

According to the Pre Publication Rules, every patent application received by the United States Patent and Trademark Office after November 29, 2000 will be pre-published at eighteen months from the effective filing date. When the application is published the contents, including the sequences, will become prior art.

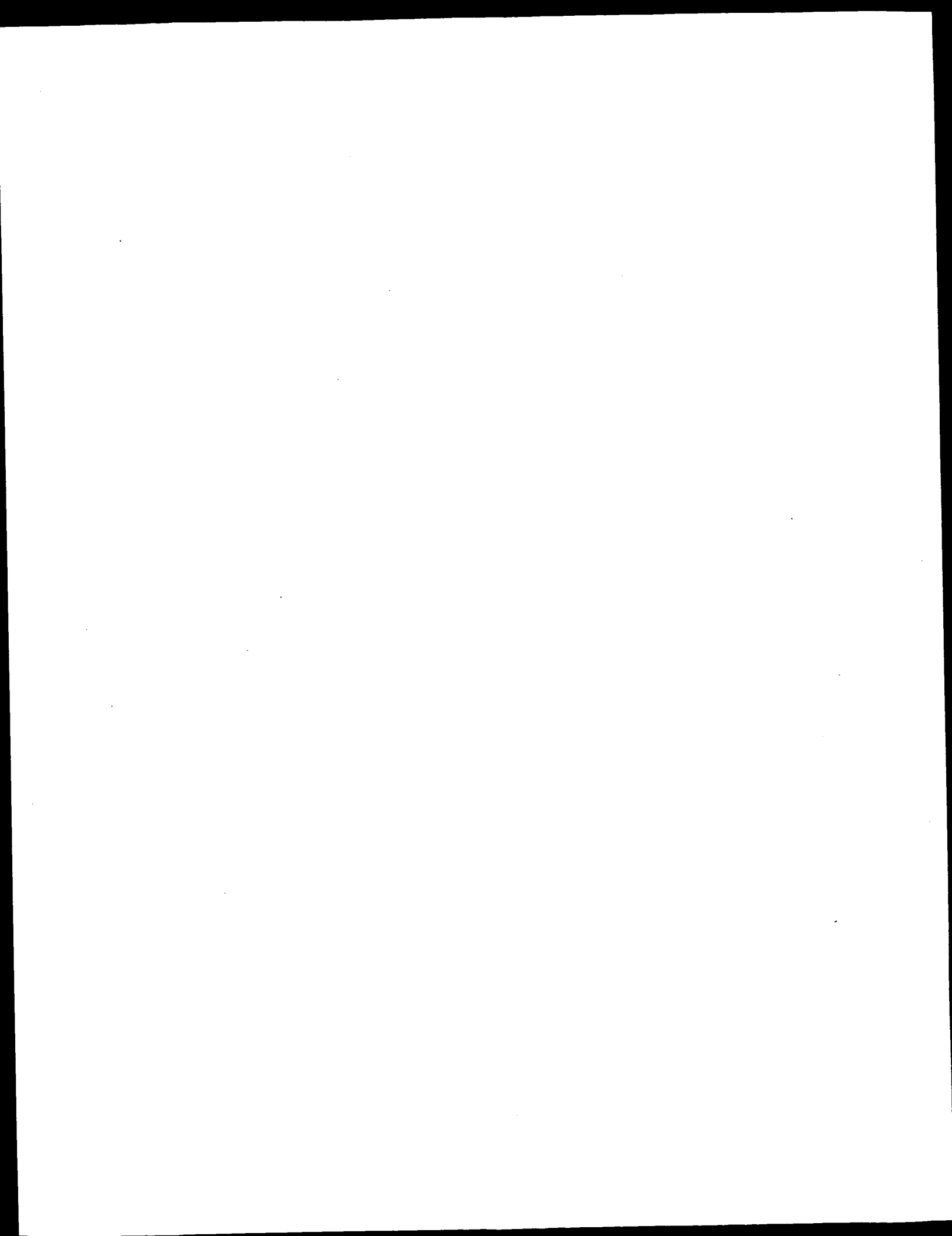
Two new databases have been created to hold the pre-published sequences:

Published_Applications_NA contains nucleic acid sequences; the search results will have the extension **.rnpb**.

Published_Applications_AA contains amino acid sequences; the search results will have the extension **.rapb**.

Each pre-published application is given a unique Publication Number. An example of a Publication Number is US20021234567A1. The "US" indicates the application was a U.S. application. The first 4 digits show the calendar year the application was published. The next 7 digits represent when the application was published. This 7-digit number starts at zero at the beginning of each calendar year. Each application published is given the next number in order. The "A" indicates a utility patent application and the "1" shows that this was the first time the application had been published. If the applicants submit changes to the application, they may request that the changed application be published again. In such instances, the "1" at the end of the number would be replaced by a "2".

Sequences in the PGPub database are public information; it is permissible to leave these results in the case.



GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 28, 2002, 02:51:13 ; Search time 47.9411 Seconds
(without alignments)
7168.683 Million cell updates/sec

Title: US-09-709-103-1

Perfect score: 846

Sequence: 1 atgaactggccgcatgat.....agcgtgcgtcatcagctag 846

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 363474 seqs, 203117208 residues

Total number of hits satisfying chosen parameters: 726948

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	405.8	48.0	3082	10	US-09-778-963A-1
2	278	32.9	405	10	US-09-960-352-10273
3	240.2	28.4	11221	10	US-09-778-963A-3
4	173.2	20.5	368	10	US-09-864-761-21643
5	99	11.7	454	10	US-09-960-352-5830
6	97	11.5	452	10	US-09-960-352-4253
7	92.6	10.9	551	10	US-09-765-298A-25
8	92.6	10.9	570	12	US-10-104-484-1
9	92.6	10.9	570	12	US-10-104-484-3
10	91	10.8	570	10	US-09-765-298A-27
11	74.6	8.8	688	9	US-09-764-868-490
12	74.6	8.8	3346	9	US-09-764-868-67
13	66.6	7.9	1119	9	US-10-067-813-1
14	64.2	7.6	2310	10	US-09-476-242-21
15	64.2	7.6	2535	10	US-09-476-242-13
16	64	7.6	1248	9	US-09-860-846-7
17	64	7.6	1248	10	US-09-861-289-7
18	64	7.6	13613	9	US-09-860-846-3
19	64	7.6	13613	10	US-09-861-289-3

20	61.4	7.3	2298	10	US-09-476-242-22	Sequence 22, Appl
21	61.4	7.3	2298	10	US-09-476-242-23	Sequence 23, Appl
22	61.4	7.3	2298	10	US-09-476-242-24	Sequence 24, Appl
23	61.4	7.3	2529	10	US-09-476-242-14	Sequence 14, Appl
24	61	7.2	2322	10	US-09-476-242-18	Sequence 18, Appl
25	61	7.2	2322	10	US-09-476-242-19	Sequence 19, Appl
26	61	7.2	2322	10	US-09-476-242-20	Sequence 20, Appl
27	61	7.2	2541	10	US-09-476-242-9	Sequence 9, Appl
28	61	7.2	2541	10	US-09-476-242-10	Sequence 10, Appl
29	61	7.2	2541	10	US-09-476-242-11	Sequence 11, Appl
30	61	7.2	2541	10	US-09-476-242-12	Sequence 12, Appl
31	59.8	7.1	309	10	US-09-783-590-4328	Sequence 26, Appl
32	59.4	7.0	2352	10	US-09-476-242-26	Sequence 3, Appl
33	59.2	7.0	1085	9	US-10-067-813-3	Sequence 7960, Ap
34	58.2	6.9	1914	10	US-09-815-242-7960	Sequence 358, Ap
35	57.4	6.8	1594	10	US-09-969-708-358	Sequence 15, Appl
36	57.4	6.8	2523	10	US-09-476-242-15	Sequence 40, Appl
37	56	6.6	612	10	US-09-972-529-3	Sequence 7866, Ap
38	56	6.6	847	10	US-09-822-849A-40	Sequence 1, Appl
39	56	6.6	1164	10	US-09-815-242-7866	Sequence 17, Appl
40	56	6.6	1224	10	US-09-972-529-1	Sequence 3, Appl
41	56	6.6	2517	10	US-09-476-242-17	Sequence 1, Appl
42	56	6.6	3192	10	US-09-788-654A-1	Sequence 3, Appl
43	55.4	6.5	2310	10	US-09-476-242-3	Sequence 4, Appl
44	55.4	6.5	2316	10	US-09-476-242-4	Sequence 8, Appl
45	55.4	6.5	2316	10	US-09-476-242-8	

ALIGNMENTS

RESULT 1

US-09-778-963A-1
; Sequence 1, Application US/09778963A
; Patent No. US20020115172A1
; GENERAL INFORMATION:
; APPLICANT: NEELAM, Beena et al
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001112
; CURRENT APPLICATION NUMBER: US/09/778,963A
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-778-963A-1

QY	13	GCATCATCAAGAAGATGCGCGAGCGACTCGGAGCTGAGTATCCCGCCCAAGAACTGC	72
Db	208	GCATCATGAAGACTTTGTCCAGCGGAACTGCACGCTCAGTGTGCGCCCAAAACTCA	267
QY	73	TATCGCATCGTCTCATCTCGGCTCGTCCAAAGTGGGCAAGAGCGCCATCGTCTCGCGTTC	132
Db	268	TACCGCATGCTGCTGCTGGTGCTCTCGGTTGGCAAGAGCTCCATCGTCTCGCTTC	327
QY	133	CTCAGCGCGCGCTTCGAGAGCGCTTACACGCTTACCATCGAGAGCTTCCACCGCAAGTTC	192
Db	328	CTCAATGGCGCGCTTTGAGGACAGGTACACACCCACCATCGAGAGCTTCCACCGTAAGTA	387
QY	193	TACTTCATCCGCGCGAGGTCTACAGCTCGACATCTCGACAGCTCCGCGCAACCCCG	252
Db	388	TACACATCCGCGCGAGGTCTACAGCTCGACATCTCGACATCTCGGTAACCTTGGCAACCCCG	447
QY	253	TTCCCGCGCATCGCGCGCGCTCTCCATCTCACAGAGAGCTTTTCATCCCTGGTTCAGT	312

Query Match 48.0%; Score 405.8; DB 10; Length 3082;
Best Local Similarity 71.4%; Pred No. 1.7e-76;
Matches 593; Conservative 0; Mismatches 202; Indels 36; Gaps 3;

	Query Match	32.9%	Score 278;	DB 10;	Length 405;	
	Best Local Similarity	89.5%;	Pred. No. 6.7e-50;			
	Matches 299; Conservative		Mismatches 35;	Indels	0;	Gaps
QY	1	ATGAAACTGGCCGGCATGCATCAAGAAGATGTGCCCGAGGACCTCGGAGCTGATGATCCCG	60			
Db	72	ATGAACAATGTGGCGATGATCAAGAAAATGTGCCCGAGGACCTCGGATGTAGGAGTCCCG	131			

	Query Match	28.4%;	Score 240.2;	DB 10;	Length 11221;
	Best Local Similarity	68.7%;	Pred. No. 7.9e-42;		
	Matches 392;	Conservative	0;	Mismatches 143;	Indels 36; Gaps 3;
QY	273	CTCCATCTCCACGAGACGCTTTTCACTCCGGGTGTTTCAGTCTGGACAACCGCACTCCTT	332		
Db	7680	CTCTCTCCTCGAGGGGATGCTTCACTCTGGTGTTCAGCTGGGATACCGGAGTCCCT	7739		
QY	333	CGAGGAGGTGACGGGGCTTCAGGCAAGCAGATCCTCGACACCAAGTCTTGCTTCAAGAACAA	392		
Db	7740	CGATGAGTCAAGCGCTTTCAGAAGCAGATCCTGGAGGTCAAGTCGTGGCTGAAGAACA	7799		
QY	393	AACCAAGAGAACGTGACGTGCCCTGGTCACTCGGGCAACAAGGGTGACC--	449	--GCCA	449
Db	7800	GACCAGGAGGGGGGAGTGCCTTCCATGGTCACTGTGGCAACAGACACCACGCCGA	7859		
QY	450	CTTCTACGCGAGGTGGACCAAGCGAGATGAGCAGCTGGTGGGCGACACCCCCAGCG	509		
Db	7860	GCTGTGCCCGCAGGTGCCACACCGAGCGCGAGCTGCTGGTTCGGGGCA--	7916	--CGAGAA	7916
QY	510	CTGCGGCTACTTCGAGATCTCGGCCAAGAAGAACAGCAGCTGGACCAAGATGTCGCGCG	569		
Db	7917	CTGCGGCTACTTCGAGGTGTGGCCCAAGAAGAACCAACGTGGACGAGATGTTCTACGT	7976		
QY	570	GCCTTTTCGCATGGCCAAAGCTGCCACGCGAGATGAGCCCAAGACTGCACCGCAAGGTCTC	629		
Db	7977	GCCTTTCAAGATGGCCAAAGCTGCCACAGAGATGAGCCCGCCCTGATCGCAAGATCTC	8036		
QY	630	GGTGAGTACTGGACGTGCTGCACAAGACAGCGCTGGGAAACAAGAGCTGCTGCGGGC	689		
Db	8037	CGTGCAGTACGGTAGCGCCTTCAACCCACAGGCC-----	8069		

Mon Dec 30 09:16:51 2002

Sequence 25, Application US/09765298A
Patent No. US20020137017A1
GENERAL INFORMATION:
APPLICANT: ARONHEIM, AMI
TITLE OF INVENTION: METHOD FOR DETECTION OF PROTEIN-PROTEIN INTERACTIONS AND A KIT TH
FILE REFERENCE: 108387.01
CURRENT APPLICATION NUMBER: US/09/765,298A
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: IL 125456
PRIOR FILING DATE: 1998-07-22
PRIOR APPLICATION NUMBER: IL 128017
PRIOR FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SEQ ID NO 25
LENGTH: 551
TYPE: DNA
ORGANISM: Homo sapiens
US-09-765-298A-25

Query Match 10.9%; Score 92.6; DB 10; Length 551;
Best Local Similarity 57.4%; Pred. No. 3.7e-11;
Matches 167; Conservative 0; Mismatches 124; Indels 0; Gaps 0;
QY 73 TATCGCATGGTCATCTCGGCTGTCCTCAAGTGGGCAAGAGCGCCATCGTGTCTCGCGTTC 132
DB 4 TATAAGCTGGTGGTGGCGCGCGGTGTGGCAAGAGTGGCTGACCATCCAGCTG 63
QY 133 CTCACCGCGCGCTTCGAGGACGCCCTACAGCGCTACCATCGAGGACTTCCACCGCAAGTTC 192
DB 64 ATCCAGAACCAATTTGTGGACCAATACGACCCCACTATAGAGAGTTCCTACCGGAAGCAG 123
QY 193 TACTCATCGCGGCGAGGTCTACGAGCTCGACATCTCGACAGTCCGCGCAACACCGC 252
DB 124 GTGGTCAATTGATGGGAGAGCGTCTGTGGACATCTCGGATACCGCGCGCAGGAGGAG 183
QY 253 TTCCCGCATCGCGCGCTCTCCATCTCTACAGGAGAGTTCACAGGAGAGCTTTTCATCTGTTCACT 312
DB 184 TACAGCGCATCGCGGACCAAGTACATGTCGACCGGGGAGGGCTTCTCTGTGTGTTC 243
QY 313 CTGGACAAACCGGACTCTCTCGAGGAGGTGTCAGCGGCTCAGGACAGCATC 363
DB 244 ATCAACAACACCAAGTCTTTTGGAGGACATCCACCATACAGGAGGAGCATC 294

RESULT 8
US-10-104-484-1
Sequence 1, Application US/10104484
Patent No. US20020150566A1
GENERAL INFORMATION:
APPLICANT: Guan, Kun-Lian
TITLE OF INVENTION: METHOD OF INHIBITING CANCEROUS CELL PROLIFERATION USING RAS MU
TITLE OF INVENTION: GDP-BOUND CONFORMATION
FILE REFERENCE: UMICH-0010
CURRENT APPLICATION NUMBER: US/10/104,484
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: 60/277,959
PRIOR FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 570
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Nucleotide sequence of the GDP-bound Ras mutant, RasN17N69.
US-10-104-484-1

Query Match 10.9%; Score 92.6; DB 12; Length 570;
Best Local Similarity 57.4%; Pred. No. 3.7e-11;
Matches 167; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

Db 131 CGCGCACTTCCTGAGCGTACCTGCCGACCATCGAAGATACCTACCGNCAGCGCTA 190
QY 196 TCCATCGCGCGGAGGTCTACAGCTGACATCTCGACAGTCCGCGCAACACCGGTTTC 255
DB 191 GCGTCGACCAACAAGGCGTCTGCATCAGGACACACCGGTCGCGGCGCTAC 250
QY 256 CCCGCCATCGCGCGCTCTCCATCTCACAGGAGACGTTTTCATCTCTGGTTCAGTCTG 315
DB 251 CGGGCCCTGACAGCGCTTGCATTTGCGAGGTACGCGCTTCATCTCTGGTTTATCTATC 310
QY 316 GACAAACCGGACTCTCTGAGGAGGTGAGCGGCTCAGGAGAGATCTCTCGACACCAAG 375
DB 311 ACCAGGAGCAAAACCTGGAGGAGTGAAGCGCTCTTTGAGTGTATCCGTCAACTCAA 370
QY 376 TCTTGCTCAAGAAACCAAGGAGACGTGG 409
DB 371 GGTAACAACCCGACANAAGTGCCCGTCACTCTGG 404

RESULT 6
US-09-960-352-4253
Sequence 4253, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 4253
LENGTH: 452
TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 18-LIB34-086-Q1-E1-E5
US-09-960-352-4253

Query Match 11.5%; Score 97; DB 10; Length 452;
Best Local Similarity 56.4%; Pred. No. 4.3e-12;
Matches 181; Conservative 0; Mismatches 140; Indels 0; Gaps 0;
QY 89 TCGGCTGCTCCAGGTGGGCAAGCGCCATCGTGTGCGCTTCTCCACCGCGCGCTTGG 148
DB 5 TCGGCTGCGCGCGGTGGGCAAGAGCGCTCTGGTGGCAAGGTGGTGGCGGCACTTCC 64
QY 149 AGGAGCGCTACACGCTACCATCGAGGACTTCCACCGCAAGTTCTACTCATCCGCGGG 208
DB 65 GTGAGCGTACTCGCGACCATCGAAGTACCTACCGCAGCGGTAGGTGAGGCCACA 124
QY 209 AGGTCTACAGTGCATCTCCAGAGTCCGCGCAACACCGTTCGCCCGCCATCGCGC 268
DB 125 AGCGGGTGCCTGCATCACCAGCACCGCGGTGCGCGCGCTACCGGGGCTGAGC 184
QY 269 GCCTCTCATCTCACAGGAGACGTTTTCATCTCTGGTTCAGTCTGTGAGCAACCGGACT 328
DB 185 GCCTTGCATCTCCAGGAGTCAAGGCTTCACTCTGTTTATTCATCACCAGGAAGCAA 244
QY 329 CCTTCGAGGAGGTGAGCGGCTCAGGAGAGATCTCTCGACACCAAGTCTGCTCAAGA 388
DB 245 CCTTGAGGAGTGAAGCGCTCTATGAGCTGATCCGCTCAACTCAAGGTAAACACCCGC 304
QY 389 ACAAAACCAAGGAGACGTGG 409
DB 305 AAAAGTGGCCCGTCACTCTGG 325

RESULT 7
US-09-765-298A-25


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QY 73 TATCGCATGGTCTATCTCGGCTCTCCCAAGGTGGCAAGACGGCCATCGTGTGCGGCTTC 132
Db 10 TATAAGCTGGTGGTGGCGCCGCGGTGTGGCAAGATGGCTGACCATCCAGCTG 69
QY 133 CTCACGGCGCGCTTCGAGGACGCCCTACAGCCTACCATCGAGGACTTCCACCGCAAGTTC 192
Db 70 ATCCAGAACCAATTTGTGACGAATACCAACCCACTATAGAGGATTCCTACCGGAAGCAG 129
QY 193 TACTCCATCCGGCGGAGGTCTACAGCTCGACATCTCTCGACAGTCCGGCAACACCCG 252
Db 130 GTGGTCATTGATGGGAGACGTGCTGTGGACATCTCTGGATACCGCGCGCAGGAGGAG 189
QY 253 TTCCCGCGCATCGCGCGCTCTCCATCTCTACAGGACGTTTTCATCTCTGGTTCAGT 312
Db 190 TACAGCGCATCGGGAACCACTATAGCAGCCGCGGAGGGCTTCCTGTGTGTGTTGCC 249
QY 313 CTGGACAACCGGAGCTCTCTCGAGGAGTGCAGCGGCTCAGGAGCAGATC 363
Db 250 ATCAACAACACCAAGTCTTTTGAGGACATCCACAGTACAGGAGCAGATC 300

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RESULT 9
US-10-104-484-3
; Sequence 3, Application US/10104484
; Patent No. US20020150566A1
; GENERAL INFORMATION:
; APPLICANT: Guan, Kun-Lian
; TITLE OF INVENTION: METHOD OF INHIBITING CANCEROUS CELL PROLIFERATION USING RAS MUTAN
; FILE REFERENCE: UNICH-0010
; CURRENT FILING DATE: 2002-03-25
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 60/277,959
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence of the wild type Ras mutant, RasN17N69.
US-10-104-484-3

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Query Match 10.9%; Score 92.6; DB 12; Length 570;
Best Local Similarity 57.4%; Pred. No. 3.7e-11;
Matches 167; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

QY 73 TATCGCATGGTCTATCTCGGCTCTCCCAAGGTGGCAAGACGGCCATCGTGTGCGGCTTC 132
Db 10 TATAAGCTGGTGGTGGCGCCGCGGTGTGGCAAGATGGCTGACCATCCAGCTG 69
QY 133 CTCACGGCGCGCTTCGAGGACGCCCTACAGCCTACCATCGAGGACTTCCACCGCAAGTTC 192
Db 70 ATCCAGAACCAATTTGTGACGAATACCAACCCACTATAGAGGATTCCTACCGGAAGCAG 129
QY 193 TACTCCATCCGGCGGAGGTCTACAGCTCGACATCTCTCGACAGTCCGGCAACACCCG 252
Db 130 GTGGTCATTGATGGGAGACGTGCTGTGGACATCTCTGGATACCGCGCGCAGGAGGAG 189
QY 253 TTCCCGCGCATCGCGCGCTCTCCATCTCTACAGGACGTTTTCATCTCTGGTTCAGT 312
Db 190 TACAGCGCATCGGGAACCACTATAGCAGCCGCGGAGGGCTTCCTGTGTGTGTTGCC 249
QY 313 CTGGACAACCGGAGCTCTCTCGAGGAGTGCAGCGGCTCAGGAGCAGATC 363
Db 250 ATCAACAACACCAAGTCTTTTGAGGACATCCACAGTACAGGAGCAGATC 300

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RESULT 10
US-09-765-298A-27
; Sequence 27, Application US/09765298A

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; Patent No. US20020137017A1
; GENERAL INFORMATION:
; APPLICANT: ARONHEIM, AMI
; TITLE OF INVENTION: METHOD FOR DETECTION PROTEIN-PROTEIN INTERACTIONS AND A KIT TH
; FILE REFERENCE: 108387.01
; CURRENT FILING DATE: 2001-01-22
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: IL 125456
; PRIOR FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-765-298A-27

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Query Match 10.8%; Score 91; DB 10; Length 570;
Best Local Similarity 57.0%; Pred. No. 7.9e-11;
Matches 166; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

QY 73 TATCGCATGGTCTATCTCGGCTCTCCCAAGGTGGCAAGACGGCCATCGTGTGCGGCTTC 132
Db 10 TATAAGCTGGTGGTGGCGCGCGGTGTGGCAAGATGGCTGACCATCCAGCTG 69
QY 133 CTCACGGCGCGCTTCGAGGACGCCCTACAGCCTACCATCGAGGACTTCCACCGCAAGTTC 192
Db 70 ATCCAGAACCAATTTGTGAGCAATACGACCCCACTATAGAGGATTCCTACCGGAAGCAG 129
QY 193 TACTCCATCCGGCGGAGGTCTACAGCTCGACATCTCTCGACAGTCCGGCAACACCCG 252
Db 130 GTGGTCATTGATGGGAGACGTGCTGTGGACATCTCTGGATACCGCGCGCAGGAGGAG 189
QY 253 TTCCCGCGCATCGCGCGCTCTCCATCTCTACAGGAGGAGTTCATCTCTGGTTCAGT 312
Db 190 TACAGCGCATCGGGAACCACTATAGCAGCCGCGGAGGGCTTCCTGTGTGTGTTGCC 249
QY 313 CTGGACAACCGGAGCTCTCTCGAGGAGTGCAGCGGCTCAGGAGCAGATC 363
Db 250 ATCAACAACACCAAGTCTTTTGAGGACATCCACAGTACAGGAGCAGATC 300

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RESULT 11
US-09-764-868-490
; Sequence 490, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION DATA REMOVED - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 490
; LENGTH: 688
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (579)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (610)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (669)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-868-490

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Mon Dec 30 09:16:51 2002

us-09-709-103-1-1.rnpb

Query Match 8.8%; Score 74.6; DB 9; Length 688;
 Best Local Similarity 55.1%; Pred. No. 2.2e-07;
 Matches 146; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 102 GGTGGGCAAGACGGCCATCGTGGCGCTTCCTACCGGGCGGCTTCGAGGACGCCCTACAC 161
 DB 223 GGTGGCAATCTGCCCTTACTGTGCAATTTGTCACTGGGACTTTTCATTGAGAAATATGA 282

QY 162 GCCTACCATCGAGACTTCACCGCAAGTTCTACTCCATCCGGGGGAGGTCTTACCAGCT 221
 DB 283 CCCCAACATGAAGATTTCTACCCCAAGAGATCGAAGTGGACTCTTCCCTCCGTGCT 342

QY 222 CGACATCTCGACAGCTCCGGCAACCCCGCTTCGCCGCGCATCGGGGCGCTCTCCATCCT 281
 DB 343 GGAATTTCTGGACACCGCAGCAACTGGAGCTTTTGCCTCCATGAGAGATCTTACATCAA 402

QY 282 CACAGGACAGCTTTTCATCTCTGGTTCAGTCTGGCAACCGGACACCTCTTCGAGGAGGT 341
 DB 403 AAACGGCCAAAGTTTCATCTCTGGTTATAGCTGGTTAATCAACAGTCTTTTCAGGATAT 462

QY 342 GCAGGGCTCAGGCGAGCATCCTC 366
 DB 463 CRAAGCAATGAGAGATCAAAATGTGTC 487

RESULT 12
 US-09-764-868-67
 ; Sequence 67, Application US/09764868
 ; Patent No. US20020168711A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PT232
 ; CURRENT APPLICATION NUMBER: US/09/764,868
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - refer to PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 1510
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 67
 ; LENGTH: 3346
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (2787)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: SITE
 ; LOCATION: (2795)
 ; OTHER INFORMATION: n equals a,t,g, or c
 US-09-764-868-67

Query Match 8.8%; Score 74.6; DB 9; Length 3346;
 Best Local Similarity 55.1%; Pred. No. 2.6e-07;
 Matches 146; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 102 GGTGGGCAAGACGGCCATCGTGGCGCTTCCTACCGGGCGGCTTCGAGGACGCCCTACAC 161
 DB 230 GGTGGCAATCTGCCCTTACTGTGCAATTTGTCACTGGGACTTTTCATTGAGAAATATGA 289

QY 162 GCCTACCATCGAGACTTCACCGCAAGTTCTACTCCATCCGGGGGAGGTCTTACCAGCT 221
 DB 290 CCCCAACATGAAGATTTCTACCCCAAGAGATCGAAGTGGACTCTTCCCTCCGTGCT 349

QY 222 CGACATCTCGACAGCTCCGGCAACCCCGCTTCGCCGCGCATCGGGGCGCTCTCCATCCT 281
 DB 350 GGAATTTCTGGACACCGCAGCAACTGGAGCTTTTGCCTCCATGAGAGATCTTACATCAA 409

QY 282 CACAGGACAGCTTTTCATCTCTGGTTCAGTCTGGCAACCGGACACCTCTTCGAGGAGGT 341
 DB 410 AAACGGCCAAAGTTTCATCTCTGGTTATAGCTGGTTAATCAACAGTCTTTTCAGGATAT 469

QY 342 GCAGGGCTCAGGCGAGCATCCTC 366

DB 470 CRAAGCAATGAGAGATCAAAATGTGTC 494

RESULT 13
 US-10-067-813-1
 ; Sequence 1, Application US/10067813
 ; Patent No. US20020156013A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Renauld, Jean-Christophe
 ; APPLICANT: Louahed, Jamila
 ; APPLICANT: Grasso, Luigi
 ; APPLICANT: Levitt, Roy
 ; APPLICANT: Nicolaides, Nicholas
 ; TITLE OF INVENTION: Asthma Associated Factors as Targets for Treating
 ; TITLE OF INVENTION: Atopic Allergies and Related Disorders
 ; FILE REFERENCE: 036870-5071
 ; CURRENT APPLICATION NUMBER: US/10/067,813
 ; CURRENT FILING DATE: 2002-02-08
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/157,247
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-18
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 1119
 ; TYPE: DNA
 ; ORGANISM: Murinae gen. sp.
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (19)...(642)
 US-10-067-813-1

Query Match 7.9%; Score 66.6; DB 9; Length 1119;
 Best Local Similarity 52.7%; Pred. No. 1.1e-05;
 Matches 144; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

QY 103 GTGGGCAAGACGGCCATCGTGGCGCTTCCTACCGGGCGGCTTCGAGGACGCCCTACACG 162
 DB 88 GTGGGCAAGAGTGGCTCACTATTTCAGTTTTCAGAAAGATCTTTGTGCTGACTACGAC 147

QY 163 CTTACCATCGAGACTTCCACCGCAAGTTCTACTCCATCCCGGGGAGGTCTACACAGCTC 222
 DB 148 CCCACCATGAAGACTCTTACCTGAAGCATACAGAGATTGACATCATGTGGCCATCTTG 207

QY 223 GACATCTCGACAGCTCCGGCAACACCGCTTCCCGGCGCATCGCGGCTCTCCATCCTC 282
 DB 208 GATGTTCTGGACACACCGCGGCGAGGAGTTCACTGTCATCGGGAACAATACATGCGC 267

QY 283 ACAGGAGACGTTTTTCATCTCTGGTGTTCAGTCTGGACACCGGACTCTCTCGAGGAGTG 342
 DB 268 ACAGGGGATGGCTTCTCTCATTTGTCTACTCCGTCACCGCAAGGCCAGCTTCGAGCACGTG 327

QY 343 CAGGGGCTCAGGCGAGATCCTTCGACACCAAG 375
 DB 328 GACCGCTTCCACCGACTCATCTTCGCTGTCAAG 360

RESULT 14
 US-09-476-242-21
 ; Sequence 21, Application US/09476242
 ; Patent No. US20020146683A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BARNETT, Susan
 ; APPLICANT: HARTOG, Karin
 ; APPLICANT: MARTIN, Eric
 ; TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES
 ; FILE REFERENCE: 1605.002
 ; CURRENT APPLICATION NUMBER: US/09/476,242
 ; CURRENT FILING DATE: 1999-12-30
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 21
 ; LENGTH: 2310
 ; TYPE: DNA

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 30, 2002, 16:35:36 ; Search time 357 Seconds
(without alignment)
2094.295 Million cell updates/sec

Title: US-09-709-103-3f1

Perfect score: 1731

Sequence: 1 GIPGAGAPSPRAQPEQSP.....IREKASAGQAKDKRCVIS 332

Scoring table:

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Ygapop 10.0			0.5
Fgapop 6.0			7.0
Delop 6.0			7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-NO_XUPXY -NO_WMAP -LARGQUERY -NEG SCORES=0 -WAIT -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1731	100.0	1801	21	AAZ36893	cDNA encoding an a
2	1714	99.0	1740	21	AAZ36914	DNA encoding an ac
3	1713	99.0	1841	20	AAZ23022	Human kd312 polype
4	1692	97.7	1776	21	AAA49177	cDNA encoding huma
5	1651	95.4	3986	20	AAZ23023	Human kd312 genomi
6	1449	83.7	846	21	AAZ36892	cDNA encoding an a
7	1435.5	82.9	1689	20	AAZ23024	Rat kd312 polypept
8	1388.5	80.2	3079	20	AAZ23025	Rat kd312 genomic
9	930.5	53.8	3427	24	ABK71563	Human ditthp polynu
10	929.5	53.7	2973	24	ABL92087	Human Tumour Endot
11	898	51.9	837	21	AAZ36913	DNA encoding a hom
12	898	51.9	2832	24	ABL92076	Human Tumour Endot
13	867	50.1	3020	24	ABL92134	Mouse Tumour Endot
14	717	41.4	951	23	AAZ36914	DNA encoding novel
15	630.5	36.4	1305	23	ABL07789	Drosophila melanog
16	494	28.5	624	24	ABQ28318	Oligonucleotide fo
17	494	28.5	624	24	ABQ28319	Oligonucleotide fo
18	459	26.5	624	24	ABQ28320	Oligonucleotide fo
19	459	26.5	624	24	ABQ28321	Oligonucleotide fo
20	376	21.7	368	22	ABA51382	Human breast cell
21	376	21.7	368	22	ABA51382	Human breast cell
22	376	21.7	368	22	ABA69388	Human foetal liver
23	376	21.7	368	22	ABA63233	Probe #14789 for g
24	376	21.7	368	22	AAK17661	Human brain expres
25	376	21.7	368	22	AAK43477	Human bone marrow
26	376	21.7	368	22	AAI24259	Probe #14192 for g
27	376	21.7	368	22	AAI49541	Probe #18227 used
28	376	21.7	368	22	AAI09818	Probe #9809 used t
29	359.5	20.8	4543	23	ABS17600	Human genome-deriv
30	354.5	20.5	1087	22	ABL07788	Drosophila melanog
31	354.5	20.5	1108	22	AAI60838	Human polynucleoti
32	354.5	20.5	1108	22	AAI59052	Human polynucleoti
33	343	19.8	4167	24	AD37605	Human intracellular
34	330.5	19.1	2340	22	AAH33981	Human colon cancer
35	329.5	19.0	960	23	ABL22541	Drosophila melanog
36	319.5	18.5	4933	22	ABQ72648	Human MDTT encodin
37	319.5	18.5	4933	22	AAK81235	Human immune/haema
38	317.5	18.3	2238	22	AAH41603	Human immune/haema
39	317.5	18.3	2238	24	ABL50190	Human Rap1A, RaIGD
40	317.5	18.3	2238	24	ABL50222	Human Rap1A, RaIGD
41	313	18.1	2205	24	ABL50199	Human Rap1A, C-Raf
42	313	18.1	2205	24	ABL50231	Human Rap1A, C-Raf
43	313	18.1	2277	24	ABL50202	Human Rap1A, C-Raf
44	313	18.1	2277	24	ABL50234	Human Rap1A, C-Raf
45	312.5	18.1	3346	22	AAZ27032	cDNA encoding nove

ALIGNMENTS

RESULT 1
AAZ36893
ID AAZ36893 standard; cDNA; 1801 BP.
XX
XX AAZ36893;
AC
XX
XX
DT 13-MAR-2000 (first entry)
DE
DE cDNA encoding an activator of G protein signalling (AGS) protein.
KW Activator of G protein signalling; AGS; ras-related G protein;
KW GTP hydrolysis; G protein activity; pheromone response pathway;
KW G protein-coupled signal transduction; G-gamma selectivity;
KW cellular signal transduction; ss.
XX
OS Homo sapiens.
XX
XX
FH Location/Qualifiers

FT 5'UTR 7..153
 FT /*tag= a
 FT CDS 154..999
 FT /tag= b
 FT /product= "activator of G protein signalling (AGS)
 protein"
 FT 3'UTR 1000..1801
 FT /tag= c
 PN MO958670-A1.
 XX 18-NOV-1999.
 PD 07-MAY-1999; 99MO-US10151.
 XX 08-MAY-1998; 98US-0084842.
 PR 07-OCT-1998; 98US-0103355.
 XX (CADU-) CADUS PHARM CORP.
 PA Cismowski M, Duzic E;
 PI WPI: 2000-072337/06.
 DR P-PSDB; AAY53921.
 XX A new activator of G protein signalling used to treat disorders
 PT characterized by an aberrant AGS protein activity -
 PS Claim 3; Page 133-135; 162pp; English.
 CC The present sequence encodes an activator of G protein signalling (AGS)
 CC protein. The cDNA sequence was isolated from a human liver cDNA
 CC library. The AGS protein exhibits homology to ras-related G proteins,
 CC and contains alterations in conserved amino acids consistent with a
 CC deficiency in GTP hydrolysis activity. AGS stimulates G protein
 CC activity, G protein-coupled signal transduction and the pheromone
 CC response pathway in a receptor-independent manner. The AGS protein
 CC also shows G-gamma selectivity, as measured by growth assays in
 CC yeast expressing various mammalian G-gamma constructs, and
 CC tissue-specific expression, as measured by Northern blot analysis.
 CC The AGS protein can be used to screen for compounds that modulate
 CC cellular signal transduction. The protein is used to treat disorders
 CC characterized by an aberrant AGS protein activity or AGS nucleic acid
 CC expression.
 XX
 SQ Sequence 1801 BP; 437 A; 561 C; 500 G; 303 T; 0 other;
 Alignment Scores:
 Pred. No.: 4,44e-125 Length: 1801
 Score: 1731.00 Matches: 332
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0
 US-09-709-103-3f1 (1-332) x AA236893 (1-1801)
 QY 1 GYIILPProserGlylaGlylaProserProserArgAlaGlnProGlnSerPro 20
 DB 1 GGAAITTCGAGCGGAGCCGAGCCCAAGCCGAGCGGCCCGCCGAGGAGAGCCCT 60
 QY 21 ProAlaAlaHisProAlaCysHisProSerAspProGlnProLeuSerAlaLeuSer 40
 DB 61 CCAAGCGGCTCAACCCGCGTCCACCCAGCGACCTCAGCGGCTCTCTGCTCTCG 120
 QY 41 AlaProArgProProSerArgProLeuCysProMetIleuAlaMetIleuLys 60
 DB 121 GCCCGCGCGCCGCTCTGCGGCTCTGCGCAATGAACTGGCCCGGAGAGCAAGAG 180
 QY 61 MetCysProSerAspSerGlnLeuSerIleProAlaLysAsnGlyTyrArgMetValIle 80
 DB 181 ATGTGCCGAGCACTCGAGCTGAGTATCCGCGCAAGAACTGATCCGATGTCATC 240

QY 81 LeuGlySerSerIysValGlyLeuThrAlaIleValSerArgPheLeuThrGlyArgPhe 100
 DB 241 CTCGGCTGCTCCAGAGTGGGCAAGCCGCAATGCTGCGCTTCTCACGGGCGGCTTC 300
 QY 101 GluAspAlaTyrThrProThrIleGluAspPheHisArgLysPheTyrSerIleArgGly 120
 DB 301 GAGAGCGGCTTACACGCCCTTACCATCGAGACTTCCACCGCAAGTTCTCATCTCATCGGGC 360
 QY 121 GluValIlyrGlnLeuAspIleLeuAspThrSerGlyAsnHisProPheProAlaMetArg 140
 DB 361 GAGGTCTACAGACTCGACATCTCGACACGTCGCGCAACCCCGCTTCCCGCATCGG 420
 QY 141 ArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSerLeuAspAsnArgAsp 160
 DB 421 CGCCTCTCATCTCCACAGAGACGTTTCACTCTGTTGTTCACTTGGACACACCGGAC 480
 QY 161 SerPheGluGluValGlnArgLeuArgGlnIleLeuAspThrIlySerCysLeuLys 180
 DB 481 TCCTTCAGAGAGGTGTCAGGGGCTCAGCGACAGATCTCGACACCAAGTCTGCTCAG 540
 QY 181 AsnLysThrLysGluAsnValAspValProLeuValIleCysGlyAsnLysGlyAspArg 200
 DB 541 AACAAACCAAGAGAGAACCTGAGCGTCCCTCGTCACTTGGCGCAAGAGGTGACCCG 600
 QY 201 AspPheTyrArgGluValAspGlnArgGlnIleGlnLeuValGlyAspAspProGln 220
 DB 601 GACTTTCACGAGGTGACCAAGCGGACGATCGAGCTGTGTGGCGAGACCCCGAG 660
 QY 221 ArgCysAlaTyrPheGlnIleSerAlaLysLysAsnSerSerLeuAspGlnMetPheArg 240
 DB 661 CGCTGCGCTACTTCAGATCTCGGCAAGAAACAGCAGCTGACAGATGTTCCGC 720
 QY 241 AlaLeuPheAlaMetAlaLysLeuProSerGlnMetSerProAspLeuHisArgLysVal 260
 DB 721 GCCTCTTCCGCTGAGCTGCAAGCTGCCACGAGATGAGCCAGACTGACACCGCAAGGTC 780
 QY 261 SerValGlnTyrCysAspValLeuHisLysLysAlaLeuArgAsnLysLeuLeuArg 280
 DB 781 TCGGTGACGACTCGACAGTGTGTCGCAAGAGGCGCTCGGAAACAAGCTGTGCGG 840
 QY 281 AlaGlySerGlyGlyGlyGlyAspProGlyAspAlaPheGlyIleValAlaProPhe 300
 DB 841 GCGGCGAGCGCGCGCGCGCGCGGACCGCGGAGAGCTTTGGCAATCGTGGACCCCTTC 900
 QY 301 AlaArgProSerValHisSerAspLeuMetTyrIleArgGlnLysAlaSerAlaGly 320
 DB 901 GCGGCGCGCGCGCGCTTACACGACGACCTCATCTATCATCCGCAAGAGCGCGCGG 960
 QY 321 SerGlnAlaLysAspLysGlnArgCysValIleSer 332
 DB 961 AGCCAGGCCAAGAGCAAGAGAGCGCTGCTCATCAGC 996
 RESULT 2
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 ID AA236914 standard; DNA; 1740 BP.
 XX
 AC AA236914;
 XX
 DT 13-MAR-2000 (first entry)
 XX
 DE DNA encoding an activator of G protein signalling (AGS) protein.
 XX
 KW Activator of G protein signalling; AGS; ras-related G protein;
 KW GTP hydrolysis; G protein activity; pheromone response pathway;
 KW G protein-coupled signal transduction; G-gamma selectivity;
 KW cellular signal transduction; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 145..991
 FT /*tag= a
 FT /product= "activator of G protein signalling (AGS)"

FT

protein"

XX PN WO9958670-A1.

XX PD 18-NOV-1999.

XX PF 07-MAY-1999; 99WO-US10151.

XX XX 08-MAY-1998; 98US-0084842.

PR 07-OCT-1998; 98US-0103355.

XX XX (CADU-) CADUS PHARM CORP.

XX PA Cismowski M, Duzic E;

XX PI WPI; 2000-072337/06.

XX DR P-PSDB; AAY53924.

XX XX A new activator of G protein signalling used to treat disorders

PT characterized by an aberrant AGS protein activity -

PT character

PS Disclosure; Page 146-148; 162pp; English.

XX CC The present sequence encodes an activator of G protein signalling (AGS)

CC protein. The cDNA sequence was isolated from a human liver cDNA

CC library. The AGS protein exhibits homology to ras-related G proteins,

CC and contains alterations in conserved amino acids consistent with a

CC deficiency in GTP hydrolysis activity. AGS stimulates G protein

CC activity, G protein-coupled signal transduction and the pheromone

CC response pathway in a receptor-independent manner. The AGS protein

CC also shows G-gamma selectivity, as measured by growth assays in

CC yeast expressing various mammalian G-gamma constructs, and

CC tissue-specific expression, as measured by Northern blot analysis.

CC The AGS protein can be used to screen for compounds that modulate

CC cellular signal transduction. The protein is used to treat disorders

CC characterized by an aberrant AGS protein activity or AGS nucleic acid

CC expression.

XX XX

SQ Sequence 1740 BP; 422 A; 546 C; 483 G; 289 T; 0 other;

XX XX

XX XX

XX XX

XX XX

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QY 124 GlnLeuAspIleLeuAspThrSerGlyAsnHisProPheProAlaMetArgArgLeuSer 143

Db 362 CAGCTCGACATCTCGACACAGTCCGGCAACACCCGTTCCCGCCATGCGCGCTCTCC 421

QY 144 IleLeuThrGlyAspValPheIleLeuValPheSerLeuAspAsnArgAspSerPheGlu 163

Db 422 ATCTCTCACAGGAGAGCTTTTTCATCTCTGGTGTTCAGTCTGGACACACCGGACTCTCTTCGAG 481

QY 164 GluValGlnArgLeuArgGlnGlnIleLeuAspThrLysSerCysLeuLysAsnLysThr 183

Db 482 GAGGTGCGAGCGCTCAGCGACAGATCTCTGACACCAAGTCTTGGCTCAAGAAACAAAC 541

QY 184 LysGluAsnValAspValProLeuValIleCysGlyAsnLysGlyAspArgAspPheTyr 203

Db 542 AAGGAGAACGTGGACGTGCCCTCTGTCTCATCTCGGCAACCAAGGTGACCGGACTTCTAC 601

QY 204 ArgGluValAspGlnArgGluGlnLeuValGlyAspAspProGlnArgCysAla 223

Db 602 CGCAGGTGGACCGACGCGAGATCGAGCAGCTGTGGGCGACGACCCCGAGCGCTCGCC 661

QY 224 TyrPheGluIleSerAlaLysLysAsnSerSerLeuAspGlnMetPheArgAlaLeuPhe 243

Db 662 TACTTCGAGATCTCGGCAAGAGACAGCAGCTGTGACAGATGTTCGCGCGCTCTTC 721

QY 244 AlaMetAlaLysLeuProSerGluMetSerProAspLeuHisArgLysValSerValGln 263

Db 722 GCCATGCCCAAGTGTCCAGCAGATGAGCCAGACTGCACCGCAAGGTCTCGGTGCGAG 781

QY 264 TyrCysAspValLeuHisLysLysAlaLeuArgAsnLysLysLeuLeuArgAlaGlySer 283

Db 782 TACTTCGACGTGTGCAAGAGGCGTCCGGAACAAGAGCTGTGCGGCGCGCGAGC 841

QY 284 GlyGlyGlyGlyGlyAspProGlyAspAlaPheGlyValAlaProPheAlaArg 303

Db 842 GCG 901

QY 304 ProSerValHisSerAspLeuMetTyrIleArgGluLysAlaSerAlaGlySerGlnAla 323

Db 902 CCCAGCGTACACAGCGACCTCATGTACATCCGCGAAGAGCGCGCGCGCGCGCGCG 961

QY 324 LysAspLysGluArgCysValIleSer 332

Db 962 AAGGACAAGGCGCTGCGTCATCAGC 988

RESULT 3

AAZ23022

ID AAZ23022 standard; cDNA; 1841 BP.

XX AC AAZ23022;

XX XX AAZ23022;

DT 17-JAN-2000 (first entry)

XX XX Human kd312 polypeptide encoding cDNA.

DE kd312 polypeptide; cancer; immunodeficiency disorder; AIDS; stroke;

XX heart attack; head trauma; neurodegenerative disease; human;

KW Parkinson's disease; Alzheimer's disease; ss.

XX OS Homo sapiens.

XX XX WO9950288-A2.

PN 07-OCT-1999.

XX PD 30-MAR-1999; 99WO-US06993.

PF 31-MAR-1998; 98US-0053374.

PR (AMGE-) AMGEN INC.

XX PA Yen K;

XX PI

XX XX

Alignment Scores:

Pred. No.: 8,87e-124 Length: 1740
 Score: 1714.00 Matches: 329
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.02% Indels: 0
 DB: 21 Gaps: 0

US-09-709-103-3F1 (1-332) x AAZ36914 (1-1740)

QY 4 SerGlyAlaGlyAlaProSerProSerArgAlaGlnProGluGlnSerProProAlaAla 23

Db 2 AGCGGCGCGAGCCCGACAGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 61

QY 24 HisProAlaCysHisProSerAspProGlnProLeuSerAlaLeuLeuSerAlaProArg 43

Db 62 CACCCGCGGTGCCACCGAGCGCTCAGCGCTCTCTGCGCTTCTCTGCGCCCGCGCGC 121

QY 44 ProProSerArgProLeuCysProMetLysLeuAlaAlaMetIleLysLysMetCysPro 63

Db 122 CCGCCCTCGCGCGCCCTCTGCGCCAACTGAACCTGGCGCGCGATCAAGAGATGTGCCG 181

QY 64 SerAspSerGluLeuSerIleProAlaLysAsnCysTyrArgMetValIleLeuGlySer 83

Db 182 AGCGACTCGAGCTGAGTATCCCGCCAGAACTGCTATCGATGGTTCATCTCGCGCTCG 241

QY 84 SerLysValGlyLysThrAlaIleValSerArgPheLeuThrGlyArgPheGluAspAla 103

Db 242 TCAGAGTGGGCAAGACGCGCCATCGTGTGCGCTTCTCACCAGCGCGCTTCGAGAGCGCC 301

QY 104 TyrThrProThrIleLeuAspPheHisArgLysPheTyrSerIleArgGlyGluValTyr 123

Db 302 TACAGCGCTACCATCGAGACTTCCACCGCAAGTTCTACTCCATCCGCGCGAGGTCTAC 361

DR MPI: 1999-601322/51.
 DR P-PSDB; AAY42693.
 XX kd312 polypeptides useful for treating diseases and disorders
 PT associated with alterations in cell proliferation and cell death
 XX
 XX Claim 1; Fig 8; 85pp; English.
 CC The invention provides nucleic acid molecules encoding human and rat
 CC kd312 polypeptides. The kd312 polypeptides can be expressed by standard
 CC recombinant methodology. The kd312 sequences, and the antibodies against
 CC the proteins may be used to treat or diagnose the presence or progression
 CC of various diseases, e.g., cancer, immunodeficiency disorders (e.g., AIDS),
 CC stroke, heart attack, head trauma, and neurodegenerative diseases (e.g.,
 CC Parkinson's disease and Alzheimer's disease). The present sequence
 CC represents the human kd312 cDNA sequence.
 XX
 XX Sequence 1841 BP; 398 A; 605 C; 530 G; 308 T; 0 other;
 SQ
 Alignment Scores:
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 Score: 1713.00 Matches: 329
 Percent Similarity: 99.70% Conservative: 0
 Best Local Similarity: 99.70% Mismatches: 1
 Query Match: 98.96% Indels: 0
 Gaps: 0
 DB:
 US-09-709-103-3f1 (1-332) x AA223022 (1-1841)
 QY 3 ProsergiyalaialaProserProserArghlaInProgluInserProProa1a 22
 Db CCGAGCGAAGCGCGAGCCCGCAAGCCCGCGCGCGCGAGAGCGAGAGCCCTCCAGCC 167
 QY 23 AlaHisProAlaCyHisProSerArspProgluInProleuSerAlaLeuSerAlaPro 42
 Db GGTCAACCCCGCGCTGCCACCCAGCGACCTTCCGCTTCCCTTCCGCGCCCG 227
 QY 43 ArgProProSerArspProleuCyProMetLysLeuAlaMetLysLysMetCys 62
 Db CCGCCGCGCTCCGCGCGCTTCCGCGCAATGAACCTGCGCGAGATGATCAAGAAATGTGC 287
 QY 228 CCGCCGCGCTCCGCGCGCTTCCGCGCAATGAACCTGCGCGAGATGATCAAGAAATGTGC 287
 QY 63 ProSerArspSerGluleuSerLleProAlaLysanCytyrArgMetValLleuGly 82
 Db CCGAGCGACTCGAGCTGATGCCGCGCAAGAACTGATGCGATGATGATCTCGGC 347
 QY 83 SerSerLysValGlyLysThrAlaLleValSerArgPheLeuThrGlyArgPheGluasp 102
 Db TCGTCCAGGTGGGCAAGCGGCCATCGTGGCGCTTCCACCGCGCTTCCAGAGAC 407
 QY 103 AlaTyThrProThrLleGluaspPheHisArgLysPheTySerLleArgGlyGluVal 122
 Db GCCTACACGCTTACATCGAGACTTCCACCGCAAGTTCTTACTCTCATCCGCGCGAGGTC 467
 QY 123 TyrGlnLeuaspLleLeuaspThrSerGlyVasnhisProPheProAlaMetArgThrLeu 142
 Db TACCAGCTCCACATCTCGACAGCTCCGCGACACCCCTTCCCGCATGGGCGCTTC 527
 QY 468 TACCAGCTCCACATCTCGACAGCTCCGCGACACCCCTTCCCGCATGGGCGCTTC 527
 QY 143 SerLleLeuThrGlyaspValPheLleLeuValPheSerLeuaspAspAspSerPhe 162
 Db TCCATCTCCACAGAGAGCGTTTTCATCTGTGTCTGATCTGAGACACCGCACTCTTC 587
 QY 163 GluGluValGlnArgLeuArgGlnGlnLleLeuaspThrLysSerCysLeuLysAsnLys 182
 Db GAGAGGTGCGAGCGCTCCAGCGACAGATCTCGACACCAAGTCTTCCCTCAAGAAACAA 647
 QY 183 ThrArgLysLeuValaspValProLeuValLleCysGlyAsnLysGlyAspArgPhe 202
 Db ACCAAGAGAAAGTGAAGTCCCTGTCTATCTGGGCAACAAAGGTGACCGCGACTTC 707
 QY 203 TyrArgLysValaspGlnArgGlnLleGlnGlnLeuValGlyaspAspProgluInArgCys 222
 Db TACCGGAGGTGAGACAGCGCGAGATCGAGAGCTGTGTGGGCAACACCCCGCGCTGC 767

QY 223 AlaTyPheGluLleSerAlaLysLysSerSerLleuaspGlnMetPheArgAlaLeu 242
 Db GCCTACTTCAGATCTCGCGCCAGAGAACGAGCGCTTGACACAGATGTCCCGCGCTC 827
 QY 243 PheAlaMetAlaLysLeuProSerGluMetSerProAspPheHisArgLysValSerVal 262
 Db TTGGCCATGGCCCAAGCTTCCAGCGAGATGAGCCCAAGCTTCCAGCGAGATGAGCTG 887
 QY 263 GlnTyCysAspValLleuHisLysAlaLeuArgAsnLysLysLeuLeuArgAlaGly 282
 Db CAGTATCTGAGCTGTGACACAGAGCGCTGCGGAACAGAGCTGTGCGGCGGCG 947
 QY 283 SerGlyGlyGlyGlyGlyAspProGlyAspAlaPheGlyLleValAlaProPheAlaArg 302
 Db AGCGGCGCGCGCGCGCGCGAGCCGCGGCAAGCTTGGCATCTGTGCGACCTTGGCGCG 1007
 QY 303 ArgProSerValHisSerAspPheMetTyrlleArgGlnLysAlaSerAlaGlySerGln 322
 Db 1008 CCGCGCCAGCTTACAGAGCGACCTCATGTATCCGCGAAGAGCGCGCGCGAGCCAG 1067
 QY 323 AlaLysAspLysGluArgCysValLleSer 332
 Db 1068 GCCAAGAGACAAAGAGCGCTGCTCATCAGC 1097
 RESULT 4
 AAA49177
 ID AAA49177 standard; cDNA; 1776 BP.
 AC AAA49177;
 XX
 XX 03-NOV-2000 (first entry)
 DE
 DE cDNA encoding human GTPase associated protein-7.
 XX
 XX Guanine nucleotide binding protein; GTP-binding protein; G-protein;
 KW GTPase; GTPase associated protein; GTPAP; cell proliferation;
 KW autoimmune; inflammatory; immune system disorder; cancer; AIDS;
 KW acquired immune deficiency syndrome; asthma; atherosclerosis;
 KW arthritis; systemic lupus erythematosus; psoriasis; human; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 180..1025
 FT /*tag= a
 FT /product= GTPAP7
 FT
 WO200031263-A2.
 XX
 PD 02-JUN-2000.
 XX
 PD 23-NOV-1999; 99WO-US28013.
 PF
 XX 23-NOV-1998; 98US-0109592.
 PR 04-FEB-1999; 98US-0118610.
 PR 06-APR-1999; 99US-0127990.
 XX
 PA (INCY-) INCYTE PHARM INC.
 PI Hillman JL, Tang YT, Bandman O, Lal P, Yue H, Lu DM, Baughn MR;
 PI Yang J, Azimzai Y;
 DR MPI: 2000-400073/34.
 DR P-PSDB; AAY9655.
 XX
 XX Human GTPase associated proteins, polynucleotides, and antibodies,
 PT useful for diagnosing, preventing and treating various diseases such as
 PT atherosclerosis, cancer, acquired immune deficiency syndrome (AIDS),
 PT asthma, and autoimmune diseases -
 XX
 PS Claim 9; Page 125-126; 144pp; English.
 XX Human cDNA libraries from various tissues were screened for GTPase

CC associated proteins (GTPAP). The present sequence is cDNA encoding
 CC human GTPAP-7. This sequence was derived from a cDNA library of the
 CC brain tumour tissue from the parietal lobe of a female.
 CC This protein is expressed in reproductive, nervous and
 CC gastrointestinal tissue. The GTPAP proteins may be used to define
 CC agonists and antagonists of GTPAP activity and to generate antibodies
 CC to GTPAP. This means the GTPAP proteins may be useful for treatment or
 CC prevention of diseases associated with GTPAP such as cell proliferation
 CC disorders, autoimmune disorders, inflammatory disorders, immune system
 CC disorders, cancer, AIDS, asthma, atherosclerosis, arthritis, systemic
 CC lupus erythematosus and psoriasis.
 XX

SQ Sequence 1776 BP; 430 A; 565 C; 490 G; 291 T; 0 other;

Alignment Scores:

Pred. No.: 4.63e-122 Length: 1776
 Score: 1692.00 Matches: 326
 Percent Similarity: 98.79% Conservative: 0
 Best Local Similarity: 98.79% Mismatches: 4
 Query Match: 97.75% Indels: 0
 DB: 21 Gaps: 0

US-09-709-103-3F1 (1-332) x AAA49177 (1-1776)

QY 3 ProSerGlyAlaGlyAlaProSerProSerArgAlaGlnProGluGlnSerProProAla 22
 Db 33 CGAGCGAACCAGCGAGCCAGCCAGCCGCGCCGAGCCGAGCCGCTCCAGCC 92
 QY 23 AlaHisProAlaCysHisProSerAspProGlnProLeuSerAlaLeuSerAlaPro 42
 Db 93 GCTCACCCCGGTGCCACCCAGCCGCTCAGCCGCTCTGCGCTCTCTCTGCGCCCGC 152
 QY 43 ArgProProSerArgProLeuCysProMetLysLeuAlaAlaMetLysLysMetCys 62
 Db 153 GCGCCGCTCTGCGGCCCTCTCCCAATGAAACTGGCCGCGATCATCAAGAGATGTC 212
 QY 63 ProSerAspSerGluLeuSerLysProAlaLysAsnCysTyrArgMetValLysGly 82
 Db 213 CCGAGCGACTCGGAGCTGAGTATCCGCGCCAGAACTGCTATCGCATGCTCCTCGGC 272
 QY 83 SerSerLysValGlyLysThrAlaValSerArgPheLeuThrGlyArgPheGluAsp 102
 Db 273 TCGTCCAGGTGGCAAGACGGCCATCGTGTGCGCTTCTCCTCAGCGCGCTTCGAGGAC 332
 QY 103 AlaTyrThrProThrIleGluAspPheHisArgLysPheTyrSerLysArgGlyGluVal 122
 Db 333 GCCTACACGCTACCATCGAGACTTCCACGCGAAGTTCTACTCCATCCGCGCGAGGTC 392
 QY 123 TyrGlnLeuAspIleLeuAspThrSerGlyAsnHisProPheProAlaMetArgArgLeu 142
 Db 393 TACCAGCTCGACATCTCGACAGCTCGCGCAACCCAGCCGTTCCCGCCATGCGTCCCTC 452
 QY 143 SerIleLeuThrGlyAspValPheIleLeuValPheSerLeuAspAsnArgAspPhe 162
 Db 453 TCCATCTTCACAGGAGAGCTTTTCATCTGCTGTTAGTCTGGACAAACCGGACTCTTC 512
 QY 163 GluGluValGlnArgLeuArgGlnGlnIleLeuAspThrLysSerCysLeuLysAsnLys 182
 Db 513 GAGGAGGTGCGAGCGCTCAGCAGCAGATCTCGACACCAAGCTTTCCTCAAGAACAA 572
 QY 183 ThrLysGluAsnValAspValProLeuValLysCysGlyAsnLysGlyAspArgAspPhe 202
 Db 573 ACCAAGGAGAACGTGGACGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 632
 QY 203 TyrArgGluValAspGlnArgGluIleGluGlnLeuValGlyAspAspProGlnArgCys 222
 Db 633 TACCAGGAGGTGGACAGCGAGATCGAGCAGCTGTTGGCGAGACCCCGAGCGCTGC 692
 QY 223 AlaTyrPheGluIleSerAlaLysLysAsnSerSerLeuAspGlnMetPheArgAlaLeu 242
 Db 693 GCCTACTTCGAGATCTCGGCCAAGAGAACAGCGCTGACAGATGTTCCGCGCGCTC 752
 QY 243 PheAlaMetAlaLysLeuProSerGluMetSerProAspLeuHisArgLysValSerVal 262

Db 753 TTGCCATGTCAGAGCTGCCAGCAGATGAGCCAGACCTGCACCGAAGTCTCGGTG 812
 QY 263 GlnTyrCysAspValLeuHisLysLysAlaLeuArgAsnLysLysLeuLeuArgAlaGly 282
 Db 813 CAGTACTTCCGACGCTGTCACAAAGAGCGCTGCCGAACAAGAGCTGCTCGCGGCGGC 872
 QY 283 SerGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 302
 Db 873 AGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 932
 QY 303 ArgProSerValHisSerAspLeuMetTyrIleArgGluLysAlaSerAlaGlySerGln 322
 Db 933 CGGCCAGCGGTACACAGCGACCTCATGTATCCGAGAGAGCCAGCGCGCGGAGCCAG 992
 QY 323 AlaLysAspLysGluArgCysValLysSer 332
 Db 993 GCCAAGGACAGGAGCGCTGCGTCATCAGC 1022

RESULT 5

AAZ23023

ID AAZ23023 standard; DNA; 3986 BP.

XX AC AAZ23023;

XX DT 17-JAN-2000 (first entry)

XX DE Human kd312 genomic DNA sequence.

XX KW kd312 polypeptide; cancer; immunodeficiency disorder; AIDS; stroke;
 XX KW heart attack; head trauma; neurodegenerative disease; human;
 XX KW Parkinson's disease; Alzheimer's disease; ss.

XX OS Homo sapiens.

XX PN WO9950288-A2.

XX PD 07-OCT-1999.

XX PF 30-MAR-1999; 99WO-US06993.

XX PR 31-MAR-1998; 98US-0053374.

XX PA (AMGE-) AMGEN INC.

XX PI Yen K;

XX XX

XX DR WPI; 1999-601322/51.

XX DR P-PSDB; AAY42693.

XX PT kd312 polypeptides useful for treating diseases and disorders
 XX associated with alterations in cell proliferation and cell death

XX PS Claim 1; Fig 5; 85pp; English.

XX CC The invention provides nucleic acid molecules encoding human and rat
 XX CC kd312 polypeptides. The kd312 polypeptides can be expressed by standard
 XX CC recombinant methodology. The kd312 sequences, and the antibodies against
 XX CC the proteins may be used to treat or diagnose the presence or progression
 XX CC of various diseases, e.g. cancer, immunodeficiency disorders (e.g. AIDS),
 XX CC stroke, heart attack, head trauma, and neurodegenerative diseases (e.g.
 XX CC Parkinson's disease and Alzheimer's disease). The present sequence
 XX CC represents the human kd312 genomic DNA sequence.

XX SQ Sequence 3986 BP; 856 A; 1226 C; 1172 G; 732 T; 0 other;

Alignment Scores:

Pred. No.: 1.84e-118 Length: 3986
 Score: 1651.00 Matches: 329
 Percent Similarity: 82.04% Conservative: 0
 Best Local Similarity: 82.04% Mismatches: 1
 Query Match: 95.38% Indels: 71
 DB: 20 Gaps: 1

SQ Sequence 846 BP; 176 A; 288 C; 252 G; 130 T; 0 other;

Alignment Scores:

Pred. No.: 1.35e-103 Length: 846
 Score: 1449.00 Matches: 281
 Percent Similarity: 100.00% Conservativity: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 83.71% Indels: 0
 DB: 21 Gaps: 0

US-09-709-103-3f1 (1-332) x AA236892 (1-846)

QY 52 MetLysLeuAlaAlaMetIleLysLysMetCysProSerAspSerGluLeuSerIlePro 71
 Db 1 ATGAACACTGGCGCGGATGATCAAGAAAGATGGCCGAGCTCGGAGCTGAGTATCCCG 60
 QY 72 AlaLysAsnCysTyrArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIle 91
 Db 61 GCCAAGAACTGCTATCGCATGGTTCATCTCGGCTCTCCAGGTGGCAAGACGGCCATC 120
 QY 92 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 111
 Db 121 GTGTCGGCTTCTTCACCGCGCTTTCAGAGACGCTCACACGCTTACCATCGAGGACTTC 180
 QY 112 HisArgLysPheTyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSer 131
 Db 181 CACCGCAAGTCTTACTCTCATCCGCGGAGGTCTACCGAGTGGATCTCTCGACACGTCC 240
 QY 132 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIle 151
 Db 241 GGCACACCCGCTTCCCGCGCATGCGCGCTCTCCATCTTCACAGGAGAGTTCATC 300
 QY 152 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGln 171
 Db 301 CTGGTGTTAGTCTGACCAACCGGACTCTTCGAGGAGGTGTCAGCGGCTCAGCGACGAG 360
 QY 172 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeu 191
 Db 361 ATCTCTCGACCAACAGTCTTGGCTCAAGAACAAACCAAGAGAGACGTGGAGCTGCCCTTG 420
 QY 192 ValIleCysGlyAsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIle 211
 Db 421 GTCATCTCGCGGCAACAGGGTGACCGGACTTCTACCGGAGGTGGACACCGCGAGATC 480
 QY 212 GluGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLys 231
 Db 481 GAGCAGCTGGTGGCGACGACCCCGCGCTGCGCTTCTGAGATCTCGGCCAAGAG 540
 QY 232 AsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGlu 251
 Db 541 AACACAGCTGGACCAAGATGTTCCGCGCTTTCGCCATGCGCAAGCTGCCAGCGAG 600
 QY 252 MetSerProAspLeuHisArgLysValSerValGlnTyrCysAspValLeuHisLysLys 271
 Db 601 ATGAGCCAGACCTGACCCGCAAGGTCTCGGTGAGTACTGCGACGTGTCACCAAGAG 660
 QY 272 AlaLeuArgAsnLysLysLeuLeuArgAlaGlySerGlyGlyGlyGlyGlyGlyGlyGly 291
 Db 661 GCGTGGCGGAAACAGAGAGCTGCTGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
 QY 292 AspAlaPheGlyIleValAlaProPheAlaArgAtqProSerValHisSerAspLeuMet 311
 Db 721 GACGCTTTGGCATGTGGACACCTTTCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
 QY 312 TyrlleArgGluLysAlaSerAlaGlySerGlnAlaLysAspLysGluArgCysValIle 331
 Db 781 TATATCGCGAGAGGCGCAGCGCGCGCAGCGCGCGCAGCGCGCGCAGCGCGCGTGTGTCATC 840
 QY 332 Ser 332
 Db 841 AGC 843

RESULT 7

AAZ23024

ID AAZ23024 standard; CDNA; 1689 BP.

AC AAZ23024;

DT 17-JAN-2000 (first entry)

XX Rat kd312 polypeptide encoding CDNA.

XX kd312 polypeptide; cancer; immunodeficiency disorder; AIDS; stroke;
 KW heart attack; head trauma; neurodegenerative disease; rat;
 KW Parkinson's disease; Alzheimer's disease; ss.

OS Rattus sp.

XX WO9950288-A2.

XX 07-OCT-1999.

XX 30-MAR-1999; 99WO-US06993.

XX 31-MAR-1998; 98US-0053374.

XX (AMGE-) AMGEN INC.

XX Yen K;

XX WPI; 1999-601322/51.

XX P-PSDB; AAY42694.

XX kd312 polypeptides useful for treating diseases and disorders
 associated with alterations in cell proliferation and cell death -

XX Claim 2; Fig 9; 85pp; English.

XX The invention provides nucleic acid molecules encoding human and rat
 kd312 polypeptides. The kd312 polypeptides can be expressed by standard
 recombinant methodology. The kd312 sequences, and the antibodies against
 the proteins may be used to treat or diagnose the presence or progression
 of various diseases, e.g. cancer, immunodeficiency disorders (e.g. AIDS),
 stroke, heart attack, head trauma, and neurodegenerative diseases (e.g.
 Parkinson's disease and Alzheimer's disease). The present sequence
 represents the rat kd312 CDNA sequence.

XX Sequence 1689 BP; 417 A; 462 C; 434 G; 376 T; 0 other;

Alignment Scores:

Pred. No.: 3.44e-102 Length: 1689
 Score: 1435.50 Matches: 290
 Percent Similarity: 91.38% Conservativity: 7
 Best Local Similarity: 89.23% Mismatches: 24
 Query Match: 82.93% Indels: 5
 DB: 20 Gaps: 3

US-09-709-103-3f1 (1-332) x AAZ23024 (1-1689)

QY 11 ProSerArgAlaGlnProGluGlnSerProAlaAlaHisProAlaCysHisProSer 30
 Db 1 CCGCTGCTCTACTACTCAAGATTCAGCGCTCCGCGGTCGCCAAGCAAACTCTTCC 60
 QY 31 ---AspProGlnProLeuSerAla-----LeuLeuSerAlaProArgProSerArg 47
 Db 61 ACCACTCGGCGGCTCTGCGGCTCTTCTCTCAGCCACGATCTGCCCTG-GGG 119
 QY 48 ProLeuCysProMetLysLeuAlaMetIleLysLysMetCysProSerAspSerGlu 67
 Db 120 CCCCTCTGCCCATGAATACTGGCGCGGATGATCAAGAGATGTGCCAAGGACTCTGAA 179
 QY 68 LeuSerIleProAlaLysAsnCysTyrArgMetValIleLeuGlySerSerLysValGly 87
 Db 180 CTGAGTATCCCGGCCAAGAACTGTACAGATGGTCTACCTCTCGGCTCATCCAAAGTGGC 239
 QY 88 LysThrAlaIleValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThr 107


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Db 240 AAGACGGCGCATCGTGGCGCTTCTCAGCGGCGCTTGAGAGACCGCTTACACCCCTTACC 299
QY 108 ILeuIAspPheHisArgLysPheTyrSerIleArgGlyIleValTyrGlnIleuAspIle 127
Db 300 ATTGAAGCTTCCACCCGAAAGTTTACTCCGATCCGCGCGAAGCTTACCAAGTTGGACATTA 359
QY 128 LeuAspThrSerGlyAsnHisProPheProIleMetArgIleuSerIleLeuThrGly 147
Db 360 CTGACACATCTGGCAATCATCTGTTCCGCCATTCGGGGCGCTCTTATCTCCACAGGA 419
QY 148 AspValPheIleLeuValPheSerLeuAspAsnArgAspSerPheGlyIleValGlnArg 167
Db 420 GAGCTTTCTATTCTGCTGTTGAGCTTACACAAACCGGACTCTCTGAGAGAGTCCAAAG 479
QY 168 LeuArgGlnGlnIleLeuAspThrLysSerCysLeuLysAsnLysThrLysGlnAsnVal 187
Db 480 CTCAAACACAGCATCTTACACACCAAGTCTCTTCMAAGAACCAACCAAGAGATGTG 539
QY 188 AspValProLeuValIleCysGlyAsnLysGlyAspArgAspPheTyrArgIleValAsp 207
Db 540 GACGTGCGCTGTCATTTGCGGTACAAAGGAGACCGGACTTCTTACCGGAGATGGAG 599
QY 208 GlnArgGlnIleGlnIleuValGlyAspAspProGlnArgCysAlaTyrPheGlnIle 227
Db 600 CAGCGGAGATGAGCGAGCTGTGGCGGATGACCTTACCGCTTACCTTACCTGAGATC 659
QY 228 SerAlaLysLysAsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLys 247
Db 660 TCGGCCAAGAAATACACAGCTCGACACAGATCTCCGTCGCTCTTCCATGGCCAG 719
QY 248 LeuProSerGlnMetSerProAspLeuHisArgLysValSerValGlnTyrCysAspVal 267
Db 720 CTGCTTACCGAGATGAGCGCTGACTTGCACCGCAAGTGTCTGTGCAAGTGTGACGTG 779
QY 268 LeuHisLysLysAlaLeuArgAsnLysLysLeuLeuArgLysGlyGlyGly 287
Db 780 CTGCAAAAGGCTGTGAGAAACAAAGCTTCTGCGTGGGGAGC---GGAGGTGGG 836
QY 288 GlnAspProGlyAspAlaPheGlyTleValAlaProPheAlaArgArgProSerValHis 307
Db 837 GCGGACACAGGAGATGCCCTTGGCATCTTGGCGGCGCTTGTCTCCACAGCTTACGCTCAT 896
QY 308 SerAspLeuMetTyrIleArgGlnLysAlaSerIleArgSerGlnAlaLysAspLysGln 327
Db 897 ACGGACCTCATGTACATTCGTGAGAAACCACTGTACACACCAAGGCTAAGAGACAGAG 956
QY 328 ArgCysValIleSer 332
Db 957 CGCTGTGTCTCAGT 971

RESULT 8
AAZ23025
ID AAZ23025 standard; DNA; 3079 BP.
XX
AC AAZ23025;
XX
DT 17-JAN-2000 (first entry)
XX
DE Rat kd312 genomic DNA sequence.
XX
KW kd312 polypeptide; cancer; immunodeficiency disorder; AIDS; stroke;
KW heart attack; head trauma; neurodegenerative disease; rat;
KW Parkinson's disease; Alzheimer's disease; ss.
XX
OS Rattus sp.
XX
PN MO9950288-A2.
XX
PD 07-OCT-1999.
XX
PF 30-MAR-1999; 99MO-US06993.
XX

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PR 31-MAR-1998; 98US-0053374.
XX
PA (AMGE-) AMGEN INC.
XX
PI Yen K;
XX
DR WPI; 1999-601322/51.
XX
DR P-PSDB; AAY42694.
XX
PT kd312 polypeptides useful for treating diseases and disorders
PT associated with alterations in cell proliferation and cell death
PS Claim 2; Fig 7; 85pp; English.
XX
CC The invention provides nucleic acid molecules encoding human and rat
CC kd312 polypeptides. The kd312 polypeptides can be expressed by standard
CC recombinant methodology. The kd312 sequences, and the antibodies against
CC the proteins may be used to treat or diagnose the presence or progression
CC of various diseases, e.g. cancer, immunodeficiency disorders (e.g. AIDS),
CC stroke, heart attack, head trauma, and neurodegenerative diseases (e.g.
CC Parkinson's disease and Alzheimer's disease). The present sequence
CC represents the rat kd312 genomic DNA sequence.
XX
SQ Sequence 3079 BP; 708 A; 843 C; 829 G; 699 T; 0 other;

Alignment Scores:
Pred. No.: 3,11e-98 Length: 3079
Score: 1388.50 Matches: 291
Percent Similarity: 79.47% Conservative: 7
Best Local Similarity: 77.60% Mismatches: 27
Query Match: 80.21% Indels: 52
DB: Gaps: 4

US-09-709-103-3f1 (1-332) x AAZ23025 (1-3079)
QY 7 GlnAlaProSerProSerArgAlaGlnProGlnIleuSerProProAlaAlaHisProAla 26
Db 160 GGAAGGCTGAGCGCGCTGCTGTACTCAAGATTCAGGCGCAGCGGGTCCCGAAG 219
QY 27 CysHisProSer---AspProGlnProLeuSerAla-----LeuLeuSerLalaProArg 43
Db 220 CCAAACTCTTCCACCACTCCGGCGCCCTGCGACGCTTCTTCTTCCACGACGCTAT 279
QY 44 ProProSerArgProLeuCysPrometLysLeuAlaMetIleLysLysMetCysPro 63
Db 280 CTGCCCTG-GGGCCCTCTGCTGCCAATGAACCTGCGCGCATGATCAAGAAATGTGCCCA 338
QY 64 SerAspSerGlnLeuSerIleProAlaLysAsnCysTyrArgMetValIleuGlySer 83
Db 339 ACGGACTGTGAATGATGATCCCGGCAAGATCTGACAGATGTGATCTCTCGGCTCA 398
QY 84 SerLysValGlyLysThrAlaIleValSerArgPheLeuThrGlyArgPheGlnAspAla 103
Db 399 TCCAAAGTGGCAAGACCGCATCTGTGCGCTTCTCCAGGGCGCTTCCAGAGCGCT 458
QY 104 TyrThrProThrIleGlnAspPheHisArgLysPheTyrSerIleArgGlyIleValTyr 123
Db 459 TACACCCCTTACCATTTGAGACCTTCCACGAAAGTTTACTGATCCCGGGGAGTGTAC 518
QY 124 GlnLeuAspIleLeuAspThrSerGlyAsnHisProPheProAlaMetArgArgLeuSer 143
Db 519 CAGTTGACATACTGACACATCTGCAATCATCTCGTTTCCGCCAATGCGGCGCTCTCT 578
QY 144 Ile----- 144
Db 579 ATCTCTCACAGGTGAGTGGGGACCCAGACGACCTGGGGAGGGAATCTCGGGAGCGG 638
QY 144 ----- 144
Db 639 ATGGGCGGTGTGTGTGCTTGGGCTGTGCTGTCTCTCGGTCTTGGCAGCTGCC 698
QY 145 -----LeuThrGlyAspValPheIleLeuValPheSerLeuAsp 157

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Db 699 CTCACCTTCCACCTCGTTCCTCTGTA-GGAGACGTTTTTCATTCTGTGTTCAGCTTAGAC 757
 QY 158 AsnArgAspSerPheGluGluValGlnArgLeuArgGlnGlnIleLeuAspThrIysSer 177
 Db 758 AACCGGACTCTTCGAGGAGGTGCAAGGCTCAACAGCATCTAGACACCAAGTCC 817
 QY 178 CysLeuIysAsnIysThrIysGluAenValAspValProLeuValIleCysGlyAsnLys 197
 Db 818 TGCTCAAGAACAAACCAAGAGATGTGGACGTGGCGCTGCTCATTTGGGTAAACAA 877
 QY 198 GlyAspArgAspPheTyrArgGluValAspGlnArgGluIleGluGlnLeuValGlyAsp 217
 Db 878 GGGGACCGGACTCTTACCGCGAGTGTGGAGCAGCGGAGATGACGACTGTGGCGGAT 937
 QY 218 AspProGlnArgCysAlaTyrPheGluIleSerAlaLysLysAsnSerSerLeuAspGln 237
 Db 938 GACCTTCAGCGTGTGCTTACTTCGAGATCTCGGCCAAGAGATAGCAGCTGGACCAG 997
 QY 238 MetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGluMetSerProAspLeuHis 257
 Db 998 ATGTTCCGTCGCTTTTGCCATGGCCAAAGCTGCTAGCGAGATGAGCCTGACTTGAC 1057
 QY 258 ArgLysValSerValGlnTyrCysAspValLeuHisLysLysAlaLeuArgAsnLysLys 277
 Db 1058 CGCAAGGTGTCTGTGACGTACTGTGACGTGTGCACAAAGGCTCTGAGGAACAAGAG 1117
 QY 278 LeuLeuArgAlaGlySerGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 297
 Db 1118 CTTCTGCTGCGGGCAGC--GGAGGTGGGGCGACCGAGATGCTTTGCACTTTG 1174
 QY 298 AlaProPheAlaArgArgProSerValHisSerAspLeuMetTyrIleArgGluLysAla 317
 Db 1175 GCGGCTTTGCTGCGACACCTAGGTGCTCATAGGACCTCATGTACATTGTCGAGAAACC 1234
 QY 318 SerAlaGlySerGlnAlaLysAspLysGluArgCysValIleSer 332
 Db 1235 AGTGTACGACCGAGGCTAAGGACAGGAGCGGTGTGTATCAGT 1279
 RESULT 9
 ABK71563
 ID ABK71563 standard; cDNA; 3427 BP.
 XX
 AC ABK71563;
 XX
 XX
 DT 30-JUL-2002 (first entry)
 XX
 DE Human dithp polynucleotide #29.
 XX
 KW Human; dithp; diagnostic and therapeutic polynucleotide; gene; ss; bone;
 KW cell proliferative disorder; cancer; tumour; autoimmune disorder; brain;
 KW inflammatory disorder; viral infection; bacterial infection; seizure;
 KW fungal infection; parasitic infections; developmental disorder; breast;
 KW endocrine disorder; metabolic disorder; neurological disorder; cervix;
 KW gastrointestinal disorder; transport disorder; gene therapy; kidney;
 KW adrenal gland; bone marrow; lung; ovary; pancreas; prostate; spleen;
 KW skin; testis; thymus.
 XX
 OS Homo sapiens.
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 XX 14-MAR-2002.
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 PF 29-AUG-2001; 2001WO-US27127.
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 DF 30-MAY-2002 (first entry)
 XX Human Tumour Endothelial Marker polynucleotide SEQ ID NO 197.
 DE Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytosolic;
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KW normal endothelial marker; pan-endothelial marker; immunostimulant;
 KW antiangiogenic; tumour; neovascularization; vascularised tumour;
 KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
 KW psoriasis; gene; ss.
 OS Homo sapiens.
 PN WO200210217-A2.
 PD 07-FEB-2002.
 PF 01-AUG-2001; 2001MO-US24031.
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 PR 11-APR-2001; 2001US-282850P.
 PA (UWJO) UNIV JOHNS HOPKINS.
 PI St Croix B, Kinzler KW, Vogelstein B;
 DR WPI, 2002-291856/33.
 DR P-PSDB; ABB90733.
 PT An isolated molecule comprising an antibody variable region which
 specifically binds to an extracellular domain of a tumor endothelial
 marker (TEM) protein, useful for inhibiting tumor growth -
 Claim 65; Page 152-153; 33pp; English.
 PS The invention relates to an isolated molecule comprising an antibody
 variable region which specifically binds to an extracellular domain of a
 tumor endothelial marker (TEM) protein selected from ABB90732, ABB90740,
 CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
 CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
 CC They are useful for inhibiting tumor growth, polycystic kidney disease,
 CC subjects bearing a vascularised tumour, rheumatoid arthritis and psoriasis. Human, mouse
 CC and rat TEM genes and the encoded proteins (ABL92075-ABL92041 and
 CC ABB90721-ABB90789) are disclosed, as are marker oligonucleotide
 CC sequences: tumour endothelial markers (TEM) ABL9196-ABL92041 and
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 QY 56 AlaMetIleLysLysMetCysProSerAspSerGluLeuSerIleProAlaLysAsnCys 75
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 QY 76 TyrArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIleValSerArgPhe 95


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Db 328 TTCAGCCTGGATTAACCGGAGTCTTCATGAGTCACAGCCGCTTCAAGACAGATCTCTG 387
174 AspThrLysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeuValIle 193
388 GAGGTCAAGTCTGCTGCTGAAGAACAGACCAAGAGCGCGAGCTGCCATGCTATC 447
194 CysGlyAsnLysGlyAspArg---AspPheTyrArgGluValAspLysGluIleGlu 212
448 TGTGGCAACAAAGACGACCGAGCTCTGCGCCAGGTGCCACCAAGAGCGCGAG 507
213 GluLeuValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerLysValAsn 232
508 CTGCTGTGTGGCGGAC---GAGAACCTGGCTACTTCAAGGTGTGTGGCAAGAGAAC 564
233 SerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGluMet 252
565 ACCAACGTGACGAGATGTTCTTACGTCTTCAAGCTTGCACCAAGCTGCCACAGAGATG 624
253 SerProAspLeuHisArgLysValSerValGlnTyrCysAspValLeuHisLysLys--- 271
625 ACCCCGCGCTGATCGCAAGATCTCGGTGACGTAAGGTGACGCTTCCACCCCGAGGCC 684
272 ---AlaLeuArgAsnLysLysLeuArgAlaGlySerGlyGlyGlyGlyAspPro 290
685 TTCTGCTGATCGCGCGCTCAAGAGATG----- 711
291 GlyAspAlaPheGlyIleValAlaProPheAlaArgArgProSerValHisSerAspLeu 310
712 ---GAGCGCTATGAGCATGTGCTTCGCCCTTCCGCCGCCCGCCAGCGTCAAGAGTACTC 768
311 MetTyrIleArgGluLysAlaSerAlaGlySerGlnAlaLysAspLysGluArgCysVal 330
769 AAGTACATCAAGCGCAAGGTCTTCCGGAAGGCCAGGCCCGTGAAGAGGACAGTGACCC 828
QY 331 Ile 331
DB 829 ATC 831
RESULT 12
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XX ABL92076;
XX
XX 30-MAY-2002 (first entry)
XX
XX Human Tumour Endothelial Marker polynucleotide SEQ ID NO 174.
XX
XX Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytoskeletal;
XX normal endothelial marker; pan-endothelial marker; immunostimulant;
XX antiangiogenic; tumour neovascularisation; vascularised tumour;
XX polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
XX psoriasis; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200210217-A2.
XX
XX 07-FEB-2002.
XX
XX 01-AUG-2001; 2001WO-US24031.
XX
XX 02-AUG-2000; 2000US-222599P.
XX
XX 11-AUG-2000; 2000US-22436P.
XX
XX 11-APR-2001; 2001US-282850P.
XX
XX (UJJO ) UNIV JOHNS HOPKINS.
XX
XX St Croix B, Kinzler KM, Vogelstein B;
XX
XX WPI; 2002-291856/33.
XX

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PT An isolated molecule comprising an antibody variable region which
PT specifically binds to an extracellular domain of a tumor endothelial
PT marker (TEM) protein, useful for inhibiting tumor growth -
XX
XX Disclosure: Page 119-120; 331pp; English.
XX
XX The invention relates to an isolated molecule comprising an antibody
XX variable region which specifically binds to an extracellular domain of a
XX tumor endothelial marker (TEM) protein selected from ABB90732, ABB90740,
XX ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
XX proteins have cytoskeletal, immunostimulant and antiangiogenic activity.
XX They are useful for inhibiting tumor growth, neovascularisation in
XX subjects bearing a vascularised tumour, polycystic kidney disease,
XX diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse
XX and rat TEM genes and the encoded proteins (ABL92075-ABL92041 and
XX ABB90721-ABB90789) are disclosed, as are marker oligonucleotide
XX sequences: tumor endothelial markers (TEM) ABL91996-ABL92041 and
XX ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074;
XX and pan-endothelial markers (PEM) ABL91903-ABL91995.
XX
XX Sequence 2832 BP; 602 A; 891 C; 727 G; 612 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 3,15e-60 Length: 2832
XX Score: 898.00 Matches: 179
XX Percent Similarity: 74.09% Conservative: 44
XX Best Local Similarity: 59.47% Mismatches: 50
XX Query Match: 51.88% Indels: 28
XX DB: 24 Gaps: 5
XX
XX US-09-709-103-3f1 (1-332) x ABL92076 (1-2832)
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DB 4 CTTGCTCTCTCGCTTGTGAGCCCGA----- 33
QY 54 LeuAlaAlaMetIleLysLysMetCysProSerAspSerGluLeuSerIleProAlaLys 73
DB 34 -----GCCATGATGAAAGCTTTGTCCAGCGGAACTCAGCTCAGTGTGCCGCAAA 87
QY 74 AsnCysTyrArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIleValSer 93
DB 88 AACTCATACCGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 147
QY 94 ArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPheHisArg 113
DB 148 CGTTCTCTCAATGCGCGCTTGTGAGCACGATCAACCCCATCTGAGAGATCCACCGT 207
QY 114 LysPheTyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSerGlyAsn 133
DB 208 AAGGTATACACATCCGCGCGCATGTACAGCTGCATCTGTGATCTCTGCGCAAC 267
QY 134 HisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuVal 153
DB 268 CACCCCTTCCCGCGCATGCGAGCTGTCTCATCTCAACGGAGATCTTCAATCTCGGTG 327
QY 154 PheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnIleLeu 173
DB 328 TTCAGCCTGGATTAACCGGAGTCTTCATGAGTCACAGCCGCTTCAAGACAGATCTCTG 387
QY 174 AspThrLysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeuValIle 193
DB 388 GAGGTCAAGTCTGCTGCTGAAGAACAGACCAAGAGCGCGAGCTGCCATGCTATC 447
QY 194 CysGlyAsnLysGlyAspArg---AspPheTyrArgGluValAspLysGluIleGlu 212
DB 448 TGTGGCAACAAAGACGACCGAGCTCTGCGCCAGGTGCCACCAAGAGCGCGAG 507
QY 213 GluLeuValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerLysValAsn 232
DB 508 CTGCTGTGTGGCGGAC---GAGAACCTGGCTACTTCAAGGTGTGTGGCAAGAGAAC 564
QY 233 SerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGluMet 252

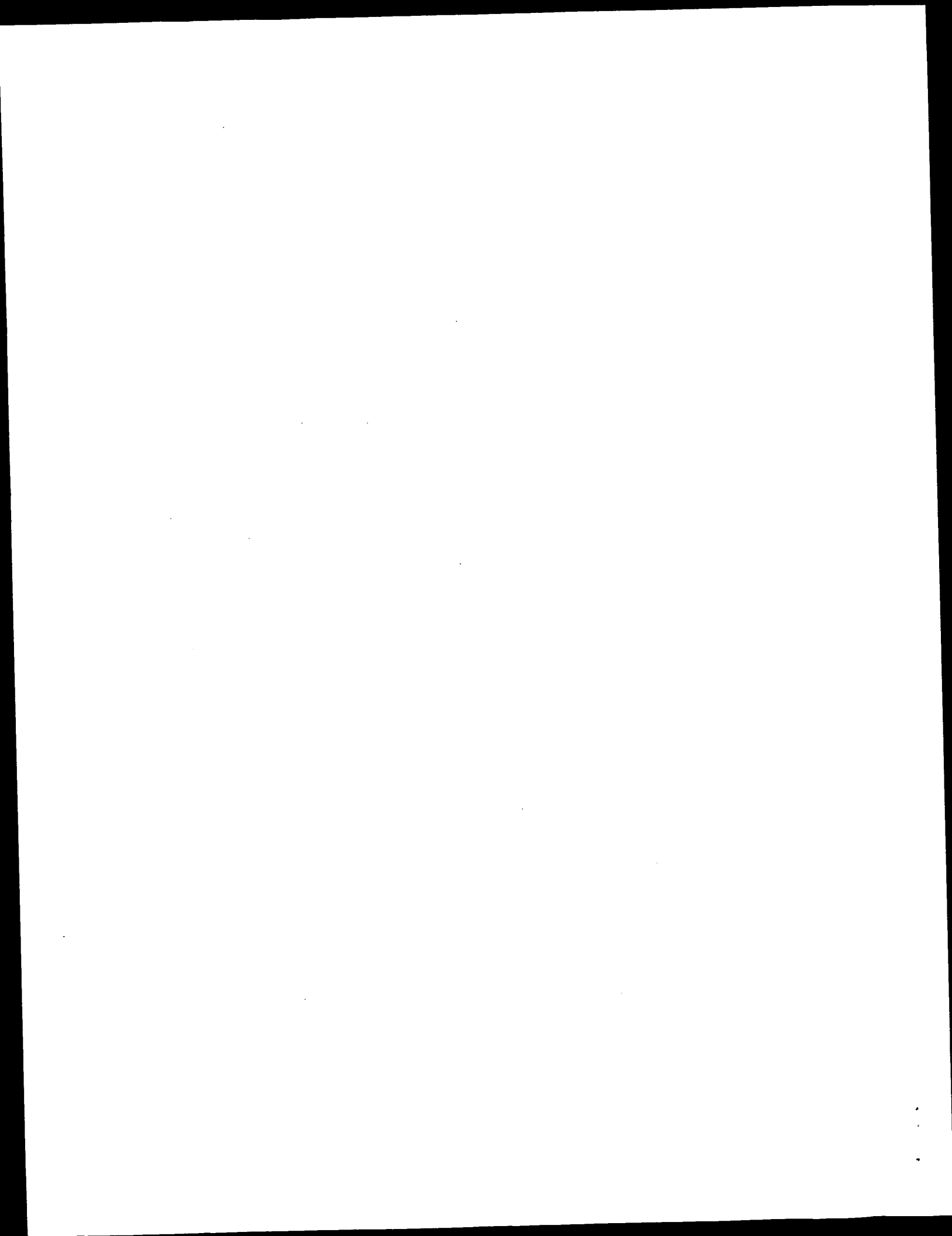
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The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740, ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, tumouricidal and antiangiogenic activity. They are useful for inhibiting tumour growth, neoangiogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABB92075-ABB92141 and

RESULT 14
 AAS90571 standard; cDNA; 951 BP.
 ID AAS90571
 AC AAS90571;
 XX
 XX
 DT 13-FEB-2002 (first entry)
 XX
 XX DNA encoding novel human diagnostic protein #26375.
 DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
 XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
 KM Homo sapiens.
 OS
 XX Homo sapiens.
 FN WO2001.75067-A2.
 PD 11-OCT-2001.
 PF 30-MAR-2001; 2001WO-US08631.
 XX 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX (HSE-) HSEQ INC.
 PA Drmanac RT, Liu C, Tang YT;
 PI MPI; 2001-639362/73.
 DR P-PSDB; ABG26384.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 PS Claim 1; SEQ ID NO 26375; 103pp; English.
 XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridization probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
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 XX Sequence 951 BP; 202 A; 291 C; 293 G; 165 T; 0 other;
 Alignment Scores: 9.39e-47 Length: 951
 Pred. No.: 717.00 Matches: 149
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 Best Local Similarity: 41.42% Indels: 36
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Db 142 CGCATGATGATGCTGGGCTCTCGGTCGAGAGCTCCATCTGCTCGCTTC 201
 Qy 97 ThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPheHisArgGlySerPheTyr 116
 Db 202 AATGGCCGCTTGAAGACCACTACACCCATCGAGAGACTTCCACCGTAAGATTATAC 261
 Qy 117 SerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisProPhe 136
 Db 262 AACATCCGCGGACATGATGACAGCTTCACATCTCGATACCTTGGCAACACCCCTTC 321
 Qy 137 ProAlaMetArgArgPheSerSerIleLeuThrGlyAspVal---PheIleLeuValPheSer 155
 Db 322 CCGCCATGGCGAGGCTGTGTCATCTCAGAGTGAAGCCCACTGCTGCTGGCTGGGACC 381
 Qy 156 LeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGln----- 170
 Db 382 -----GGCAGGCGCAGGAGCATGGGTCGAGAGTGTG 411
 Qy 171 -----GlnIleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsn 186
 Db 412 CTGGGCACTTAGCAGATCTCGAGTCAGTCAAGTCTGCTGAAGAACAGACCAAGAGGCG 471
 Qy 187 ValAspValProLeuValIleCysGlyAsnLysGlyAspArg---AspPheTyrArgGlu 205
 Db 472 GCGGAGCTGCGCATGTCATCTGTGGCACAAGACAGACGAGCGAGCTGTGGCGCCAG 531
 Qy 206 ValAspGlnArgGluIleGlnLeuValGlyAspAspProGlnArgCysAlaTyrPhe 225
 Db 532 GTGCCACACCGAGGCGGAGCTGCTGTGGGCGAC---GAGAACTGCGCTCACTTC 588
 Qy 226 GluIleSerAlaLysLysAsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMet 245
 Db 589 GAGCTGTGCGCAAGAACAGACCAACCTGAGCGAGATGTTCTACGTCCTTCACAGCATG 648
 Qy 246 AlaLysLeuProSerGlnMetSerProAspLeuHisArgLysValSerValGlnTyrCys 265
 Db 649 GCCAAGCTGCCACAGATGAGGCCCGCCCTGATCGCAAGATCTCGTGCATATACGCT 708
 Qy 266 AspValLeuHisLysLys-----AlaLeuArgAsnLysLysLeuArgAlaGlySer 283
 Db 709 GAGCCCTTCACCCAGCGCTTCATGACGCCCGCTCAGAGATG----- 756
 Qy 284 GlyGlyGlyGlyGlyAspProGlyAspAlaPheGlyIleValAlaProPheAlaArgArg 303
 Db 757 -----GACGCTATGAGATGCTCGCCCTTCGCGCGCGC 792
 Qy 304 ProSerValHisSerAspLeuMetTyrIleArgGluLysAlaSerAlaGlySerGlnAla 323
 Db 793 CCCAGCGTCAACATGACCTCAAGTACATCAAGCCAGAGTCTCTTGGGAAGCCAGCGCC 852
 Qy 324 LysAspLysGluArgCysValIle 331
 Db 853 CGTGAAGAGGACAGATGACCATC 876
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 ID ABL07789
 AC ABL07789;
 XX
 XX
 DT 26-MAR-2002 (first entry)
 XX
 XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 17849.
 DE Drosophila; developmental biology; cell signalling; insecticide;
 XX Drosophila; gene; ss.
 KM Drosophila melanogaster.
 OS
 XX WO2001.71042-A2.
 FN 27-SEP-2001.
 XX

Search completed: December 30, 2002, 18:13:49
Job time : 373 secs



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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 30, 2002, 18:04:26 ; Search time 2185 Seconds
(without alignments)
2460.825 Million cell updates/sec

Title: US-09-709-103-3f1

Perfect score: 1731

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Delop 6.0, Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: gb_ges.*
18: em_gss_hum.*
19: em_gss_inv.*
20: em_gss_pln.*
21: em_gss_prt.*
22: em_gss_fun.*
23: em_gss_mam.*
24: em_gss_mus.*
25: em_gss_other.*
26: em_gss_pro.*
27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1437	83.0	962	13	BM543472	BM543472 AGENCOURT
3	1416	81.8	1103	14	BM920514	BM920514 AGENCOURT
4	1372.5	79.3	1033	14	BM921737	BM921737 AGENCOURT
5	1368	79.0	965	9	ALS53318	ALS53318 AL533318
6	1310	75.7	1023	13	BM543630	BM543630 AGENCOURT
7	1305	75.4	1032	14	BQ067637	BQ067637 AGENCOURT
8	1190.5	68.8	1137	14	BM921656	BM921656 AGENCOURT
9	1189	68.7	814	13	BM159688	BM159688 AGENCOURT
10	1186	68.5	742	10	AW028127	AW028127 W26C07.X
11	1168.5	67.5	1160	14	BM805574	BM805574 AGENCOURT
12	1162.5	67.2	831	13	BM1596637	BM1596637 603243203
13	1114.5	64.4	958	14	BQ719566	BQ719566 AGENCOURT
14	1097	63.4	699	12	BG706012	BG706012 602669154
15	1071	61.9	699	12	BG709229	BG709229 602674615
16	1071	61.9	700	13	BM1596509	BM1596509 603243558
17	1064	61.5	649	12	BG085090	BG085090 H3108E05-
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19	994.5	57.5	726	12	BF613135	BF613135 de30e03.Y
20	994	57.4	675	13	BM1545172	BM1545172 603242791
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23	946.5	54.7	1438	14	BM807669	BM807669 AGENCOURT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1035)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1AM12776 row: j column: 10
High quality sequence stop: 658.
Location/Qualifiers

FEATURES
source

1. 1035
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/db_xref="taxon:9606"
/clone="IMAGE:5748585"
/clone_lib="NIH MGC_120"
/lab_host="DH10B"
/note="Organ: pooled pancreas and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH MGC Library."
BASE COUNT 209 a 386 c 293 g 146 t 1 others
ORIGIN

Alignment Scores: 4.75e-120 Length: 1035
Pred. No.: 1482.50 Matches: 293
Score: 95.81% Conservative: 4
Percent Similarity: 94.52% Mismatches: 8
Best Local Similarity: 85.64% Indels: 5
Query Match: 14 Gaps: 2
DB:

US-09-709-103-3f1 (1-332) x BM919341 (1-1035)

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DB 40 CCGAGCGGAGCCGAGAGCCGAGAGCCGAGAGCCGAGAGCCGAGAGCCGAGAGCCGAGAGCC 99
QY 23 AlaHisProAlaGlyHisProSerAspProGlnProLeuSerAlaLeuSerAlaPro 42
DB 100 GCTCACCCCGCGTGCACCCGAGAGCCGAGAGCCGAGAGCCGAGAGCCGAGAGCCGAGAGCC 159
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DB 160 CGCCCGGCTCGGCGCCCTCTCCCAATGAATGCGCGCATGTATCAAGAAATGTGC 219
QY 63 ProSerAspSerGlnLeuSerLeuProAlaAlaValSerCysTyrArgMetValIleuGly 82
DB 220 CCGAGCAGCTCGGAGTATTCGCGGCAAGACTGCTATGCTATGCTATGCTATGCTATGCT 279
QY 83 SerSerLeuValGlyLeuThrAlaAlaValSerArgPheLeuThrGlyArgPheGluAsp 102
DB 280 TCGTCCAGGCGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 339
QY 103 AlaTyrThrProThrIleGluAspPheHisArgGlySerLeuSerLeuArgGlyVal 122
DB 340 GCTTACACGCGCTTACATCGACAGCTCGGCAACACCGCTTCCCGCGCATGCGCGCTTC 399
QY 123 TyrGlnLeuAspIleLeuAspThrSerGIYAsnHisProPheProAlaMetArgGlu 142
DB 400 TACAGCGCTGACATCTCTGACAGCTCGGCAACACCGCTTCCCGCGCATGCGCGCTTC 459
QY 143 SerIleLeuThrGlyAspValPheIleuValPheSerLeuAspAsnArgAspSerPhe 162
DB 460 TCCATCTTCACAGGAGAGCGTTTCTCATCTGCTGATGCTGCAACACCGAGCTCTTC 519

QY 163 GluGluValGlnArgLeuArgGlnGlnIleLeuAspThrIleSerCysLeuValAsnLys 182
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QY 203 TyrArgGluValAspGlnArgGlnIleGluIleuValGlyAspAspProGlnArgCys 222
DB 640 TACCGAGAGTGAACAGCGGAGATCGAGCTGTGTGGGAGAGAGAGAGAGAGAGAGAGAGAG 699
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DB 700 GCTTACTTCAGATCTCGGCAAGAAACAGAGCTGAGACCAATGTTCCGCGCTTC 759
QY 243 PheAlaMetAlaLysLeuProSerGlnMetSerProAspLeuHisArgLysValSerVal 262
DB 760 TTCCGCTGCGCAAGCTGCGCCAGAGATGAGCCAGACTGACCGGCAAGGTTCTCGGTTG 819
QY 263 GlnTyrCysAspValLeuHisLysLysValAlaLeuArgAsnLysLeuLeuArgAlaGly 282
DB 820 CAGTACTGCGAGCTGCTGCAACAGAAAGCGCTGCGGAAACAGAACTGCTGCGGCGCGC 879
QY 283 SerGly-GlyGly-GlyGlyAspProGlyAspAlaPheGlyIleValAla-----Prop 300
DB 880 AACG 939
QY 300 hea1aArg--ArgProSerValHis 307
DB 940 TCG 965

RESULT 2
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DEFINITION
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5', mRNA sequence.
BM543472
BM543472.1 GI:18773895
VERSION
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 962)
NIH-MGC http://mgc.nci.nih.gov/
TITLE
JOURNAL
COMMENT
Email: cgabs-remail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1AM12719 row: d column: 11
High quality sequence start: 18
High quality sequence stop: 692.
Location/Qualifiers

FEATURES
source

1. 962
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5726554"
/clone_lib="NIH MGC_124"
/tissue_type="hippocampus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: EcoRV (destroyed); Site_2: NotI; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is

normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012." 141 t 1 others

BASE COUNT 185 a 363 c 272 g 141 t 1 others
ORIGIN

Alignment Scores:

Pred. No.: 4.26e-116 Length: 962
Score: 1437.00 Matches: 283
Percent Similarity: 93.75% Conservative: 2
Best Local Similarity: 93.09% Mismatches: 9
Query Match: 83.02% Indels: 10
DB: 13 Gaps: 1

US-09-709-103-3F1 (1-332) x BM543472 (1-962)

QY 3 ProSerGlyAlaGlyAlaProSerProSerArgAlaGlnProGluGlnSerProProAla 22
Db 77 CCGAGCGGAGCGGAGCGCCGAGCCGAGCGCGCCGAGCGCCGAGCGCGCTCCAGCC 136
QY 23 AlaHisProAlaCysHisProSerAspProGlnProLeuSerAlaLeuSerAlaPro 42
Db 137 GCTCACCCTCGGCGGCTCCAGCGGAGCGCTCCAGCGCTCTCTGCGGCGCG 196
QY 43 ArgProProSerArgProLeuCysProMetLysLeuAlaAlaMetLysLysMetCys 62
Db 197 CGCCCGGCTCGGCGGCTCTGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 256
QY 63 ProSerAspSerGluLeuSerLysProAlaLysAsnCysTyrArgMetValLysLeuGly 82
Db 257 CCGAGCGACTCGGAGCTGAGTATCCCGGCGGAGCGGAGCGGAGCGGAGCGG 316
QY 83 SerSerLysValGlyLysThrAlaLeuValSerArgPheLeuThrGlyArgPheGluAsp 102
Db 317 TCGTCAAGGTGGGAGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 376
QY 103 AlaTyrThrProThrIleGluAspPheHisArgLysPheTyrSerIleArgGlyVal 122
Db 377 GCCTACAGCGCTACCTACGAGGAGCTTCCACCGAGGAGCTTCTCTCTCTCTCT 436
QY 123 TyrGluLeuAspIleLeuAspThrSerGlyAsnHisProPheProAlaMetArgArgLeu 142
Db 437 TACAGCTCGACATCTCCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 496
QY 143 SerIleLeuThrGlyAspValPheIleLeuValPheSerLeuAspAsnArgAspPhe 162
Db 497 TCATCTCTCACAGGAGAGCTTTTCACTCTGGTGTTCAGTCTGGGAGCGGAGCTTC 556
QY 163 GluGluValGlnArgLeuArgGlnGlnIleLeuAspThrLysSerCysLeuLysAsnLys 182
Db 557 GAGGAGGTGAGCGGCTCAGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 616
QY 183 ThrLysGluAsnValAspValProLeuValIleCysGlyAsnLysGlyAspArgPhe 202
Db 617 ACCAGGAGAGAGCTGGAGCTGCCCTGGTCTATCTGGGAGCGGAGCGGAGCTTC 676
QY 203 TyrArgGluValAspGlnArgGluIleGluGlnLeuValGlyAspAspProGlnArgCys 222
Db 677 TACCGGAGGTGGAGCGGAGAGTCCGAGCGTGTGGGAGCGGAGCGGAGCGGAGCTG 736
QY 223 AlaTyrPheGluIleSerAlaLysLysSerSerLeuAspGlnMetPheArgAlaLeu 242
Db 737 GCCTACTTCGAGATCTCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 796
QY 243 PheAlaMetAlaLysLeuProSerGluMetSerProAspLeuHisArgLysValSerVal 262
Db 797 TTCGCATGGCCAGCTGCCAGCGAGATGAGCCCGAGAGCTTCAGCGGAGGAGCTTC 856
QY 263 GlnTyrCysAspValLeuHisLysLysAlaLeuArgAsnLysLysLeuLeuArgAlaG 282
Db 857 CAGTACTGCGAGCTGCTGCAAGAGAGCGTCCGGAACAGAGAGCTGCTCGGCGGCG 916
QY 282 LysSerGlyGlyGlyGlyAspProGlyAspAlaPheGlyLysLeuAlaProPheAla 302

Db 917 GGCAACCG 952
QY 302 rGAtgPro 304
Db 953 GACGCCCT 960

RESULT 3

BM920514

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 1103)

NIH-MGC http://mgi.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Cloning Distribution: Agencourt Bioscience Corporation

Cloned through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM12781 row: j column: 12

High quality sequence stop: 676

Location/Qualifiers

1..1103

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5750507"

/lab_host="DH10B"

/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;

Site 1: NotI; Site 2: EcoRV (destroyed); RNA source

anonymous pool of 24 week female lung, 16 week female

spleen, and 20-22 week male spleens. Library is oligo-dT

primed and directionally cloned (EcoRV site is destroyed

upon cloning). Average insert size 1.4 kb, insert size

range 1-3 kb. Library is normalized and enriched for

full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 026. Note:

this is a NIH MGC library."

BASE COUNT 230 a 402 c 314 g 156 t

ORIGIN

Alignment Scores:

Pred. No.: 3.5e-114 Length: 1103

Score: 1416.00 Matches: 295

Percent Similarity: 90.36% Conservative: 5

Best Local Similarity: 88.86% Mismatches: 24

Query Match: 81.80% Indels: 9

DB: 14 Gaps: 3

US-09-709-103-3F1 (1-332) x BM920514 (1-1103)

QY 3 ProSerGlyAlaGlyAlaProSerProSerArgAlaGlnProGluGlnSerProProAla 22

Db 54 CCGAGCGGAGCGGAGCGCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 113

QY 23 AlaHisProAlaCysHisProSerAspProGlnProLeuSerAlaLeuSerAlaPro 42

Db 114 GCTCACCCTCGGCGGCTCCAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 173

QY 43 ArgProProSerArgProLeuCysProMetLysLeuAlaAlaMetLysLysMetCys 62


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Db 174 CCGCCGCCCTCGGGCCCTCTGCCCAATGAACCTGGCGGATGATCAAAAGATGTC 233
Qy 63 ProSerAspSerGluLeuSerIleProAlaLysAsnCyTYrArgMetValIleLeuGly 82
Db 234 CCGAGGAGCTCGGAGCTGATCCGGCCGCAAGAACTGTATCCGATGCTATCTCGGC 293
Qy 83 SerSerIleValGlyIleThrAlaIleValSerArgPheLeuThrGlyArgPheGluAsp 102
Db 294 TCGTCAAGGTGGCAAGACGGCCATCGTGGCGCTTCTCCACCGCGCGCTTCAGAGAC 353
Qy 103 AlaTYrThrProThrIleGluAspPheHISArgGlySerIleArgGlyGluVal 122
Db 354 GCTACACGCGCTACATCCAGAGCTTCACCGCAAGCTTCTTACTTCATCCGCGGAGGTC 413
Qy 123 TYrGluLeuAspIleLeuAspThrSerGlyAsnHISProPheProAlaMetArgArgLeu 142
Db 414 TACCACTTCGACATCTCCGACACGTCGGCAACCCGCTCCCGCGCGCGCTTC 473
Qy 143 SerIleLeuThrGlyAspValPheIleLeuValPheSerIleuAspAsnArgAspSerPhe 162
Db 474 TCCATCTCCACAGAGAGAGTTCATCTCTGTTGATCTGAGACACCTGATCTCTTC 533
Qy 163 GluGluValGlnArgLeuArgGlnGlnIleLeuAspThrIleSerCySerLeuLysAsnLys 182
Db 534 GAGAGAGTGCAGCGGCTCAGGACACATCTCTGACACCAAGCTTGCTCAAGAACAA 593
Qy 183 ThrIleGluAsnValAspValProLeuValIleCySerGlyAsnLysGlyAspArgAspPhe 202
Db 594 ACCAAGAGAAAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 653
Qy 203 TYrArgGluValAspGlnArgGlnIleGluGlnLeuValGlyAspAspProGlnArgCys 222
Db 654 TACCCGCGAGTGCAGCACCGGAGATCGACGATCGGTGGCGCGACGCCCGCGCGCTGC 713
Qy 223 AlaTYrPheGluIleSerAlaLysLysAsnSerSerIleuAspGlnMetPheArgAlaLeu 242
Db 714 GCTTACTTCGATCTCGGCGCAAGAAAG-AGCAGCCTGGAACCAAGTGTTCGCGCGCTC 772
Qy 243 PheAlaMetAlaLysLeu-ProSerGluMetSerProAspLeuHISArgLysValSerVal 262
Db 773 TTGCGCATGCGCCAGCTGCGCGCGAGATGAGCCCAAGCTTCGACCGCAAGGTCTCGGT 832
Qy 262 IGHTrCYrAspValIleuHIS-LysLysAlaLeuArgAsnLys-LysLeuLeuArgAla 281
Db 833 GCGATCTCGAGCTGCTCCACAAAGAGGCTTCGGAACCAAGAACTCTTTCGCGGC 892
Qy 282 GlySerGlyGlyGlyGlyGlyAspProGlyAspAla-----PheGlyIleValAlaPro 299
Db 893 CCGGCAACCGCGCGCGCGCGCGCGCAACCGCGCGCAACCCCTTGGCATCTGCGGACCC 952
Qy 300 Phe---AlaArgArgProSerValHIS-SerAspLeuMetTYrIleArgGlyLysAlaSer 318
Db 953 TTTCGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 1012
Qy 318 r---AlaGlySerGlnAlaLysAspLys 326
Db 1013 ACCGCCGCGNACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1040

RESULT 4
BM921737 1053 bp mRNA linear EST 12-MAR-2002
LOCUS BM921737
AGENCY NCUR 6708101 NIH_MGC_115 Homo sapiens CDNA clone IMAGE:5753301
DEFINITION 5', mRNA sequence.
ACCESSION BM921737
VERSION BM921737
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1053)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.

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TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
CONTACT Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1AM12788 row: n column: 22
High quality sequence stop: 600.
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source
location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5753301"
/clone_id="NIH_MGC_115"
/lab_host="MDH10B"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-Sport; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male testis, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb.
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH-MGC Library."
BASE COUNT 215 a 390 c 297 g 150 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 2,176-110 Length: 1053
Score: 1372.50 Matches: 277
Percent Similarity: 90.10% Conservative: 5
Best Local Similarity: 88.50% Mismatches: 22
Query Match: 79.29% Indels: 9
DB: 14 Gaps: 3
US-09-709-103-3fl (1-332) x BM921737 (1-1053)
Qy 3 ProSerGlyAlaGlyAlaProSerProSerArgAlaGlnProGlnGlnSerProProAla 22
Db 53 CCGAGCGGAGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 112
Qy 23 AlaHISProAlaCySHISProSerAspProGlnProLeuSerAlaLeuLeuSerAlaPro 42
Db 113 GCTCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 172
Qy 43 ArgProProSerArgProLeuCySProMetLysLeuAlaMetIleLysLysMetCys 62
Db 173 CCGCCGCCCTCGGGCCCTCTGCCCAATGAACCTGGCGCGGAGATGATGTC 232
Qy 63 ProSerAspSerGluLeuSerIleProAlaLysAsnCyTYrArgMetValIleLeuGly 82
Db 233 CCGAGGAGCTCGGAGCTGATCCGGCCGCAAGAACTGTATCCGATGCTATCTCGGC 292
Qy 83 SerSerIleValGlyIleThrAlaIleValSerArgPheLeuThrGlyArgPheGluAsp 102
Db 293 TCGTCAAGGTGGCAAGACGGCCATCGTGGCGCTTCTCCACCGCGCGCTTCAGAGAC 352
Qy 103 AlaTYrThrProThrIleGluAspPheHISArgGlySerIleArgGlyGluVal 122
Db 353 GCTACACGCGCTACATCCAGAGCTTCACCGCAAGCTTCTTACTTCATCCGCGGAGGTC 412
Qy 123 TYrGluLeuAspIleLeuAspThrSerGlyAsnHISProPheProAlaMetArgArgLeu 142
Db 413 TACCACTTCGACATCTCCGACACGTCGGCAACCCGCTCCCGCGCGCGCTTC 472
Qy 143 SerIleLeuThrGlyAspValPheIleLeuValPheSerIleuAspAsnArgAspSerPhe 162

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Db 473 TCCATCTCTCAGGAGACGCTTTTCATCTCTGGTGTTCAGTCTGGACACCGGACTCCTTC 532
Qy 163 GluGluValGlnArgLeuArgGlnGlnLeuAspThrLysSerCysLeuLysAsnLys 182
Db 533 GAGGAGTGCAGGGCTCAGGAGCAGAGATCTTCACACCAAGTCTTGCCTCAAGAACAAA 592
Qy 183 ThrLysGluAsnValAspValProLeuValLysCysGlyAsnLysGlyAspArgAspPhe 202
Db 593 ACCAAGAGAACGTCGAGCTGCCCTGGTCTCTCGGCAACAGGCTGCCCGGACTTC 652
Qy 203 TyrArgGluValAspGlnArgGluLeuLeuValGlyAspAspProGlnArgCys 222
Db 653 TACCGGAGGTGCACACCGGAGATCGAGCAGTGTGGCGCAGCACCAGCGCTGC 712
Qy 223 AlaTyrPheGluLeuSerAlaLysAsnSerSerLeuAspGlnMetPheArgAlaLeu 242
Db 713 GCCTACTTTCGAGATCTCGGCCAAAAGAACAGCAGACCTGCACCGCAAGGGTCTCGG 772
Qy 242 uPheAlaMetAlaLysLeuProSerGluMetSerProAspLeuHisArgLys---Valse 261
Db 773 CTGCGCATGCCCAAGTGTCCAGCGAGATGAGCCAGACCTGCACCGCAAGGGTCTCGG 832
Qy 261 rValGlnTyrCysAspValLeuHisLysLys---AlaLeuArgAsnLysLysLeuLeuAr 280
Db 833 GGCAGTACTGCGCAGCTGTGCACAAAAGAGGGCTGCGGGAACAAAACACTGCTGCG 892
Qy 280 g-AlaGlySer-----GlyGlyGlyGlyGlyAspProGlyAspAlaPheG 295
Db 893 GGGCGGTATACCGTGTGGCGGCGCGGAGGAAACCGGCGCAACCCCTTTGGGGAATCG 952
Qy 295 lylleValAlaPropheAlaArgArgProSerVal 306
Db 953 GGGGCAACCTTCTGTGGGCGCGGAGCAACAGGTA 987

RESULT 5
LOCUS AL533318
DEFINITION AL533318 LTI_FLO15_Brn1 Homo sapiens cDNA clone CS0DN003YJ19 5
prime, mRNA sequence.
ACCESSION AL533318
VERSION AL533318.1 GI:12796811
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li.W.B., Gruber.C., Jesse,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. 965
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DN003YJ19"
/clone_lib="LTI_FLO15_Brn1"
/sex="male"
/tissue type="Adult brain"
/notes="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo (dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was constructed by Life Technologies.
Contact : Feng Liang Life Technologies, a division of
Invitrogen 9800 Medical Center Drive Rockville, Maryland
20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 189 a 352 c 273 g 144 t 7 others

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ORIGIN

Alignment Scores:
 Score: 4.83e-110 Length: 965
 Pred. No.: 1368.00 Matches: 282
 Percent Similarity: 95.00% Conservative: 3
 Best Local Similarity: 94.00% Mismatches: 14
 Query Match: 79.03% Indels: 5
 DB: 9 Gaps: 1

US-09-709-103-3P1 (1-332) x AL533318 (1-965)

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Qy 3 ProSerGlyAlaGlyValaProSerProSerArgAlaGlnProGluGlnSerProAla 22
Db 44 CCGAGCGGAGCGGAGCCCAAGCCCGAGCGCGCCGAGCAGAGCCCTCCAGCC 103
Qy 23 AlaHisProAlaCysHisProSerAspProGlnProLeuSerAlaLeuLeuSerAlaPro 42
Db 104 GCTCACCCCGGTGCCACCCCGAGCGACCTCAGCCGCTCTCTGCCCCCTTCTTCGGCCCTG 163
Qy 43 ArgProProSerArgProLeuCysProMetLysLeuAlaAlaMetLysLysMetCys 62
Db 164 CGCCCGCCCTCGCGGCCCTCTGCCCAATGAACTGGCCGCGATGATCAAGAAGATGTC 223
Qy 63 ProSerAspSerGluLeuSerIleProAlaLysAsnCysTyrArgMetValIleLeuGly 82
Db 224 CCGAGCGGACTCGGAGCTGAGTATCCCGGCCCAAGACTGATATCGCATGGTTCATCTCGGC 283
Qy 83 SerSerLysValGlyLysThrAlaIleValSerArgPheLeuThrGlyArgPheGluAsp 102
Db 284 TCGTCCAGGTGGGCAAGACGGCCATCGTGTGCGCTTCTCACCGGCGCTTCGAGGAC 343
Qy 103 AlaTyrThrProThrIleGluAspPheHisArgLysPheTyrSerIleArgGlyGluVal 122
Db 344 GCCTACAGCTACCATCGAGACTTCCACCGCAAGTCTACTCATCCGCGGCGAGGTC 403
Qy 123 TyrGlnLeuAspIleLeuAspThrSerGlyAsnHisProPheProAlaMetArgArgLeu 142
Db 404 TACCAGCTCGACATCTCCGACAGCTCCGCGCAACCAACCGCTTCCCGCGCATGCG-CGCTC 462
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Db 463 TCCATCTCACAGGAGAGCTTTTCATCTCTGGTTCAGTCTGGACAAACCGGACTCCTTC 522
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Qy 183 ThrLysGluAsnValAspValProLeuValIleCysGlyAsnLysGlyAspArgAspPhe 202
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Qy 203 TyrArgGluValAspGlnArgGluIleGluLeuValGlyAspAspProGlnArgCys 222
Db 643 TACCGGAGGTGGACCGCGAGATCGAGCAGTGTGGCGCAGCACCACCGCGCTGC 702
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Db 763 TCCGCCATGCGCAAGTGTGCCAGCAGATGAGCCAGACCTGCACCGCAAGTCTTCGGTG 821
Qy 263 GlnTyrCysAspValLeuHisLysLysAlaLeuArgAsnLysLysLeuLeuArgAlaGly 282
Db 822 CAGTACTGCGAGCTGTGCAAAARAARGCGCTGCGGAACAA-AARCTGCTCGGCGCGCA 880
Qy 283 SerGlyGlyGlyGlyAspProGlyAspAlaPheGlyIleValAlaProPheAlaArg 302
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RESULT 6

BM543630 1023 bp mRNA linear EST 20-PEB-2002
 LOCUS 6492527 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5726764
 DEFINITION 5', mRNA sequence.
 ACCESSION BM543630
 VERSION BM543630.1 GI:18774186
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1023)
 NIH-MGC http://mgs.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgabbs-remail.nih.gov
 Tissue Procurement: Invitrogen
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM12719 row: m column: 05
 http://image.llnl.gov
 Location/Qualifiers
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 /organism="Homo sapiens"
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 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMV-Sport6; Site: 1: EcorV
 (destroyed); Site 2: NotI; RNA source male hippocampus,
 age 27. Library is oligo-dT primed and directionally
 cloned (EcorV site is destroyed upon cloning). Average
 insert size 1.4 kb, insert size range 0.9-4 kb. Library is
 normalized and enriched for full-length clones and was
 constructed by C. Gruber (Invitrogen). Research Genetics
 tracking code 012."
 BASE COUNT 196 a 378 c 281 g 168 t
 ORIGIN
 Alignment Scores:
 Pared. No.: 6.36e-105 Length: 1023
 Score: 1310.00 Matches: 271
 Percent Similarity: 85.98% Conserved: 5
 Best Local Similarity: 84.42% Mismatches: 30
 Query Match: 75.68% Indels: 15
 DB: 13 Gaps: 3
 US-09-709-103-3f1 (1-332) x BM543630 (1-1023)
 QY 3 ProSeGjYlAGlYAlAProSeRProSeRArgAlAGlProGluGlnSerProProAla 22
 Db 2 CCGGCGGAGAGCCGAGCCCAAGCCGAGCCGAGCCGAGCCGAGGAGGAGGAGGAGG 61
 QY 23 AlAhiaProlaCyShisPProSeRArgProGlnProLeuSerAlaLeuSerAlaPro 42
 Db 62 GCTCACCCCGGTCGACCCAGGAGCCCTCAGCCGCTCTCTCCCTTCTCCGCGCCG 121
 QY 43 ArgProPProSeRArgProLeuCyPProMeLysLeuAlaLamelleLysLysMetCyS 62
 Db 122 CGCCGCGCTCCGCGCCCTCTGCGCAATGAATGCGCCGCGATGATCAAGAGATGTC 181
 QY 63 ProSeRArgPProSeRArgProLeuSerAlaLeuSerAlaLeuSerAlaLeuSerAla 82
 Db 182 CCGAGCGAGCTCGAGCTAGTATCCCGGCAAGAGCTGATGATGATGATGATGATGAT 241
 QY 83 SerSerLysValGlyLysThrAlaLeuSerAlaLeuSerAlaLeuSerAlaLeuSerAla 102

Db 242 TCGTCAAGGTGGCAAGACGCGCATCGTTCGCGCTTCTCACCAGCGCCCTTGAGAGAC 301
 QY 103 AlAtYrThProThrlLgluAspPheHisArgLysPheYrSerLysArgGlyGluVal 122
 Db 302 GCTTACACGCTTCCATCCAGAGACTTCCACCCGAGAGTTCTTATCTCCATCCGCGGAGGTC 361
 QY 123 TyrGlnLeuAspLleLeuAspThrSerGlyAsnHisPProPheProAlaMetArgArgLeu 142
 Db 362 TACCAAGCTCGACATCTTCGACACGTCGCGCAACACCCGCTTCCCGCAATGCGCGCTTC 421
 QY 143 SerLleuThrGlyAspValPheLleuValPheSerLeuAspAsnArgAspSerPhe 162
 Db 422 TCCATCTCCACAGAGACGTTTTCATCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 481
 QY 163 GluGluValGlnArgLeuArgGlnLleLeuAspThrLysSerCyPLeuLysAsnLys 182
 Db 482 GAGAGGTGCGAGCGCTCAGGACAGCATCTGACACCAAGCTTGTGCTCAAGACAA 541
 QY 183 ThrLysGluAsnValAspValProLeuValLleCySgLYAsnLysgLYAspArgAspPhe 202
 Db 542 ACCAAGAGAGAACGTGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601
 QY 203 TyrArgGluValAspGlnArgGlnLleGluLleuValGlyAspAspProGlnArgCyS 222
 Db 602 TACCGGAGGTGAGACCAAGGAGATCGAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 661
 QY 223 AlAtYrPheGluLleSerAlaLysLysAsnSerSerLeu-AspGlnMetPheArgAlaLe 242
 Db 662 GCTTACTTCGAGATCTCGGCGCAAGAAACACAGCTTGGGACAGATGTTCCGCGGCT 721
 QY 242 unPheAlaMetAla-LysLeu-ProSeRglnMetSerProAspLeuHisArgLys---Val 260
 Db 722 CTTCCTCCATGCGCCCAAGCTGCGCGCGAGATGAGCCAGACCTGACCGCGCAAGTTC 781
 QY 261 SerValGlnTyrCyS---AspValLeuHisLysLysAlaLeuArgAsnLysLysLeu 279
 Db 782 GGTGCGAGTACTGCGGACCGCGCTGCGCAAGAAAGGCGCTGGGGAACACAGAACTG 841
 QY 280 ArgAlaGlySerGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 289
 Db 842 GCTGTCGGGCGCGGCAATCGCGGGGCTCTCTTATGATTAACCTTGACCGAAGAGC 901
 QY 290 ProGlyAspAlaPheGlyLleValAlaProPheAlaArgProSeRValHisSer 308
 Db 902 CTTGGGCGAGCTGAGGCGCACATTTTCCGAGACAGTCCGCTCTTGTGTATCC 958
 RESULT 7
 B0067637 1032 bp mRNA linear EST 02-APR-2002
 LOCUS 6759053 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5755214
 DEFINITION 5', mRNA sequence.
 ACCESSION B0067637
 VERSION B0067637.1 GI:19896683
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1032)
 NIH-MGC http://mgs.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgabbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM12793 row: n column: 15
 High quality sequence stop: 602.

QY 63 ProSerAspSerGluLeuSerIleProAlaLysAsnCysTyrArgMetValIleLeuGly 82
 Db 253 CCGAGCGAGTCCGAGCTAGTATCCGCGCAAGAACTCTATCGCATGGTCTCTCGGC 312
 QY 83 SerSerLysValGlyLysThrAlaIleValSerArgPheLeuThrGlyArgPheGluAsp 102
 Db 313 TCGTCCAAAGTGGCAAGACGCCATCGTGTGCGCTTCCTCACCGCGCGCTTCGAGGAC 372
 QY 103 AlaTyrThrProThrIleGluAspPheHisArgLysPheTyrSerIleArgGlyVal 122
 Db 373 GCTTACACGCTTACCATCGAGGACTTCACCGCAAGTTCTACTCCATCCGCGCGCGAGTC 432
 QY 123 TyrGlnLeuAspIleLeuAspThrSerGlyAsnHisProPheProAlaMetArgArgLeu 142
 Db 433 TACCAGCTCGATCTCGACAGCTCCGCGCAACACCGCTTCCTCCCGCATCGCGCGCTC 492
 QY 143 SerIleLeuThrGlyAspValPheIleLeuValPheSerLeuAspAsnArgSerPhe 162
 Db 493 TCAATCTCTACAGGAGAGCTTTTCACTCTGTTGTTCACTGTGAGTGGACAAACCGCGACTCTTC 552
 QY 163 GluGluValGlnArgLeuArgGlnGlnIleLeuAspThrLysSerCysLeuLysAsnLys 182
 Db 553 GAGGAGGTGCAGCGCTCAGGCGACAGATCTCTGACACCAAGTCTTGCTCAAGAACAA 612
 QY 183 ThrLysGluAsnValAspValProLeuValIleCysGlyAsnLysGlyAspArgAspPhe 202
 Db 613 ACCAAGGAGAACGTGGAGCTGCCCTGTGTCATCTGCGGCAACAAAGGTGACCGCGACTTC 672
 QY 203 TyrArgGluValAspGlnArgGluIleGlnLeuValGlyAspAsp-ProGlnArgCy 222
 Db 673 TACCGGAGGTGGACCGCGGAGATCGAGCAGCTGTGTGGGGCGAGACCCCGCGCGCTG 732
 QY 222 sAlaTyrPheGlu-IleSerAlaLysLysAsnSerSerLeuAspGlnMetPheArgAlaL 242
 Db 733 CGCCTACTTCAGAAATCTCGGCCAAGAACACGACCCG-GACCAGATGTC-CGCGCGC 790
 QY 242 euPheAlaMetAlaLysLeu 248
 Db 791 TCTTCGCCCATGGCAAGCTG 810

RESULT 10
 AW028127
 LOCUS
 DEFINITION
 wv26c07.x1 NCI_CGAP Kid11 Homo sapiens cDNA clone IMAGE:2530668 3',
 similar to TR:035626 035626 RAS, DEXAMETHASONE-INDUCED 1 ;, mRNA
 sequence.
 AW028127
 VERSION
 EST.
 SOURCE
 human.
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 742)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL
 Unpublished (1997)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Sequencing by: Greg Lennon, Ph.D.
 Clone Distribution: NCI-CGAP University Genome Sequencing Center
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: -40UP from Gibco
 High quality sequence stop: 445.
 Location/Qualifiers
 1. .742

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2530668"
 /clone_lib="NCI_CGAP_Kid11"
 /lab_host="DH10B"
 /note="Organ: kidney; Vector: p77T3D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not 1; Site 2: Eco RI;
 Plasmid DNA from the normalized library NCI_CGAP Kid3 was
 prepared, and ss circles were made in vitro. Following HAP
 purification, this DNA was used as tracer in a subtractive
 hybridization reaction. The driver was PCR-amplified cDNAs
 from a pool of 5,000 clones made from the same library
 (clones IDs 1322376-1323911, 1456007-1456775, and
 1500552-1502855). Subtraction by Bento Soares and M.
 Fatima Bonaldo. "

BASE COUNT 149 a 260 c 208 g 122 t 3 others
 ORIGIN

Alignment Scores:
 Pred. No.: 3,25e-94 Length: 742
 Score: 1186.00 Matches: 231
 Percent Similarity: 95.93% Conservative: 5
 Best Local Similarity: 93.90% Mismatches: 10
 Query Match: 68.52% Indels: 0
 DB: 10 Gaps: 0

US-09-709-103-3F1 (1-332) x AW028127 (1-742)

QY 41 AlaProArgProSerArgProLeuCysProMetLysLeuAlaMetIleLysLys 60
 Db 2 GCCCGCGCGCGCTCGCGCGCCCTCTGCCCATGAACTGGCCGCGATGATCAAGAG 61
 QY 61 MetCysProSerAspSerGluLeuSerIleProAlaLysAsnCysTyrArgMetValIle 80
 Db 62 ATGTCGCCGAGCGACTCGGAGCTGAGTATCCGCGCAAGACTGCTATCGCATGTCATC 121
 QY 81 LeuGlySerSerLysValGlyLysThrAlaIleValSerArgPheLeuThrGlyArgPhe 100
 Db 122 CTGGCTCTCGAAGTGGCAAGACGCGCATCGTGTGCGCTTCTCCTCGCGCGCTTC 181
 QY 101 GluAspAlaTyrThrProThrIleGluAspPheHisArgLysPheTyrSerIleArgGly 120
 Db 182 GAGGAGCGCTTACACGCTACCATCGAGGACTTCCACCGCAAGTCTTACTCCATCCGCGC 241
 QY 121 GluValTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisProPheProAlaMetArg 140
 Db 242 GAGTCTTACGAGCTCGACATCTCTGACACGCTCCGCAACACCCGCTTCCCGCCATGCGG 301
 QY 141 ArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSerLeuAspAsnArgAsp 160
 Db 302 CGCCTCTCCATCTCACAGGAGACGTTTTCATCTCTGTTGTTTCAGTCTGGACACCGCGAC 361
 QY 161 SerPheGluGluValGlnArgLeuArgGlnGlnIleLeuAspThrLysSerCysLysLys 180
 Db 362 TCCCTTCGAGGAGTGCAGCGCTCAGGCGAGCATCTCCGACCAAGTCTTGGCTCAAG 421
 QY 181 AsnLysThrLysGluAsnValAspValProLeuValIleCysGlyAsnLysGlyAspArg 200
 Db 422 AACAAACCAAGAGAACGTGACGTGCCCTCTGTCATCTCGGCAACCAAGGGTGACGC 481
 QY 201 AspPheTyrArgGluValAspGlnArgGluIleGluGlnLeuValGlyAspAspProGln 220
 Db 482 GACTTCTACCGGAGTGGACCGCGCGAGATCGAGCAGCTGGTGGCGAGCACCCCGCAG 541
 QY 221 ArgCysAlaTyrPheGluIleSerAlaLysLysAsnSerSerLeuAspGlnMetPheArg 240
 Db 542 CGCTGCGCTACTTTCAGATCTTCGCAAGAGAACACGACGCTGGACCATGTTTCCGC 601
 QY 241 AlaLeuPheAlaMetAlaLysLeuProSerGluMetSerProAspLeuHisArgLysVal 260
 Db 602 GCGCTCTTCGCATGCGCCAGCTGCCAGCAGATGAGCCAGACCTGACCCCGCAAGGTC 661
 QY 261 SerValGlnTyrCysAspValLeuHisLysLysAlaLeuArgAsnLysLysLeuLeuArg 280


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Db 662 TCNGTGAAGTACCTGAGCGTCCCTGCACAGAGCGCTGCCGAAGAAGAGCTGTGCGG 721
Qy 281 AAGlyserglyglygly 286
Db 722 TCCGACAGCGGCGTGGT 739

RESULT 11
BM805574 1160 bp mRNA linear EST 05-MAR-2002
LOCUS AGENCOURT 6498388 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5729129
DEFINITION 5', mRNA sequence.
ACCESSION BM805574
VERSION BM805574.1 GI:19122397
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1160)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM12725 row: o column: 18
High quality sequence stop: 23
High quality sequence stop: 501.
Location/Qualifiers
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/clone="IMAGE:5729129"
/clone_11b="NIH_MGC_124"
/tissue_type="hippocampus"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pCMV-SPORT6; Site: 1: EcoRV
(destructed); Site 2: NotI; RNA source male hippocampus,
age 27. Library is oligo-dT primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 1.4 kb, insert size range 0.9-4 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 012."

BASE COUNT 207 a 473 c 279 g 201 t
ORIGIN

Alignment Scores:
Pred. No.: 1..92e-92 Length: 1160
Score: 1168.50 Matches: 229
Percent Similarity: 94.55% Conservative: 14
Best Local Similarity: 89.11% Mismatches: 10
Query Match: 67.50% Indels: 4
DB: 14 Gaps: 1

US-09-709-103-3f1 (1-332) x BM805574 (1-1160)
Qy 3 ProSerGlyAlaGlyAlaProSerProSerArgAlaGlnProGlnGlnSerProProAla 22
Db 50 CCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 109
Qy 23 AlaHisProAlaGlyHisProSerArgProGlnProLeuSerAlaLeuSerAlaPro 42
Db 110 GCTACCCCGGCTGCGACCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 169
Qy 43 ArgProSerArgProLeuCyProMetLeuAlaMetLeuLysLysMetCys 62

FEATURES
source 1..831
Location/Qualifiers

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Db      61 GTGGGCAAGACGGCCATCGTGTGCGCTTCTTCACCGCGCGCTTCGAGAGACGCCCTACAGC 120
Qy      106 ProthrillegluaspPheH1sArgLysPheTySer11leargLylgluVal1TyrgInleu 125
Db      121 CTRACATTCAGAGACTTCCACCGCAAGTCTACTCCATCCGCGCGAGGTCTACAGCTTC 180
Qy      126 Aspl1leuaspThrseryAsnH1sProPheProAlaMetArGArgLeuSer11leu 145
Db      181 GACATCTCGACAGCTCCGGCAACACCCGTTCCCGCCATCGCGCCCTCTCATCTTC 240
Qy      146 ThrglYAspVal1Phe1leuVal1PheSerleuaspAsnH1sArgSerPhegluVal 155
Db      241 ACAGAGACAGCTTTTCATCTCTGTGTTCAGTGTGACAAACCGGACTCTTCGAGAGAGTG 300
Qy      166 GluHArgLeuArgInglIn1leuaspThrlYsSerCySleuLysAsnLysThrlYsGlu 185
Db      301 CAGGGGCTCAGAGCAGATCCTCGACACCAAGTCTTGCTCAAGAAACAAACCAAGGAG 360
Qy      186 AsnValAspVal1ProleuVal11leCyaglYAsnLysglYAspArGAspPheTyArgGlu 205
Db      361 AACGTGACGTGCCCTGTGTCTGTGCGGCAACAAAGGTGACCCGACTTCTACCGGAG 420
Qy      206 ValAspGlnArgGlu1leuGluInleuVal1glYAspAspProGlnArgCySAlATyrPhe 225
Db      421 GTGACCAAGCGGAGATCGAGCAGCTGGTGGGCGACGACCCCGAGCGCTGCGCTACTTC 480
Qy      226 Glu1leSerAlaLysLysAsnSerSerleuaspGlnMetPheArgAlaLeuPheAlaMet 245
Db      481 GAGATCTCGCGCCAAAGAACGAGCCTGAGCCAGATGTTCCGGCGCTCTTCGCCATG 540
Qy      246 AlaLysleuProSerGlnMetSerProAspLeuH1sArgLysVal1SerVal1GlnTyrCys 265
Db      541 GCGAAGCTGCCAGAGCATGAGCCAGACCTGCCCGGAAAGTCTCGGTGAGAAATGC 600
Qy      266 AspVal1leuH1sLysLysAlaLeuArgAsnLysLysleuLeuArg-AlaGlySerGly-G 285
Db      601 GACGTCTCTCAACAGAGCGCTGCGGAAACAAAGCTGCTCGGCGCGGCAACGAGAG 660
Qy      285 lYglYglYglYAspPro---GlyAspAlaPheGly11leValAlaPhePheAlaAGArg 303
Db      661 GCCGCGCGCTGAGCCCGCGGAGACCTTTTGGGATCGGGGGCCCCCTTTCGGCGCG 719

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RESULT 14      699 bp      mRNA      linear      EST 07-MAY-2001
LOCUS      BG706012
DEFINITION      602669154Fl NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4792069 5',
                mRNA sequence.
ACCESSION      BG706012
VERSION      BG706012.1 GI:13980932
KEYWORDS
SOURCE
ORGANISM      human.
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS      1 (bases 1 to 699)
TITLE      NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL      National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT      Unpublished (1999)
                Contact: Robert Strausberg, Ph.D.
                Email: cgaabs-r@mail.nih.gov
                Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
                cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki
                Toshitaki and Piero Carninci (RIKEN)
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: Incyte Genomics, Inc.
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
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                Location/Qualifiers
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/tissue_type="hypothalamus"
/lab_host="DH10B"
/notes="Organ: brain; Vector: Bluescript (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTAA-3',
size selected for average insert size 2.3 kb and
normalized to ROP 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC library."
BASE COUNT      135 a      270 c      189 g      104 t
ORIGIN
Alignment Scores:
Pred. No.:      1,94e-86      Length:      699
Score:      1097.00      Matches:      209
Percent Similarity:      100.00%      Conservative:      0
Best Local Similarity:      100.00%      Mismatches:      0
Query Match:      63.37%      Indels:      0
DB:      12      Gaps:      0
US-09-709-103-3fl (1-332) x BG706012 (1-699)

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Qy      3 ProSerGlyAlaGlyAlaProSerProSerArGAlaGlnProGluGlnSerProProAla 22
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Qy      23 AlaH1sProAlaGlyH1sProSerAspProGlnProleuSerAlaLeuDeuSerAlaPro 42
Db      131 GCTCACCCCGGTGACACCCACGACCTTCAGCCGCTCTGCTGCTTCGCGCCCG 190
Qy      43 ArgProProSerArgProleuCySPrometLysLeuAlaAlaMetLysLysMetCys 62
Db      191 CGCCCGCCCTCGGGGCCCTCTGCCCAATGAACCTGGCCGATGATCAAGAAAGTGC 250
Qy      63 ProSerAspSerGluLeuSer11leProAlaLysAsnCyTyArgMetVal11leuGly 82
Db      251 CCGAGCAGCTCGGAGCTGAGTATCCCGGCCAAGACTGCTATGCAATGATCTCTCGG 310
Qy      83 SerSerLysVal1GlyLysThrlAla1leVal1SerArGpHeuThrgLylArgPhegluasp 102
Db      311 TCGTCAAGGTGGCAAGACGCCCATGTCTCGGCTCTTCACCGCGCTTCGAGAGAC 370
Qy      103 AlaTyrThrProthrillegluaspPheH1sArgLysPheTySer11leargLylgluVal 122
Db      371 GCTTACAGCCTTACCATCGAGACTTCACCGCAAGTCTTACTTCATCCCGCGAGGTC 430
Qy      123 TyrGlnleuasp11leuaspThrseryAsnH1sProPheProAlaMetArGArgLeu 142
Db      431 TACAGCTCGACATCTCGACATCCGGAACCAACCCGTTCCCGGCATCGCGCGCTC 490
Qy      143 Ser1leuThrgLylAspVal1Phe1leuVal1PheSerleuaspAsnH1sArgSerPhe 162
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Qy      163 GluGluVal1GlnArgLeuArgInglIn1leuaspThrlYsSerCySleuLysAsnLys 182
Db      551 GAGGAGGTGAGCGGCTCAGACAGATCTTCACACCAAGTCTTCCTCAAGAAACAA 610
Qy      183 ThrlYsGluAsnValAspVal1ProleuVal11leCyaglYAsnLysglYAspArGAspPhe 202
Db      611 ACCAAGAGAAAGTGAAGTGCCTCCCTGTGTCTGTGCGGCAACAAAGGTGACCCGAGCTTC 670
Qy      203 TyrArgGluValAspGlnArgGlu1le 211
Db      671 TACCGGAGGTGACCAAGCGGAGATC 697
RESULT 15
BG709229

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LOCUS BG709229 699 bp mRNA linear EST 07-MAY-2001
DEFINITION 602674615F1 NIH_MGC_96 Homo sapiens CDNA clone IMAGE:4797482 5',
mRNA sequence.
ACCESSION BG709229
VERSION BG709229.1 GI:13987357
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 699)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM10683 row: m column: 03
High quality sequence stop: 699.
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/clone_lib="NIH_MGC_96"
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/lab_host="DH10B"
/notes="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-xhoI (gtcagag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.3 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
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ORIGIN

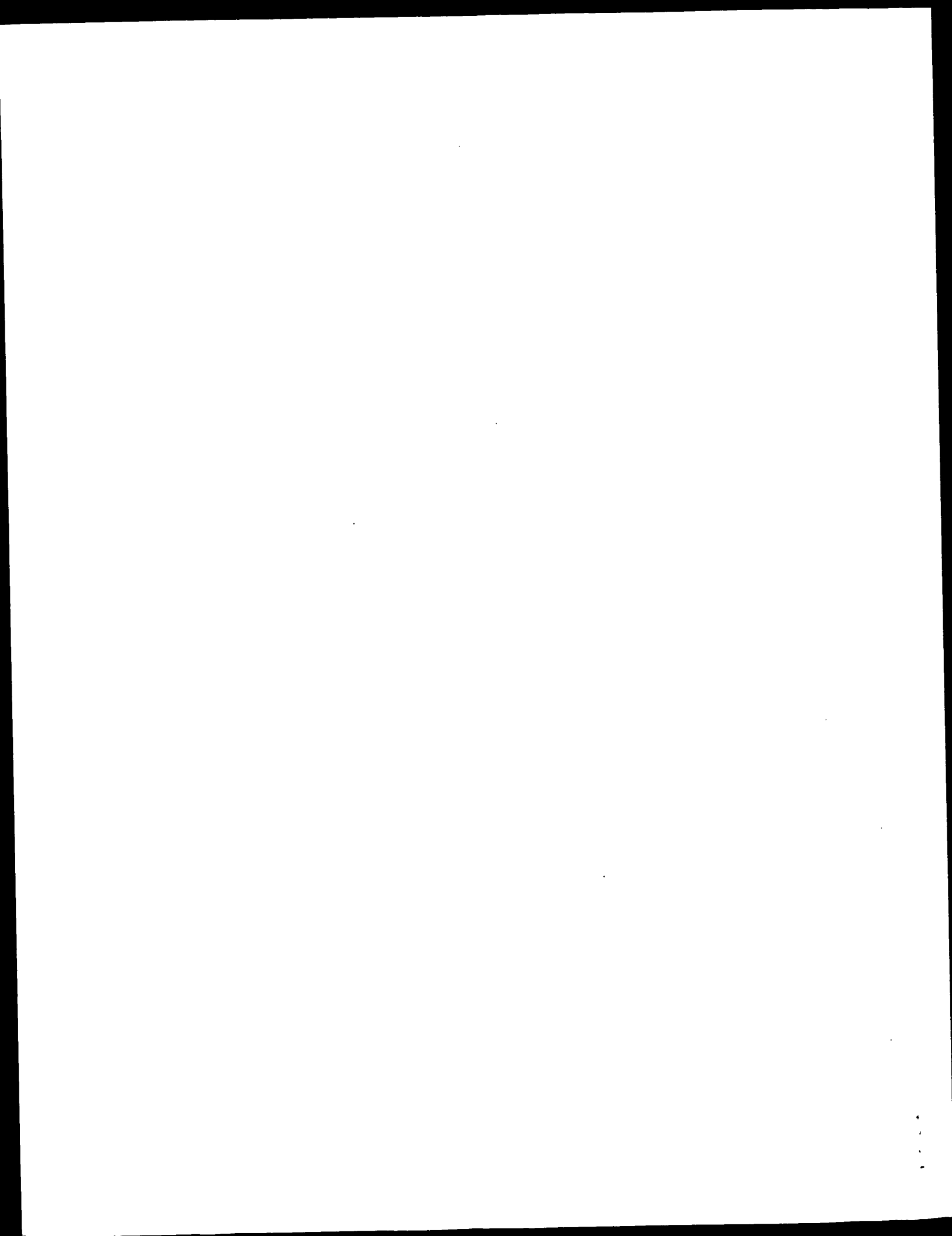
Alignment Scores:
Pred. No.: 3,71e-84 Length: 699
Score: 1071.00 Matches: 209
Percent Similarity: 99.05% Conservative: 0
Best Local Similarity: 99.05% Mismatches: 0
Query Match: 61.87% Indels: 2
DB: 12 Gaps: 0

US-09-709-103-3Fl (1-332) x BG709229 (1-699)

QY 3 ProSerGlyAlaGlyAlaProSerProSerArgAlaGln-ProGluGlnSerProAl 22
Db 71 CCGAGCGGAGCGGAGCGCCCAAGCGCGAGCGCCCGCCAGCCCTGAGCAGCCCTCCAGC 130
QY 22 aAlaHisProAlaCysHisProSerAspProGlnProLeuSerAlaLeuLeuSerAlaPr 42
Db 131 CGCTACCCCGCGGTGCCACCCAGGAGCCCTCAGCGGCTCTCTGCCCTCTCTCGGCCCC 190
QY 42 oArgProProSerArgProLeuCysProMetLysLeuAlaMetLysLysMetCy 62
Db 191 GCGCCCGCCCTCGCGGCCCTCTGCCCAATGAACTGGCCGCGATGATCAAGAAGATGTG 250
QY 62 sProSerAspSerGluLeuSerIleProAlaLysAsnCysTyrArgMetValIleLeuGl 82
Db 251 CCGGAGCGACTCGGAGCTGAGTATCCCGGCCAAGAACTGCTATCGCAIGGTGTCCTCGG 310
QY 82 y-SerSerLysValGlyLysThrAlaIleValSerArgPheLeuThrGlyArgPheGluA 102

Db 311 ACTCGTCCAAGTGGGGAAGCGCCATCGTGTGCGCTTCTCACCGCGGCTTCGAGG 370
QY 102 spAlaTyrThrProThrIleGluAspPheHisArgLysPheTyrSerIleArgGlyGluV 122
Db 371 ACGCCTACAGCGCTACCATCGAGACTTCCACCGCAAGTTCTACTCTCATCCGCGGCGAGG 430
QY 122 alTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisProPheProAlaMetArgArgL 142
Db 431 TCTACCACTCGACATCTCTGACAGCTCCGCGCAACACCGCTTCCCGCCATCGCGGCC 490
QY 142 euSerIleLeuThrGlyAspValPheIleLeuValPheSerLeuAspAsnArgAspSerP 162
Db 491 TCTTCATCTCACAGGAGACGTTTTCATCTGCTGTTTTCAGTCTGGACCAACCGCGACTCCT 550
QY 162 heGluGluValGlnArgLeuArgGlnGlnIleLeuAspThrLysSerCysLeuLysAsnL 182
Db 551 TCGAGGAGTGCAGCGCTCAGGCGAGCATCTTCGACACCAAGTCTTGCTCAAGAAC 610
QY 182 ysThrLysGluAsnValAspValProLeuValIleCysGlyAsnLysGlyAspArgAsp 202
Db 611 AAACCAAGGAGAACCTGGACGTGCCCTGCTGTCATCTGCGGCAACAAAGGTGACCGGACT 670
QY 202 heTyrArgGluValAspGlnArgGluIle 211
Db 671 TCTACCGGAGGTGGACCGCGGAGATC 699

Search completed: December 30, 2002, 19:42:40
Job time : 2189 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 30, 2002, 18:06:06 ; Search time 76 Seconds
(without alignments)
1339.693 Million cell updates/sec

Title: US-09-709-103-3F1

Perfect score: 1731

Sequence: 1 GIPGAGAPSPRAQPEQSP.....IREKASAGSQAQKRCRVIS 332

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-O=/cgn2_1/USPRO.spool/SULLIVAN3F1/runat_30122002.144155.22165/app_query.fasta_1.519
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=SULLIVAN3F1 @CNG 1.1 31 @runat_30122002.144155.22165 -NCPU=6 -ICPU=3
-NO XLPXY -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*

1: /cgn2_6/prodata/1/ina/5A.COMB.seq:*

2: /cgn2_6/prodata/1/ina/5B.COMB.seq:*

3: /cgn2_6/prodata/1/ina/6A.COMB.seq:*

4: /cgn2_6/prodata/1/ina/6B.COMB.seq:*

5: /cgn2_6/prodata/1/ina/6C.COMB.seq:*

6: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1713	99.0	1841	4	US-09-053-374A-1
2	1651	95.4	3986	4	US-09-053-374A-3
3	1435.5	82.9	1689	4	US-09-053-374A-4
4	1388.5	80.2	3079	4	US-09-053-374A-6
5	300	17.3	615	1	US-08-247-946A-5
6	300	17.3	615	5	PCT-US95-06420-5
7	279	16.1	5775	1	US-08-306-691B-15
8	279	16.1	5775	5	PCT-US93-06251-29
9	277.5	16.0	570	4	US-08-884-866A-2
10	277.5	16.0	570	4	US-08-884-866A-11
11	276	15.9	607	2	US-08-429-964-85
12	275.5	15.9	480	4	US-08-884-866A-9
					Sequence 1, Appli
					Sequence 3, Appli
					Sequence 4, Appli
					Sequence 5, Appli
					Sequence 6, Appli
					Sequence 7, Appli
					Sequence 8, Appli
					Sequence 9, Appli
					Sequence 10, Appli
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					Sequence 36, Appli
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					Sequence 38, Appli
					Sequence 39, Appli
					Sequence 40, Appli
					Sequence 41, Appli
					Sequence 42, Appli
					Sequence 43, Appli
					Sequence 44, Appli
					Sequence 45, Appli

13	275.5	15.9	4480	4	US-09-167-322-12	Sequence 12, Appli
14	266.5	15.4	450	4	US-08-884-866A-10	Sequence 10, Appli
15	266.5	15.4	574	2	US-08-429-964-83	Sequence 83, Appli
16	265.5	15.3	2436	1	US-08-306-691B-16	Sequence 16, Appli
17	237	13.7	2309	3	US-09-078-317-3	Sequence 3, Appli
18	237	13.7	2309	3	US-09-454-818-3	Sequence 3, Appli
19	234.5	13.5	600	3	US-09-078-317-1	Sequence 1, Appli
20	234.5	13.5	600	4	US-09-454-818-1	Sequence 1, Appli
21	220	12.7	3497	4	US-09-503-505A-2	Sequence 2, Appli
22	219.5	12.7	563	4	US-09-385-982-426	Sequence 426, App
23	203	11.7	897	2	US-09-006-535-2	Sequence 2, Appli
24	203	11.7	1525	2	US-09-006-535-1	Sequence 1, Appli
25	201	11.6	6453	1	US-08-306-691B-14	Sequence 14, Appli
26	201	11.6	6453	3	US-09-209-668-10	Sequence 10, Appli
27	201	11.6	6453	3	US-09-356-952-8	Sequence 8, Appli
28	198	11.4	897	2	US-09-006-535-7	Sequence 7, Appli
29	193	11.1	1443	1	US-08-076-089-1	Sequence 1, Appli
30	193	11.1	1443	2	US-08-707-200-1	Sequence 1, Appli
31	193	11.1	1443	4	US-08-896-565-1	Sequence 1, Appli
32	193	11.1	1443	5	PCT-US93-05643-1	Sequence 1, Appli
33	188	10.9	702	3	US-08-842-976-2	Sequence 2, Appli
34	188	10.9	702	3	US-09-213-397-2	Sequence 2, Appli
35	188	10.9	702	3	US-09-416-489-2	Sequence 2, Appli
36	187	10.8	1098	2	US-08-948-616-6	Sequence 6, Appli
37	187	10.8	1098	2	US-09-193-510-6	Sequence 6, Appli
38	187	10.8	1098	4	US-09-368-402-6	Sequence 6, Appli
39	185.5	10.7	2964	2	US-08-846-790A-2	Sequence 2, Appli
40	185.5	10.7	2964	3	US-08-935-333-2	Sequence 2, Appli
41	178	10.3	1074	2	US-09-156-424-1	Sequence 1, Appli
42	178	10.3	1074	4	US-09-387-341-1	Sequence 1, Appli
43	177.5	10.3	1166	5	PCT-US96-12129B-1	Sequence 1, Appli
44	175.5	10.1	603	4	US-09-325-932A-29	Sequence 29, Appli
45	175.5	10.1	932	4	US-09-325-932A-28	Sequence 28, Appli

ALIGNMENTS

RESULT 1

US-09-053-374A-1
; Sequence 1, Application US/09053374A
; Patent No. 6462177
; GENERAL INFORMATION:
; APPLICANT: YEN, KWANG-MU
; TITLE OF INVENTION: MAMMALIAN BLOOD LOSS-INDUCED GENE, KD312
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: US
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/053,374A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-514
; INFORMATION FOR SEQ ID NO. 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1841 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:

NAME/KEY: CDS
LOCATION: 255..1097
US-09-053-374A-1

Alignment Scores:
Pred. No.: 1,156-146 Length: 1841
Score: 1713.00 Matches: 329
Percent Similarity: 99.70% Conservative: 0
Best Local Similarity: 98.96% Mismatches: 1
Query Match: 98.96% Indels: 0
Gaps: 0

US-09-709-103-3f1 (1-332) x US-09-053-374A-1 (1-1841)

QY 3 ProSerGlyAlaGlyAlaProSerProSerArgAlaGlnProGluGlnSerProProAla 22
DB 108 CCGAGCGAAGCGGAGCCCGAAGCCCGAGCCCGCCGAGCAGAGCCCTCCAGCC 167
QY 23 AlaHisProAlaCyHisProSerAspProGlnProLeuSerAlaLeuLeuSerAlaPro 42
DB 168 GCTCAACCCGCGGCGCAGCCAGCAGCCTCCAGCCCTCTCTGCCCCCTCTCTGCCCCCG 227
QY 43 ArgProProSerArgProLeuCySPrometLysLeuAlaMetLysLysMetCys 62
DB 228 CGCCCGCCCTCGGCGCCCTCTCCCAATGAAACTGCGCGCATGATCAAGAGATGTC 287
QY 63 ProSerAspSerGluLeuSerLleProAlaLysAncCysTyraMetValLleLeuGly 82
DB 288 CCGAGCGACTCGAGCGAGTATCCCGCGCAAGAACTGCTATCGCATGTCTCTCCGCGC 347
QY 83 SerSerLysValGlyLysThrAlaIleValSerArgPheLeuThrglyArgPheGluAsp 102
DB 348 TCGTCGAAGTGGGCAAGACGCGCATCTGTCTGCGCTTCCACCGCGCGCTTCGAGAGC 407
QY 103 AlaTyThrProThrLleGluAspPheHisArgLysPheTyraSerLleArgGlyGluVal 122
DB 408 GCCACACGCTTACATCATCGAGACTTCCACCGCAAGTCTTACTCCATCCGCGGAGATC 467
QY 123 TyrgLnuAspLleLeuAspThrSerGlyAsnHisProPheProAlaMetArgArgLnu 142
DB 468 TACCAAGCTCGACATCTCGACAGCTCCGCGACACACCGCTCCCGCGCATGCGCGCTTC 527
QY 143 SerLleLeuThrGlyAspValPheLleLeuValPheSerLleAspAsnArgAspSerPhe 162
DB 528 TCCATCTTCAACAGAGAGCTTTTCACTCTGCTGCTTCACTGAGCAACCGCGACTCTTC 587
QY 163 GluGluValGlnArgLnuArgGlnGlnLleLeuAspThrLysSerCysLeuLysAsnLys 182
DB 588 GAGGAGGTGCAAGCGCTCGAGCGAGATCTTCCAGACCAAGTCTTCCCTCAAGAACAA 647
QY 183 ThrLysGluAsnValAspValProLeuValLleCysGlyAsnLysGlyAspArgAspPhe 202
DB 648 ACCAAGAGAGAGTGGAGCGTCCCTGCTCATCTGCGGCAACAGGGGTGAGCGGACTTC 707
QY 203 TyraGlyValAspGlnArgGlnLleGluGlnLeuValGlyAspAspProGlnArgCys 222
DB 708 TACCGGAGGTGAGCGAGCGCGAGATCGAGCTGTGTGGCGAGACACCCCGCGCTGC 767
QY 223 AlaTyThrPheGluLleSerAlaLysLysAsnSerSerLleAspGlnMetPheArgAlaLeu 242
DB 768 GCCTACTTGAATCTCGGCGCAAGAGACAGACGCTGAGACCAATGTTCCGCGCTC 827
QY 243 PheAlaMetAlaLysLeuProSerGluMetSerProAspLeuHisArgLysValSerVal 262
DB 828 TTGGCATGCGCAAGCTGCGCCAGCGAGATGAGCCAGACTTCAACCGCAAGTCTCGGTG 887
QY 263 GlnTyCysAspValLeuHisLysLysAlaLeuArgAsnLysLysLeuLeuArgAlaGly 282
DB 888 CAGAGTGCACGCTGTGCAAGAGGCGCTCGGAGAACAGAGTGTGTGCGGCGCGC 947
QY 283 SerGlyGlyGlyGlyAspProGlyAspAlaPheGlyLleValAlaProPheAlaArg 302
DB 948 AGCGCGCGCGCGCGCGAGACCGCGCGAGCGCTTTGGCATCGTGGACCTTCCGCGCGC 1007

QY 303 ArgProSerValHisSerAspLeuMetTyrlleArgGluLysAlaSerAlaGlySerGln 322
DB 1008 CGGCCGAGCTGACACAGCAGCCTCATGTATCATCCCGGAGAGCCAGCGCGGAGCCAG 1067
QY 323 AlaLysAspLysGluArgCysValLleSer 332
DB 1068 GCCAAGAGCAAGAGCGCTGCTCATCAGC 1097

RESULT 2

US-09-053-374A-3
Sequence 3, Application US/09053374A

Patent No. 6462177

GENERAL INFORMATION:
APPLICANT: YEN, KWANG-MU

TITLE OF INVENTION: MAMMALIAN BLOOD LOSS-INDUCED GENE, KD312

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.

STREET: ONE AMGEN CENTER DRIVE
CITY: THOUSAND OAKS

STATE: CA
COUNTRY: US

ZIP: 91320

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/053,374A

FILING DATE:
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.

REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-514

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

LENGTH: 3986 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-09-053-374A-3

Alignment Scores:

Pred. No.: 1,496-140 Length: 3986
Score: 1651.00 Matches: 329

Percent Similarity: 82.04% Conservative: 0
Best Local Similarity: 95.38% Mismatches: 1

Query Match: 95.38% Indels: 71
Gaps: 1

US-09-709-103-3f1 (1-332) x US-09-053-374A-3 (1-3986)

QY 3 ProSerGlyAlaGlyAlaProSerProSerArgAlaGlnProGluGlnSerProProAla 22
DB 627 CCGAGCGAAGCGGAGCCCGCAAGCCCGAGCCCGCGAGCCCGAGCAGAGCCCTCCAGCC 686
QY 23 AlaHisProAlaCyHisProSerAspProGlnProLeuSerAlaLeuLeuSerAlaPro 42
DB 687 GCTCAACCCGCGGCGCAGCCAGCAGCCTTCAGCCCTCTCTGCCCCCTCTCTGCCCCCG 746
QY 43 ArgProProSerArgProLeuCySPrometLysLeuAlaMetLysLysMetCys 62
DB 747 CGCCCGCCCTCGGCGCCCTCTCCCAATGAAACTGCGCGGAGATCAAGAGATGTC 806
QY 63 ProSerAspSerGluLeuSerLleProAlaLysAncCysTyraMetValLleLeuGly 82
DB 807 CCGAGCGACTCGAGCGTGAATCCCGCGCAAGAACTGCTATCCAGATGCTATCTCGCGC 866
QY 83 SerSerLysValGlyLysThrAlaIleValSerArgPheLeuThrglyArgPheGluAsp 102

RESULT 4
US-09-053-374A-6
Sequence 6, Application US/09053374A

APPLICANT: YEN, KWANG-MU
 TITLE OF INVENTION: MAMMALIAN BLOOD LOSS-INDUCED GENE, KD312
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: AMGEN INC.
 STREET: ONE AMGEN CENTER DRIVE
 CITY: THOUSAND OAKS
 STATE: CA
 COUNTRY: US
 ZIP: 91320
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/053,374A

1 FILING DATE:
 2 CLASSIFICATION: 435
 3 ATTORNEY/AGENT INFORMATION:
 4 NAME: COOK, ROBERT R.
 5 REGISTRATION NUMBER: 31,602
 6 REFERENCE/DOCKET NUMBER: A-514
 7 INFORMATION FOR SEQ ID NO: 6:
 8 SEQUENCE CHARACTERISTICS:
 9 LENGTH: 3079 base pairs
 10 TYPE: nucleic acid
 11 STRANDEDNESS: single
 12 TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-09-053-374A-6

Alignment Scores:	
Pred. No.:	7,79e-117
Score:	1388.50
Percent Similarity:	79.47%
Best Local Similarity:	77.60%
Query Match:	80.21%
DB:	4
Length:	3078
Matches:	291
Conservative:	27
Mismatches:	52
Indels:	4
Gaps:	

US-09-709-103-3F1 (1-332) x US-09-053-374A-6 (1-3079)

[illegible]

Qy 258 ArgLysValSerValGlnTyrCysAspValLeuHisLysLysAlaLeuArgAsnLysLys 277
 Db 1058 CGCAAGGTGTCTGTGACAGTACTGTGACGTCTGCACAAAAGGCTCTGAGGAACAAGAG 1117
 Qy 278 LeuLeuArgAlaGlySerGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 297
 Db 1118 CTTCTGCTGGCGGACGAC---GGAGGTGGGGGGGACACGAGAGTGCCTTTGGCATCTTG 1174
 Qy 298 AlaProPheAlaArgProSerValHisSerAspLeuMetTyrIleArgGluLysAla 317
 Db 1175 GCGCCCTTTGCTCGCAGACCTACGCTGCATAGCAGCCTCATGTACATTGCTGAGAAAACC 1234
 Qy 318 SerAlaGlySerGlnAlaLysAspLysGluArgCysValIleSer 332
 Db 1235 AGTGTACAGCAGCCAGGCTAAGGACAAGGAGCGCTGTGTATCATCAGT 1279

RESULT 5

US-08-247-946A-5
 ; Sequence 5, Application US/08247946A
 ; Patent No. 5792638
 ; GENERAL INFORMATION:
 ; APPLICANT: AARONSON, S.A.; CHAN, A.;
 ; APPLICANT: MIKI, T.
 ; TITLE OF INVENTION: NOVEL HUMAN RAS-RELATED
 ; TITLE OF INVENTION: ONCOGENES UNMASKED BY EXPRESSION OF CDNA
 ; TITLE OF INVENTION: CLONING
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORGAN & FINNEGAN
 ; STREET: 345 PARK AVENUE
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; COUNTRY: USA
 ; ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORDPERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/247,946A
 FILING DATE: 24-MAY-1994
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: DOROTHY R. AUTH
 REGISTRATION NUMBER: 36,434
 REFERENCE/DOCKET NUMBER: 2026-4150
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-4800
 TELEFAX: (212) 751-6849
 TELEX: 421792

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 615

TYPE: Nucleic acid

STRANDEDNESS: Double

TOPOLOGY: Unknown

MOLECULE TYPE: CDNA

HYPOTHETICAL: No

ORGANISM: Human

STRAIN:

INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE:

HAPLOTYPE:

TISSUE TYPE:

CELL TYPE:

CELL LINE:

ORGANELLE:

FEATURE:

NAME/KEY: TC21 gene

LOCATION:

IDENTIFICATION METHOD:

; OTHER INFORMATION:

US-08-247-946A-5

Alignment Scores:

Pred. No.: 8,27e-19 Length: 615
 Score: 300.00 Matches: 71
 Percent Similarity: 55.32% Conservative: 33
 Best Local Similarity: 37.77% Mismatches: 70
 Query Match: 17.33% Indels: 14
 DB: 1 Gaps: 3

US-09-709-103-3f1 (1-332) x US-08-247-946A-5 (1-615)

Qy 76 TyrArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIleValSerArgPhe 95
 Db 43 TACCGGCTCGTGTGTCGGGGGGCGGCGTGGCAAGTCGGCGCTCACCATCAGTTC 102
 Qy 96 LeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPheHisArgLysPhe 115
 Db 103 ATCCAGTCCCTATTGTAAACGGATTATGATCCAAACCAATTGAAGATTCTTACACAAAGCAG 162
 Qy 116 TyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisPro 135
 Db 163 TGTGTGATAGATGACAGACAGCCCGCTAGATATTTGGATACAGCAGGANNNGAAGAG 222
 Qy 136 PheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSer 155
 Db 223 TTTGGAGCCCATGAGAGAACAGTATATGAGGACTGGCGAAGCTTCTGTGGTCTTTTCA 282
 Qy 156 LeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGlnIleLeuAspThr 175
 Db 283 GTCACAGATAGAGCGAGTTTGAAGAAATCTATAAGTTTCAAAGACAGATTCTC----- 336
 Qy 176 LysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeuValIleCysGly 195
 Db 337 -----AGAGTAAAGGATCGTGATGAGTTCCCAATGATTTTAATTGGT 378
 Qy 196 AsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIleGluGlnLeuVal 215
 Db 379 AATAAAGCAGATCTGGATCATCAAAAGACAGGTAAACACAGGAAGAGGACACAGTTAGCA 438
 Qy 216 GlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLysAsnSerSerLeu 235
 Db 439 CGGCAG-----CTTAAGTTAAACATACATCGAGGCATCAGCAAGATTAGGATGAATGA 492
 Qy 236 AspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGluMet----- 252
 Db 493 GATCAAGCTTTCCATGAACCTTGTCCGGGTTATCAGGAAATTTCAAGAGCAGGAATGCTCCT 552
 Qy 253 ---SerProAspLeuHisArgLys 259
 Db 553 CTTTACCAGAACCAACACGGA 576

RESULT 6

PCT-US95-06420-5

; Sequence 5, Application PC/TUS9506420

; GENERAL INFORMATION:

; APPLICANT: AARONSON, S.A.; CHAN, A.;

; APPLICANT: MIKI, T.

; TITLE OF INVENTION: NOVEL HUMAN RAS-RELATED

; TITLE OF INVENTION: ONCOGENES UNMASKED BY EXPRESSION OF CDNA

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORGAN & FINNEGAN

; STREET: 345 PARK AVENUE

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 10154

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK

; COMPUTER: IBM PC COMPATIBLE


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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06420
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/247,946
FILING DATE: 24-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4150PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 615
TYPE: Nucleic acid
STRANDEDNESS: Double
TOPOLOGY: Unknown
MOLECULE TYPE: cDNA
HYPOTHETICAL: No
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL LINE:
ORGANELLE:
FEATURE:
NAME/KEY: TC21 gene
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PCT-US95-06420-5

Alignment Scores:
Pred. No.: 8,276-19 Length: 615
Score: 300.00 Matches: 71
Percent Similarity: 55.32% Conservative: 33
Best Local Similarity: 37.77% Mismatches: 70
Query Match: 17.33% Indels: 14
DB: Gaps: 3

US-09-709-103-3f1 (1-332) x PCT-US95-06420-5 (1-615)
QY 76 TYRARGMETVALLELENGLYSERISERLYSVALGLYETHRALALEVALSERARGPHE 95
DB 43 TACCGGCTCTGTGTGGCGGGCGGCGGCGGCGGCAAGTCGCGCGCTCACATCCAGTTTC 102
QY 96 LEUETHGLIYARGPHEGLIUSPALATYTRHPROTHIRLEGLIUSPHEHISARGLYSPHE 115
DB 103 ATCCAGTCCATTGTTGAACGATTTGATTCACCAACATTGAAATCTTACCAACAGCAG 162
QY 116 TYRSETHLEARGGLIUALVALYRGLINLEUASPHELEUASPHEHISARGLYSPHE 135
DB 163 TGTGTGATATGATGACAGAGCAGCCCGCTGATATTTGATTCACGACAGANNNGAAGAG 222
QY 136 PHEPROBLAMELARGARGLEUSERILELEUTHIRGLIYASPVALPHEILEUVALPHESER 155
DB 223 TTTGGAGCCCTAGACAGAACAGTATATGAGACTGCGCAAGCTTCCTGTTGGTTTTC 282
QY 156 LEUASPANARGASPERPHEGLIULVALGLINARGLEUARGINGINILEUASPETHR 175
DB 283 GTCCAGATAGAGCGAGTTTGAAGAAATCTATTAAGATTTC----- 336
QY 176 LYSERCYSEUYSANLSTHLYSGLIUSVALSPVALPROLEUVALILECYSGLY 195

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DB 337 -----AGAGTAAGGATCTGATGACGTTCCCATGATTATTTGCT 378
QY 196 ASNLVSGLIYASPARGASPERPHELYRARGGLIUALASPGLINARGLIUGLINLEUVAL 215
DB 379 AATTAAGCAGATCTGATTCATCAAAAGACAGTAAACAGAGAAAGACAAACAGTTTGA 438
QY 216 GLIYASPARPROGLINARGYSAIATYRPHGLIULESERIALYSLYSANSESERLEU 235
DB 439 CGGCAG-----CTTAAGGTAACTACATGAGGACATCGCAAGATTAGATGATGTA 492
QY 226 ASPGINMETPHEARGALALEUPHEALAMEALALYSLEUPROSERGIUMET----- 252
DB 493 GATCAAGCTTTCCATGAACTTGTCCGGGTTATACGAAATTTCAGAAAGCAGGAATGCT 552
QY 253 ---SERPROASPLEUHSIARGLYS 259
DB 553 CCTTACCACCAAGCAACACAGGAAA 576

RESULT 7
US-08-306-691B-15
Sequence 15, Application US/08306691B
Patent No. 5734039
GENERAL INFORMATION:
APPLICANT: Calabretta, Bruno
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P. C.
STREET: Two Penn Center, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,691B
FILING DATE: September 15, 1994
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: NO. 5734039e
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 5775 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-306-691B-15

Alignment Scores:
Pred. No.: 1,586-15 Length: 5775
Score: 279.00 Matches: 67
Percent Similarity: 54.59% Conservative: 34
Best Local Similarity: 36.22% Mismatches: 72
Query Match: 16.12% Indels: 12
DB: Gaps: 4

```


US-09-709-103-3F1 (1-332) x US-08-306-691B-15 (1-5775)

```

QY 76 TyrArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIleValSerArgPhe 95
Db 202 TATAAACTTGTGTAGTGTGGCTAGGCAAGAGTGCCTTGACGATACAGCTA 261
QY 96 LeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPheHisArgLysPhe 115
Db 262 ATTCAAGATCATTTTGTGGACGAATATGATCCAAATAGAGGATTCCTACAGGAACAA 321
QY 116 TyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisPro 135
Db 322 GTAGTAATTCATCGAGAAACCTCTCTTGGATATTCGACACAGCAGGTCAAGAGGAG 381
QY 136 PheProAlaMetArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSer 155
Db 382 TACAGTGCAATGAGGACCATGATACAGGACTGGGAGGGCTTCTTGTGTATTTGCC 441
QY 156 LeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGlnIleLeuAspThr 175
Db 442 ATAAATAAATACTAAATCATTTGAGATATTCACCAATTATAGAGAACAAATT----- 492
QY 176 LysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeuValIleCysGly 195
Db 493 -----AAAAGAGTTAGGACTCTGGAAGATGTACCTATGATGCTAGTAGGA 537
QY 196 AsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIleGluGlnLeuVal 215
Db 538 AATAAATGTGATTTGGCT--TCTAGACAGTAGACACAAACAGGCTCAGGACTTAGCA 594
QY 216 GlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLysAsnSerSerLeu 235
Db 595 AGAAGT-----TATGGAATTCCTTTTAAACATCAGCAAAAGACAGAGGTGT 648
QY 236 AspGlnMetPheArgAlaLeuPhe---AlaMetAlaLysLeuProSerGluMetSerPro 254
Db 649 GATGATGCTCTTATACATTAGTTCGAGAAATTCGAAATTCGAAACATATAAGAAAGATGAGCAA 708
QY 255 AspLeuHisArgLys 259
Db 709 GATGTAAGAAAGAG 723

```

RESULT 8

```

PCT-US93-06251-29
; Sequence 29, Application PC/TUS9306251
; GENERAL INFORMATION:
; APPLICANT: Wickstrom, Eric and Rife, Jason P.
; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
; TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: NY
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06251
; FILING DATE: 19930630
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8586
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366

```

RESULT 9

```

US-08-884-866A-2
; Sequence 2, Application US/08884866A
; GENERAL INFORMATION:
; APPLICANT: Chien, Shu
; APPLICANT: Shyy, John Y-J
; TITLE OF INVENTION: GENE THERAPY IN CORONARY ANGIOPLASTY AND
; TITLE OF INVENTION: BYPASS
; FILE REFERENCE: UCSD1100-1
; CURRENT APPLICATION NUMBER: US/08/884,866A
; CURRENT FILING DATE: 1997-06-30
; PRIOR APPLICATION NUMBER: 60/030,358
; PRIOR FILING DATE: 1996-11-08

```

```

; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5775 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US93-06251-29

```

```

Alignment Scores:
Pred. No.: 1-58e-15 Length: 5775
Score: 279.00 Matches: 67
Percent Similarity: 54.59% Conservative: 34
Best Local Similarity: 36.22% Mismatches: 72
Query Match: 16.12% Indels: 12
DB: 5 Gaps: 4

```

US-09-709-103-3F1 (1-332) x PCT-US93-06251-29 (1-5775)

```

QY 76 TyrArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIleValSerArgPhe 95
Db 202 TATAAACTTGTGTAGTGTGGCTAGGCAAGAGTGCCTTGACGATACAGCTA 261
QY 96 LeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPheHisArgLysPhe 115
Db 262 ATTCAAGATCATTTTGTGGACGAATATGATCCAAATAGAGGATTCCTACAGGAACAA 321
QY 116 TyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisPro 135
Db 322 GTAGTAATTCATCGAGAAACCTCTCTTGGATATTCGACACAGCAGGTCAAGAGGAG 381
QY 136 PheProAlaMetArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSer 155
Db 382 TACAGTGCAATGAGGACCATGATACAGGACTGGGAGGGCTTCTTGTGTATTTGCC 441
QY 156 LeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGlnIleLeuAspThr 175
Db 442 ATAAATAAATACTAAATCATTTGAGATATTCACCAATTATAGAGAACAAATT----- 492
QY 176 LysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeuValIleCysGly 195
Db 493 -----AAAAGAGTTAGGACTCTGGAAGATGTACCTATGATGCTAGTAGGA 537
QY 196 AsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIleGluGlnLeuVal 215
Db 538 AATAAATGTGATTTGGCT--TCTAGACAGTAGACACAAACAGGCTCAGGACTTAGCA 594
QY 216 GlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLysAsnSerSerLeu 235
Db 595 AGAAGT-----TATGGAATTCCTTTTAAACATCAGCAAAAGACAGAGGTGT 648
QY 236 AspGlnMetPheArgAlaLeuPhe---AlaMetAlaLysLeuProSerGluMetSerPro 254
Db 649 GATGATGCTCTTATACATTAGTTCGAGAAATTCGAAATTCGAAACATATAAGAAAGATGAGCAA 708
QY 255 AspLeuHisArgLys 259
Db 709 GATGTAAGAAAGAG 723

```



```

; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (570)
; US-08-866A-2

```

```

Alignment Scores:
Pred. No.: 8.28e-17 Length: 570
Score: 277.50 Matches: 73
Percent Similarity: 53.23% Conservative: 34
Best Local Similarity: 36.32% Mismatches: 72
Query Match: 16.03% Indels: 23
DB: 4 Gaps: 6

```

US-09-709-103-3f1 (1-332) x US-08-866A-2 (1-570)

```

QY 76 TyrArgMetValIleLeuGlySerSerlySValGlyThrAlaIleValSerArgPhe 95
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 10 TATAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 69
QY 96 LeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPheHisArgLysPhe 115
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 70 ATCCAGAACCATTTGTGTGAGCAATACGACCCCACTATAGAGATTCTTACCGAGAGCAG 129
QY 116 TySerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisPro 135
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 130 GTGGTCATTGATGGGAGAGCGTGGTGTGACATCTGTGATACCGCGCGCTGGAGGAG 189
QY 136 PheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSer 155
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 190 TACAGCGGCATCGGGAGCCAGTCAATGCGCACCGGGAGGGCTTCTGTGTGTGTGTGCC 249
QY 156 LeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGlnIleLeuAspThr 175
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 250 ATCAACAACCAAGCTTTTGAAGACATCCACAGTACGAGAGCAGATC----- 300
QY 176 LysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeuValIleCysGly 195
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 -----AAACGGGTGAAGGAGCTCGAGTACGTGCTCCATGTGTGTGTGTGTGGG 345
QY 196 AsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGlnIleGluGlnLeuVal 215
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 346 AACCAAGTGTGACCTG---GCTGCACGCACTGTGTGAATCTCGGACAGCTCAGGACCTCGCC 402
QY 216 GlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLysAsnSerSerLeu 235
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 403 CGAAGC-----TACGGCATCCCTTACATCGAGACCTCGGCGCAAGCCCGGAGGGAGGTG 456
QY 236 AspGlnMetPheArgAlaLeu-----PheAlaMetAlaLysLeu--- 248
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 457 GAGGATGCTCTTACACAGTGTGTGCGTGAAGATCCGGACAGCAGCTGGGAGAGCTGAAAC 516
QY 249 ---ProSerGlnMetSerProAspLeuHisArgLysValSerValGlnTyrCysAspVal 267
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 517 CCTCTGTATGAGAGTGGCCCCGG-CTGCAT-----GAGCTGCAAGTGTGTGTCTTC 566
QY 268 Leu 268
   |||
Db 567 CTG 569

```

```

RESULT 10
; US-08-866A-11
; Sequence 11, Application US/08884866A
; GENERAL INFORMATION:
; APPLICANT: Shyy, John Y-J
; APPLICANT: Chien, Shu
; TITLE OF INVENTION: GENE THERAPY IN CORONARY ANGIOPLASTY AND
; TITLE OF INVENTION: BYPASS

```

```

; FILE REFERENCE: UCSD1100-1
; CURRENT APPLICATION NUMBER: US/08/864,866A
; CURRENT FILING DATE: 1997-06-30
; PRIOR APPLICATION NUMBER: 60/030,358
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (49) ... (51)
; OTHER INFORMATION: nnn = Any nucleic acid triplet, except for UCA,
; OTHER INFORMATION: UCC, UCG, UCU, AGC, or AGU
; OTHER INFORMATION: Variation of SEQ ID NO:2
; US-08-866A-11

```

```

Alignment Scores:
Pred. No.: 8.28e-17 Length: 570
Score: 277.50 Matches: 73
Percent Similarity: 53.23% Conservative: 34
Best Local Similarity: 36.32% Mismatches: 72
Query Match: 16.03% Indels: 23
DB: 4 Gaps: 6

```

US-09-709-103-3f1 (1-332) x US-08-866A-11 (1-570)

```

QY 76 TyrArgMetValIleLeuGlySerSerlySValGlyThrAlaIleValSerArgPhe 95
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 10 TATAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 69
QY 96 LeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPheHisArgLysPhe 115
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 70 ATCCAGAACCATTTGTGTGAGCAATACGACCCCACTATAGAGATTCTTACCGAGAGCAG 129
QY 116 TySerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisPro 135
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 130 GTGGTCATTGATGGGAGAGCGTGGTGTGACATCTGTGATACCGCGCGCTGGAGGAG 189
QY 136 PheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSer 155
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 190 TACAGCGGCATCGGGAGCCAGTCAATGCGCACCGGGAGGGCTTCTGTGTGTGTGTGCC 249
QY 156 LeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGlnIleLeuAspThr 175
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 250 ATCAACAACCAAGCTTTTGAAGACATCCACAGTACGAGAGCAGATC----- 300
QY 176 LysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeuValIleCysGly 195
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 -----AAACGGGTGAAGGAGCTCGAGTACGTGCTCCATGTGTGTGTGTGTGGG 345
QY 196 AsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGlnIleGluGlnLeuVal 215
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 346 AACCAAGTGTGACCTG---GCTGCACGCACTGTGTGAATCTCGGACAGCTCAGGACCTCGCC 402
QY 216 GlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLysAsnSerSerLeu 235
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 403 CGAAGC-----TACGGCATCCCTTACATCGAGACCTCGGCGCAAGCCCGGAGGGAGGTG 456
QY 236 AspGlnMetPheArgAlaLeu-----PheAlaMetAlaLysLeu--- 248
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 457 GAGGATGCTCTTACACAGTGTGTGCGTGAAGATCCGGACAGCAGCTGGGAGAGCTGAAAC 516
QY 249 ---ProSerGlnMetSerProAspLeuHisArgLysValSerValGlnTyrCysAspVal 267
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 517 CCTCTGTATGAGAGTGGCCCCGG-CTGCAT-----GAGCTGCAAGTGTGTCTTC 566
QY 268 Leu 268
   |||
Db 567 CTG 569

```


RESULT 11

US-08-429-964-85
 ; Sequence 85, Application US/08429964
 ; Patent No. 5962243
 ; GENERAL INFORMATION:
 ; APPLICANT: BROWN, MICHAEL S.
 ; APPLICANT: GOLDSTEIN, JOSEPH L.
 ; APPLICANT: REISS, YUVAL
 ; APPLICANT: JAMES, GUY L.
 ; TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF FARNESYL
 ; NUMBER OF INVENTIONS: TRANSFERASE INHIBITORS
 ; NUMBER OF SEQUENCES: 85
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ARNOLD, WHITE & DURKEE
 ; STREET: P.O. BOX 4433
 ; CITY: HOUSTON
 ; STATE: TEXAS
 ; COUNTRY: UNITED STATES OF AMERICA
 ; ZIP: 77210

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/429,964
 ; FILING DATE: 27-APR-1995
 ; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/021,625
 ; FILING DATE: 16-FEB-1993
 ; CLASSIFICATION: 435

APPLICATION NUMBER: US 07/822,011
 FILING DATE: ABANDONED

APPLICATION NUMBER: 435
 FILING DATE: 18-APR-1991

APPLICATION NUMBER: 435
 FILING DATE: 20-NOV-1990

APPLICATION NUMBER: 435
 FILING DATE: 18-APR-1990 (ABANDONED)

ATTORNEY/AGENT INFORMATION:
 ; NAME: PARKER, DAVID L.
 ; REGISTRATION NUMBER: 32,165

REFERENCE/DOCKET NUMBER: UTSD:432/PAR
 TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (512) 418-3000
 ; TELEFAX: (713) 789-2679
 ; TELEX: 79-0924

INFORMATION FOR SEQ ID NO: 85:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 607 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear

US-08-429-964-85

Alignment Scores:
 Pred. No.: 1.24e-16 Length: 607
 Score: 276.00 Matches: 66
 Percent Similarity: 54.59% Conservative: 35
 Best Local Similarity: 35.68% Mismatches: 72
 Query Match: 15.94% Indels: 12
 DB: 2 Gaps: 4

US-09-709-103-3F1 (1-332) x US-08-429-964-85 (1-607)

Qy 76 TyrArgMetValIleLeuGlySerLysValGlyThrAlaIleValSerArgPhe 95

Db 10 TATAAACTTGTGGTAGTGTGGCTAGGCAAGAGTGCCTTGACGATACAGCTA 69

Qy 96 LeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPheHisArgLysPhe 115
 ;
 Db 70 ATTGACAATCATTTTGTGACGAATATGATCCAAATAGAGGATTCCTACAGCAAGCAA 129
 ;
 Qy 116 TyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisPro 135
 ;
 Db 130 GTAGTAATTTGATGGAGAAACCTGCTCTTGGATATTTCCGACACAGCGGTCAAGAGGAG 189
 ;
 Qy 136 PheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSer 155
 ;
 Db 190 TACAGTGCATGAGGACCATCATGAGGACTGGGAGGGCTTCTTGTGATTATTTGCC 249
 ;
 Qy 156 LeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGlnIleLeuAspThr 175
 ;
 Db 250 ATAATAATACTAAATCATTTGAAGATATTCACCATATATAGAACAAAT----- 300
 ;
 Qy 176 LysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeuValIleCysGly 195
 ;
 Db 301 -----AAAAGAGTTAAGGACTCTGAAGATGTACCTATGTCTCTAGTAGGA 345
 ;
 Qy 196 AsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIleGluGlnLeuVal 215
 ;
 Db 346 AATAAATGTGATTGCTCT--TCTAGAACAGTAGACACAAACAGGCTCAGGACTTAGCA 402
 ;
 Qy 216 GlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLysAsnSerSerLeu 235
 ;
 Db 403 AGAAGT-----TATGGAATTCCTTTTATCAACATCAGCAACAGACAGAGGTGT 456
 ;
 Qy 236 AspGlnMetPheArgAlaLeuPhe---AlaMetAlaLysLeuProSerGluMetSerPro 254
 ;
 Db 457 GATGATCCCTTCTATACATTAGTTCGAGAAATTCGAAAAACATAAAAGAAAGATGACCAA 516
 ;

RESULT 12

US-08-884-866A-9
 ; Sequence 9, Application US/08884866A
 ; GENERAL INFORMATION:
 ; APPLICANT: Chien, Shu
 ; APPLICANT: Shyy, John Y-J
 ; TITLE OF INVENTION: GENE THERAPY IN CORONARY ANGIOPLASTY AND
 ; FILE REFERENCE: UCSD1100-1
 ; CURRENT APPLICATION NUMBER: US/08/884,866A
 ; PRIOR FILING DATE: 1997-06-30
 ; PRIOR APPLICATION NUMBER: 60/030,358
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 9
 ; LENGTH: 480
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (49)---(51)
 ; OTHER INFORMATION: nnn = Any nucleic acid triplet, except for UCA,
 ; OTHER INFORMATION: UCC, UCG, UCU, AGC, or AGU
 ; US-08-884-866A-9

Alignment Scores:
 Pred. No.: 9.88e-17 Length: 480
 Score: 275.50 Matches: 63
 Percent Similarity: 56.25% Conservative: 31
 Best Local Similarity: 37.72% Mismatches: 62
 Query Match: 15.92% Indels: 11
 DB: 4 Gaps: 3

US-09-709-103-3F1 (1-332) x US-08-884-866A-9 (1-480)

Tue Dec 31 15:27:54 2002

us-09-709-103-3fl.p2n.rnt

Page 10

QY 76 TyrArgMetValIleLeuGlySerSerLysValGlyThrAlaIleValSerArgPhe 95
Db 10 TATAAGCTGCTGCTGGCGCGCGGCTGTGGCAAAANNNGCGCTGACCATTCAGCTG 69
QY 96 LeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPheIleArgLysPhe 115
Db 70 ATCCGAACCATTTGTGTGACGAAATACGACCCCACTATAGAGATTCCTCTACCGGAGCAG 129
QY 116 TyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisPro 135
Db 130 GTGCGATCATGATGGGAGAGCGTCTGTGGACATCTCGATACCGCGCGCTGGAGAG 189
QY 136 PheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSer 155
Db 190 TACAGCGCATGCGGACCACTCAATGCGCACCGGGAGGCGTCTCTGTGTGTGGCC 249
QY 156 LeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGlnIleLeuAspThr 175
Db 250 ATCAACAACACCAAGCTTTTGGACATCCACCAAGTACAGGAGACAGATC----- 300
QY 176 LysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeuValIleCysGly 195
Db 301 -----AAACGGTGAAGCACTCGGATGACGTGCCATGCTGCTGTGGG 345
QY 196 AsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGlnIleGluGlnLeuVal 215
Db 346 AACAAAGTGTACCTG---GCTGACGCGACTGTGGATCTCGGAGGCTCGACACTTCCG 402
QY 216 GlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLysAsnSerLeu 235
Db 403 CGAAGC-----TACGCGATCCCTTACATCGAGACCTCGGCCAAAGACCGGAGGAGTG 456
QY 236 AspGlnMetPheArgAlaLeu 242
Db 457 GAGGATGCTTCTTACAGCTTG 477
RESULT 13
US-09-167-322-12
Sequence 12, Application US/09167322
Patent No. 6365151
GENERAL INFORMATION:
APPLICANT: Allegheny University of the Health
Sciences, Halpern, Michael S.
England, James M.
TITLE OF INVENTION: CANCER VACCINE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorigna & Monaco, P.C.
SURRET: Suite 1800, Two Penn Center Plaza
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09167,322
APPLICATION NUMBER: US/09167,322
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/00582
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 7933-33 PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 4480 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-167-322-12
Alignment Scores:
Pred. No.: 2,3e-15 Length: 4480
Score: 275.50 Matches: 89
Percent Similarity: 46.01% Conservative: 38
Best Local Similarity: 32.25% Mismatches: 92
Query Match: 15.92% Indels: 58
Gaps: 10
US-09-709-103-3fl (1-332) x US-09-167-322-12 (1-4480)
QY 7 GlyAlaProSerProSer-----ArgAlaGlnProGlnGlnSerProPro 21
Db 1130 GAGCGTCCGAGACCGAGACGATGATCAGTGGTGAAGATCAAGAAAGTCTCTCGGAG 1189
QY 22 AlaAlaHisProAlaCysHisProSerAspProGln-ProLeuSerAlaLeuSerAl 41
Db 1190 GTC-----GGGACAGATGCGCGCCAGCAAGCGGTGGCGAGAGC 1228
QY 41 aProArgProProSerArgProLeuCysProMetLysLeuAlaMetIleLysLysMe 61
Db 1229 TCCT-----GGTTGGCAGCCCTCTGTAGAAAGCAT 1258
QY 61 tCysProSerAspSerGluLeuSerIleProAlaLysAsnCysTyrArgMetValIle 81
Db 1259 GACAGAA-----TCAAGCTTGTGTGTGT 1282
QY 81 uGlySerSerLysValGlyLysThrAlaIleValSerArgPheLeuThrGlyArgPheG 101
Db 1283 GGGCGCTAGAGGCGGTGGAAAGAGTCCCTGACCATCCAGCTGATCCAGAACCATTTGT 1342
QY 101 uAspAlaTyrThrProThrIleGluAspPheHisArgLysPheTyrSerIleArgGlyG 121
Db 1343 GACAGAGATGATGCCACTATAGAGAGCTCCACCGAAACAGATGATGATGGGGA 1402
QY 121 uValTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisProPheProAlaMetArg 141
Db 1403 GACGCTTACTGACATCTTAAACACAGAGGCTCAAGAAAGACTATAGTCCATGGGGA 1462
QY 141 gluSerIleLeuThrGlyAspValPheIleLeuValPheSerLeuAspAsnArgAsp 161
Db 1463 CCAGTACATGGCCACAGAGGAGGCTTCCCTGTGTATTTGCCATCAACACCAAGTC 1522
QY 161 rPheGluGluValGlnArgLeuArgGlnGlnIleLeuAspThrLysSerCysLeuLys 181
Db 1523 CTTTGAAGCATCCATCAGTACAGGAGAGCATC-----AA 1558
QY 181 nLysThrLysGluAsnValAspValProLeuValIleCysGlyAsnLysGlyAspArg 201
Db 1559 GCGGCTGAAGATTCAGATGATGTCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1618
QY 201 pPheTyrArgGluValAspGlnArgGlnIleGluGlnLeuValGlyAspAspProGln 221
Db 1619 CGGTAC---ACTGTGAGTCTCGGACAGCCAGGACCTTCTGTGCAGC-----TATGG 1669
QY 221 gCysAlaTyrPheGluIleSerAlaLysLysAsnSerSerLeuAspGlnMetPheArg 241
Db 1670 CATCCCTCATTTGAACATCAAGAGCCGACAGAGTGTGAGATGCTTCTACAC 1729
QY 241 alaLys-----PheAlaMetAlaLysLeu-----ProSerGluMetSe 253
Db 1730 ACTGATACGAGATTCGGAGAGATTAATCAAGAACTGAACCCGCTGTATGAGATGG 1789
QY 253 rProAspLeuHisArgLysValSerValGlnTyrCysAspValLeu 268
Db 1790 CCTGG-CTGCAT-----GAGCTGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1825

RESULT 14

US-08-884-866A-10
 ; Sequence 10, Application US/08884866A
 ; GENERAL INFORMATION:
 ; APPLICANT: Chien, Shu
 ; APPLICANT: Shyy, John Y-J
 ; TITLE OF INVENTION: GENE THERAPY IN CORONARY ANGIOPLASTY AND
 ; FILE REFERENCE: UCSD1100-1
 ; CURRENT APPLICATION NUMBER: US/08/884,866A
 ; CURRENT FILING DATE: 1997-06-30
 ; PRIOR APPLICATION NUMBER: 60/030,358
 ; PRIOR FILING DATE: 1996-11-08
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 10
 ; LENGTH: 450
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (49)...(51)
 ; OTHER INFORMATION: nnn = Any nucleic acid triplet, except for UCA,
 ; OTHER INFORMATION: UCC, UCG, UCU, AGC, or AGU
 US-08-884-866A-10

Alignment Scores:

Pred. No.:	5.94e-16	Length:	450
Score:	266.50	Matches:	61
Percent Similarity:	58.06%	Conservative:	29
Best Local Similarity:	39.35%	Mismatches:	54
Query Match:	15.40%	Indels:	11
DB:	4	Gaps:	3

US-09-709-103-3F1 (1-332) x US-08-884-866A-10 (1-450)

Qy	76	TyrArgMetValIleLeuGlySerLysValGlyThrAlaIleValSerArgPhe	95
Db	10	TATAAGCTGTGTGTGGCGCGCGGTGGGGAANNNGCCTGACCATCCAGCTG	69
Qy	96	LeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPheHisArgLysPhe	115
Db	70	ATCCAGAACCATTTGTGGACGAATACGACCCACTATAGAGATTCTTACCGAAGCAG	129
Qy	116	TyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisPro	135
Db	130	GTGGTCAATTGGGGAGACGCTGCTGTGGACATCTCTGGATACCGCGCGCTGGAGGAG	189
Qy	136	PheProAlaMetArgLeuSerPheIleLeuThrGlyAspValPheIleLeuValPheSer	155
Db	190	TACAGCGCCATCGGGACGACGATCAATGCGACCGGGAGGCTTCTGTGTGTGTGGG	249
Qy	156	LeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGlnIleLeuAspThr	175
Db	250	ATCAACACACCAAGTCTTTTGGAGACATCCACGACATACGAGGAGCAGATC-----	300
Qy	176	LysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeuValIleCysGly	195
Db	301	-----AAACGGGTGAGGACTCGGATACGTCGATCGGCTGCTGGTGGGG	345
Qy	196	AsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluGlnLeuVal	215
Db	346	AACAGTGTGACCTG---GCTGCAGCAGCTGTGGAATCTCGGAGGCTCAGGACCTCGCC	402
Qy	216	GlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLys	230
Db	403	CGAAGC-----TACGGCATCCCTATATGAGACCTCGGCCAAG	441

RESULT 15

US-08-429-964-83
 ; Sequence 83, Application US/08429964
 ; Patent No. 5962243

GENERAL INFORMATION:

APPLICANT: BROWN, MICHAEL S.
 APPLICANT: GOLDSTEIN, JOSEPH L.
 APPLICANT: REISS, YUVAL
 APPLICANT: JAMES, GUY L.
 TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF FARNESYL
 NUMBER OF SEQUENCES: 85
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ARNOLD, WHITE & DURKEE
 STREET: P.O. BOX 4433
 CITY: HOUSTON
 STATE: TEXAS
 COUNTRY: UNITED STATES OF AMERICA
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/429,964
 FILING DATE: 27-APR-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/021,625
 FILING DATE: 16-FEB-1993
 CLASSIFICATION: 435
 APPLICATION NUMBER: US 07/822,011
 FILING DATE: ABANDONED
 CLASSIFICATION: 435
 APPLICATION NUMBER: PCT/US/91/02650
 FILING DATE: 18-APR-1991
 CLASSIFICATION: 435
 APPLICATION NUMBER: US 07/615,715
 FILING DATE: 20-NOV-1990
 CLASSIFICATION: 435
 APPLICATION NUMBER: US 07/510,706
 FILING DATE: 18-APR-1990 (ABANDONED)
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: PARKER, DAVID L.
 REGISTRATION NUMBER: 32,165
 REFERENCE/DOCKET NUMBER: UTSD:432/PAR
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEFAX: (713) 789-2679
 TELEX: 79-0924
 INFORMATION FOR SEQ ID NO: 83:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 574 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-429-964-83

Alignment Scores:

Pred. No.:	8.37e-16	Length:	574
Score:	266.50	Matches:	62
Percent Similarity:	53.85%	Conservative:	36
Best Local Similarity:	34.07%	Mismatches:	67
Query Match:	15.40%	Indels:	17
DB:	2	Gaps:	4

US-09-709-103-3F1 (1-332) x US-08-429-964-83 (1-574)

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Db	10	TATAAACTTGTGTGTGGAGCTTGTGGCGTAGGCAAGAGTCTTGACGATACAGCTA	69
Qy	96	LeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPheHisArgLysPhe	115
Db	70	ATTGACAAATCATTTTGTGGACGAATATGATCCAAATAGAGGATTCCTACAGGAAGCAA	129

QY 116 TyrSer11ea9g1ygluvalTyrGlnLeuasp11leuaspThrSerGlyAsnHisPro 135
DB 130 GTAAGTAATTGATGGAGAAACCTGTCTCTTGATATTTCTCGACACAGCGTCAAGAGAG 189
QY 136 PheProAlaMetArgArgLeuSer11leuThrGlyaspValPhe11leuValPheSer 155
DB 190 TACAGTGCATATAGGAGCACACATACATGAGAGCTGGGGAGGCTTTCTTGTTATTTGCC 249
QY 156 LeuAspAsnArgaspSerPheGlnGluValGlnArgLeuArgGlnGln11leuaspThr 175
DB 250 ATAAATTAATTAATAATCATTTGAAGATATTCACCATTTATAGAGAAATAATT----- 300
QY 176 LysSerCysLeuLysAsnLysThrLysGlnAsnValaspValProLeuVal11leCysGly 195
DB 301 -----AAAGAGTTAAGAGACTCTGAAGATGTACCTATGTGCTCTAGTAGGA 345
QY 196 AsnLysGlyaspArgaspPheTyrArgGluValaspGlnArgGln11leGlnLeuVal 215
DB 346 AATAAATGTGATTTGGCT--TCTAGACAGTAGACACAAAACAGGCTCAGGACTTAGCA 402
QY 216 GlyaspAspProGlnArgCysAlaTyrPheGlnLysSerAlaLysLysAsnSerSerLeu 235
DB 403 AGAAGT-----TATGGAATTCCTTTATTCAAAACATCAGCAAAAGACAAACAGAGAGTG 456
QY 236 AspGlnMetPheArgAlaLeu-----PheAlaMetAlaLysLeuPro 249
DB 457 GAGGATGCTTTTATACATTTGTGAGAGAGATCCGACAAATACGATTGAAAAAATCAGC 516
QY 250 SerGlu 251
DB 517 AAAGAA 522

Search completed: December 30, 2002, 19:44:17
Job time : 88 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 30, 2002, 18:07:41 ; Search time 90 seconds
(without alignments)

1498.554 Million cell updates/sec

Title: US-09-709-103-3f1

Perfect score: 1731

Sequence: 1 GIPGAGAPSPRAQPEOSP.....IREKASAGSQAQDKRCVTS 332

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 363474 seqs, 203117208 residues

Total number of hits satisfying chosen parameters: 726948

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500
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-DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=7 -DELEXT=7

Database :

Published Applications NA:
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2: /cgn2_6/ptodata/1/pubpna/FCI_NEW_PUB.seq:
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13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	919.5	53.1	3082	10	US-09-778-963A-1 Sequence 1, Appli
2	540	31.2	405	10	US-09-960-352-10273 Sequence 10273, A
3	526	30.4	11221	10	US-09-778-963A-3 Sequence 3, Appli
4	376	21.7	368	10	US-09-864-761-21643 Sequence 21643, A

5	312.5	18.1	3346	9	US-09-764-868-67 Sequence 67, Appl
6	303.5	17.5	688	9	US-09-764-868-490 Sequence 490, App
7	283.5	16.4	2040	12	US-10-044-090-336 Sequence 336, App
8	278.5	16.1	197997	10	US-09-822-246-3 Sequence 3, Appli
9	276.5	16.0	570	12	US-10-104-484-1 Sequence 1, Appli
10	276.5	16.0	570	12	US-10-104-484-3 Sequence 3, Appli
11	275.5	15.9	551	10	US-09-765-298A-25 Sequence 25, Appli
12	272.5	15.7	570	10	US-09-765-298A-27 Sequence 27, Appl
13	268.5	15.5	942	10	US-09-962-832-256 Sequence 256, App
14	264.5	15.3	847	10	US-09-822-849A-40 Sequence 40, Appl
15	264.5	15.3	930	10	US-09-801-368-285 Sequence 285, App
16	262.5	15.2	1271	12	US-10-044-090-110 Sequence 110, App
17	259.5	15.0	536	10	US-09-867-701-5566 Sequence 5566, Ap
18	254	14.7	952	10	US-09-917-800A-1389 Sequence 1389, Ap
19	245.5	14.2	969	10	US-09-801-368-287 Sequence 287, App
20	241.5	14.0	1088	10	US-09-917-800A-1616 Sequence 1616, Ap
21	237	13.7	2418	9	US-09-764-868-84 Sequence 84, Appl
22	237	13.7	2479	9	US-09-764-868-69 Sequence 69, Appl
23	236.5	13.7	1085	9	US-10-067-813-3 Sequence 3, Appli
24	236	13.6	1119	9	US-10-067-813-1 Sequence 1, Appli
25	232	13.4	1191	12	US-10-044-090-111 Sequence 111, App
26	231.5	13.4	452	10	US-09-960-352-4253 Sequence 4253, Ap
27	228	13.2	1296	9	US-09-954-531-983 Sequence 983, App
28	228	13.2	1296	9	US-09-954-531-983 Sequence 5830, Ap
29	225.5	13.0	454	10	US-09-960-352-5830 Sequence 1378, Ap
30	222.5	12.9	1244	10	US-09-972-529-1 Sequence 1, Appli
31	222.5	12.9	3192	10	US-09-788-654A-1 Sequence 1, Appli
32	222	12.8	1157	9	US-10-108-605-44 Sequence 44, Appl
33	221.5	12.8	752	9	US-09-764-868-501 Sequence 501, App
34	211	12.2	1199	10	US-09-794-257-10 Sequence 10, Appl
35	210.5	12.2	1274	10	US-09-925-302-91 Sequence 91, Appl
36	208	12.0	412	10	US-09-960-352-6794 Sequence 6794, Ap
37	205	11.8	1964	10	US-09-925-297-367 Sequence 3, Appli
38	200.5	11.6	612	10	US-09-925-300-631 Sequence 631, App
39	200	11.6	1537	10	US-09-925-300-631 Sequence 4, Appli
40	198	11.4	1023	10	US-09-770-445-674 Sequence 674, App
41	194.5	11.2	836	10	US-09-925-300-678 Sequence 678, App
42	194.5	11.2	2667	10	US-09-962-832-224 Sequence 224, App
43	193	11.1	1443	10	US-09-960-352-6793 Sequence 6793, Ap
44	192	11.1	401	10	US-09-794-257-12 Sequence 12, Appl
45	192	11.1	552	10	

ALIGNMENTS

RESULT 1

US-09-778-963A-1

; Sequence 1, Application US/09778963A

; Patent No. US20020115172A1

; GENERAL INFORMATION:

; APPLICANT: NEELAM, Beena et al

; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE

; FILE REFERENCE: CLO01112

; CURRENT APPLICATION NUMBER: US/09778,963A

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 3082

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-778-963A-1

Alignment Scores:

Pred. No.:	2.01e-71	Length:	3082
Score:	919.50	Matches:	193
Percent Similarity:	71.39%	Conservative:	49
Best local Similarity:	56.93%	Mismatches:	72
Query Match:	53.12%	Indels:	25
DB:	10	Gaps:	8


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; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 11221
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-778-963A-3

Alignment Scores:
Pred. No.:          2,98e-36          Length:          11221
Score:              526.00            Matches:          106
Percent Similarity: 72.40%            Conservative:    37
Best Local Similarity: 55.21%          Mismatches:     33
Query Match:        30.39%            Indels:         16
DB:                 10                Gaps:           4

US-09-709-103-3Fl (1-332) x US-09-778-963A-3 (1-11221)

QY 143 SerIleLeuThrGlyAspValPheIleLeuValPheSerLeuAspAsnArgSerPhe 162
Db 7681 TCTCTCCCTGCGAGGGATGCTTCATCTCTGTTGTTTCAGCTGGATAACCGGAGTCTCTC 7740

QY 163 GluGluValGlnArgLeuArgGlnGlnIleLeuAspThrIysSerCysLeuIysAsnLys 182
Db 7741 GATGAGTCAAGCGCTTCAGAGCAGATCTGGAGTCAAGTCTCTGCTGAAGAAACAG 7800

QY 183 ThrIysGluAsnValAspValProLeuValIleCysGlyAsnLysGlyAspArg---Asp 201
Db 7801 ACCAAGGAGCGCGCGGAGTGCCTGATCTGTCGCAACAGAACGACCGCGGAG 7860

QY 202 PheTyArgGluValAspGlnArgGluIleGluGlnLeuValGlyAspAspProGlnArg 221
Db 7861 CTGTCCCGCCAGGTCCCAACCGAGCGCGAGTGTGTGTGTCGCGCGAC---GAGAAC 7917

QY 222 CysAlaTyRheGluIleSerAlaLysLysAsnSerSerLeuAspGlnMetPheArgAla 241
Db 7918 TCGCGCTACTTCGAGGTGTCGCCAAGAGAACACCAACAGTGGACGAGATGTTCTACGTG 7977

QY 242 LeuPheAlaMetAlaLysLeuProSerGluMetSerProAspLeuHisArgLysValSer 261
Db 7978 CTCCTTCAGCATGGCCAGCTGCCACAGATGAGCCCGCCGCTGTCGCAAGATCTCC 8037

QY 262 ValGlnTyCysAspValLeuHisLysLys-----AlaLeuArgAsnLysLysLeuLeu 279
Db 8038 GTGCAGTACGTGAGCGCTTCCACCCAGCGCTTCTGCAATGCGCCCGCGTCAAGGAGATG 8097

QY 280 ArgAlaGlySerGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 299
Db 8098 -----GAGCGCTATGGCATGTGCTCTGCGCC 8121

QY 300 PheAlaArgArgProSerValHisSerAspLeuMetTyRileArgGluLysAlaSerAla 319
Db 8122 TTGCGCCCGCCCGCCCGCGTCAACAGTGCACCTCAAGTACATCAAGGCCAAGGTCTCTCGG 8181

QY 320 GlySerGlnAlaLysAspLysGluArgCysValIle 331
Db 8182 GAAGCCAGGCGCGTGGAGAGGACAGTGCACCATC 8217

RESULT 4
US-09-864-761-21643
; Sequence 21643, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312

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; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 21643
; LENGTH: 368
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL022334.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3
; OTHER INFORMATION: NT HIT: g111418034, EVALUATE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: P13856, EVALUATE 8.00e-12
; OTHER INFORMATION: EST_HUMAN HIT: BE389944.1, EVALUATE 0.00e+00
US-09-864-761-21643

```

Alignment Scores:

```

Pred. No.:          4,51e-25          Length:          368
Score:              376.00            Matches:          79
Percent Similarity: 67.91%            Conservative:    12
Best Local Similarity: 21.72%          Mismatches:     28
Query Match:        21.72%            Indels:         15
DB:                 10                Gaps:           2

```

US-09-709-103-3Fl (1-332) x US-09-864-761-21643 (1-368)

```

QY 16 ProGluGlnSerProAlaAlaHisProAlaCysHisPro-----SerAspPro-G1 33
Db 4 CCTAGACAGAGCGCTAGAGAGCGCCAGAGGTGGTGGGCGCCAGGTCTGGGGGGCCCTGAT 63
QY 33 nProLeuSerAlaLeuLeuSerAlaProArgProProSerArgProLeuCysProMetLy 53

```



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Db      64  GCCTGCTTCTCTCCCTTGTGTGACCCCA----- 94
Qy      53  sIeuaAlaMeIleIlySlyMeCySProSerAspSerGluLeuSerIleProAlaIy 73
Db      95  -----GCCATGATGAAGACTTGTCCAGGGGAACTGCACGCTCAGTGTGCCCGCA 147
Qy      73  sasnCySlyrArgMeValIleLeuGlySerSerIyValGlyrThrAlaIleValse 93
Db     148  AAATCATACCGCATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 207
Qy      93  rArgPheLeuThrGlyrArgPheGluAspAlaIyTrThrProThrIleGluAspPheI 113
Db     208  TCGCTCTCTCAATGGCCGCTTTGAGACCATACACCCCATCCAGGACTTCCACCG 267
Qy     113  gLySPheYserIleArgIyGlyValIyTrGluLeuAspIleLeuAspThrSerGlyAs 133
Db     268  TAAAGTATACAAATCCGGCGGACATGTACAGCTGCACATCTCGATACCTCTGCA 327
Qy     133  nHisProPheProAlaMetArgArgLeuSerIleLeuThr 146
Db     328  CCACCCCTTCCCGCATGCGAGGCTGTCCATCTCACA 367

RESULT 5
US-09-764-868-67
; Sequence 67, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 3346
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2787)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (2795)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-868-67

Alignment Scores:
Pred. No.: 2,946-18      Length: 3346
Score: 312.50      Matches: 86
Percent Similarity: 52.38%      Conservative: 35
Best Local Similarity: 37.23%      Mismatches: 83
Query Match: 18.05%      Indels: 27
DB: 9      Gaps: 7

US-09-709-103-3f1 (1-332) x US-09-764-868-67 (1-3346)
Qy      19  SerProProAlaAlaHisProAlaCySHisProSerAspProGlnProLeuSerAlaLeu 38
Db     21  TCCCTTCCTCCCT-----CCTGTAATCTCTCTTCTCCCGGTTGGGCCCTTGTCTCT 74
Qy     39  LeuSerAlaPro-----ArgProProSerArgProLeuCySPromet 52
Db     75  CTGCACTCTCTCCCGCATGTCGAGATTTCGCCCACTTCCGCGCTGTACCGCGGCC 134
Qy     53  LysLeuAlaAlaMeIleIlySlyMeCySProSerAspSerGluLeu---SerIlePro 71
Db    135  ACAGCTTACCGGGGTGATC-----TTTCCCTCCCTCTGTGTAAGGTTGGTGAAGTGA 188
Qy     72  AlaLysAsnCySlyrArgMeValIleLeuGlySerSerIyValGlyrThrAlaIle 91

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Db     189  CTGATGAGGGAATACAAAGTATGCTGTAGCGAGTGGAGGCTTGGCAATCTGCCCTT 248
Qy     92  ValSerArgPheLeuThrGlyrArgPheGluAspAlaIyTrThrProThrIleGluAspPhe 111
Db    249  ACTGTGCACTTGTTCATCGGAGCTTTTCAATTGAGAAATATGACCCACCATTTGAAGATTTC 308
Qy    112  HisArgLysPheYrSerIleArgIyGlyValIyTrGluLeuAspIleLeuAspThrSer 131
Db    309  TACCCCAAAAGATGACATGAGTACTTCCCTCCGCTCGTGGAAATTCGGACACCGCA 368
Qy    132  GlyAsnHisProPheProAlaMetArgArgPheSerIleLeuThrGlyAspValPheIle 151
Db    369  GGAATCTAGACAGTTGCTCTCATGAGATCTTCAATCAAAAACGGCCAGGTTTATC 428
Qy    152  LeuValPheSerLeuAspAsnArgAspSerPheGluGlyValGlnArgLeuArgGln 171
Db    429  CTGGTTATAGCTGTTATATCAACAGCTTTTCAGATATCAAGCCATGAGAGATCAA 488
Qy    172  IleLeuAspThrLysSerCySLeuLysAsnLysThrLysGluAsnValAspValProLeu 191
Db    489  ATGTCT-----AGATGAAAGATATGAAAAAGTCCCACTA 524
Qy    192  ValIleCyGlyAsnLysGlyAspArgAspPheYrArgIyVal-----AspGln 208
Db    525  ATCTTAGTGAATTAAGTGTCTGAAACCAAGAGAGATTATGTCTTCAAGAGGC 584
Qy    209  ArgGluIleGluGlnLeuValGlyAspAspProGlnArgCyAlaIyTrPheGluLeuSer 228
Db    585  AGAGCTCTGCTCAAGAAATGCGGC-----TGTCTTTCATGGAACATCG 629
Qy    229  AlaLysLysAsnSerSerLeuAspGlnMetPhe 239
Db    630  GCAAAAAGTAAATCAATGTGTGATGAATCTTTT 662

```

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RESULT 6
US-09-764-868-490
; Sequence 490, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 490
; LENGTH: 688
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (579)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (610)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (669)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-868-490

Alignment Scores:
Pred. No.: 2,266-18      Length: 688
Score: 303.50      Matches: 85
Percent Similarity: 51.32%      Conservative: 32
Best Local Similarity: 37.28%      Mismatches: 90
Query Match: 17.53%      Indels: 21
DB: 9      Gaps: 6

US-09-709-103-3f1 (1-332) x US-09-764-868-490 (1-688)

```


QY	19	SerProProAlaAlaHisProAlaCysHisProSerAspProGlnProLeuSerAspLeu	38
Db	14	TCCTCTCCCT-----CCTGTAACCTCTCTCTCCCGGTGGGCCCTCTGCTCTCT	67
QY	39	LeuSerAlaPro-----ArgProProSerArgProLeuCysProMet	52
Db	68	CTGCATCTCTCTCCCACTTCGCAGATTCCTCGGCCACCTTCGCGCTCTAGCCGCGCC	127
QY	53	LysLeuAlaAlaMetIleLysLysMetCysProSerAspSerGluLeu-----SerIlePro	71
Db	128	ACAGCTAGCGGGTGATC-----TTTCCCCCTCTGCTAGGAGTTGGTCAAGGTGAGA	181
QY	72	AlaLysAsnCysTyrArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIle	91
Db	182	CTCATGAGGGAATACAGAGTAGTGGTGTAGGAGTGGAGGGTTGGCAATCTGCCTT	241
QY	92	ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe	111
Db	242	ACTGTGCAGTTTGTCACTGGGACTTTTCATTGAGAAATATGACCCACCATTTGAAGATTTC	301
QY	112	HisArgLysPheTyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSer	131
Db	302	TACGCGAAAGAGATCGAAGTGGACTTCCCTCCCTCCGCTGGAAATCTTGACACCGCA	361
QY	132	GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIle	151
Db	362	GGAACTGAGCAGTTTGCTCCATGAGAGATCTCTACATCAAAAAGCCCAAGGTTTCATC	421
QY	152	LeuValPheSerLeuAspAsnArgSerPheGluGluValGlnArgLeuArgGlnGln	171
Db	422	CTGTTTATAGCTTGTTAATCAACAGTCTTTTCAGGATATCAAGCAATGAGAGATCAA	481
QY	172	IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeu	191
Db	482	ATTGTC-----AGGTGAAGAGATATGAAAAGTCCCACTA	517
QY	192	ValIleCysGlyAsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIle	211
Db	518	ATCKAGTAGGAAATAAAGTGAATCGAACACGAAAGAGAGGTTATGTTCTTCAGAGGC	577
QY	212	GluGlnLeuValGlyAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLys	231
Db	578	ANAGCTCTGCCTCAAGAA-----TGGGGCTGCTCTTATGAGACATCGGCAAAAAGT	631
QY	232	AsnSerSerLeuAspGlnMetPhe	239
Db	632	AAATCAATGTGTGATCAACTTTT	655

```

RESULT 7
US-10-044-090-336
; Sequence 336, Application US/10044090
; Patent No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 336
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 3110662CBI
US-10-044-090-336

```

Alignment Scores:	
Pred. No.:	5.29e-16
Score:	283.50
Length:	66
Matches:	66
Conservative:	40
Percent Similarity:	55.21%

Best Local Similarity:	34.38%	Mismatches:	69
Query Match:	16.38%	Indels:	17
DB:	12	Gaps:	3
US-09-709-103-3F1 (1-332) x US-10-044-090-336 (1-2040)			
QY	76	TyArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIleValSerArgpHe	95
DB	202	TATAAGCTAGTCGTCTTGCTCAGGAGCGTGGAAAGTCTGCTTTGACTGTGACAATTT	261
QY	96	LeuThrGlyArgPheGluAspAlaTyThrProThrIleGluAspPheHisArgLysPhe	115
DB	262	GTTCAAGGAAATTTTGTAGAAAATACGATCTCAGATAGAAGATTCTTATGAAAGCAA	321
QY	116	TyrSerIleArgGlyGluValTyGinLeuAspIleLeuAspThrSerGlyAsnHisPro	135
DB	322	GTTGAAGTAGATGCACAACAGTGTATGCTTTGAAATCTTGGATACTGCAGGACGGAGCAA	381
QY	136	PheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSer	155
DB	382	TTTACAGCAATGAGGATTTATACATGAAATATGCAAGGATTTGCATTAGTTTATTC	441
QY	156	LeuAspAsnArgSerpPheGluGluValGlnArgLeuArgGlnGlnIleLeuAspThr	175
DB	442	ATCAGCAGCACGCCACATTTAAACGATTTACAGACCTGAGAGNACGATCTTT	495
QY	176	LysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeuValIleCysGly	195
DB	496	-----CGAGTTAAAGCACTCATGATGTTCCAATGATCTTGTGTGT	537
QY	196	AsnLysGlyAspArgAspPheTyArgGluValAspGlnArgGluIleGluGlnLeuVal	215
DB	538	AATAAGTGTCACTTGGAA-----CATGAAAGAGTTGTGGGAGGAGCAAA	582
QY	216	GlyAspAspProGlnArg-----CysAlaTyrrPheGluIleSerAlaLysLys	231
DB	583	GGTCAAAATCTTACAGACAAATGGAAACACTGTGCAATCTTTAGAACTCTTCTGCAAAATCA	642
QY	232	AsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGlu	251
DB	643	AAAATAAATGTTAATAGATCTTTTATGACCTAGTCGGCGAAATTAAACAGAAAAACTCCA	702
QY	252	MetSerProAspLeuHisArgLysValSerValGln	263
DB	703	GTGCCTGGGAAGCTCGCAAAAGATCATATGTCAG	738

RESULT 8

```

US-09-822-246-3/c
; Sequence 3, Application US/09822246
; Patent No. US20020142383A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001149
; CURRENT APPLICATION NUMBER: US/09/822,246
; CURRENT FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 197997
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(197997)
; OTHER INFORMATION: n = A,T,C or G
US-09-822-246-3

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Alignment Scores:
Pred. No.:      5.84e-13      Length:      197997
Score:          278.50       Matches:      65

```


OTHER INFORMATION: Nucleotide sequence of the wild type Ras mutant, RasN17N69.
US-10-104-484-3

Alignment Scores:
Pred. No.: 4, 07e-16 Length: 570
Score: 276.50 Matches: 72
Percent Similarity: 52.74% Conservativity: 34
Best Local Similarity: 35.82% Mismatches: 73
Query Match: 15.97% Indels: 23
DB: 12 Gaps: 6

US-09-709-103-3F1 (1-332) x US-10-104-484-3 (1-570)

```

QY 76 TyrArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIleValSerArgPhe 95
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 10 TATAAGCTGGTGGTGGCGCGCGGTGGGCAAGAGTGGCTGACCATCCAGCTG 69
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 96 LeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPheHisArgLysPhe 115
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 70 ATCCAGAACCATTTTGTGGACCAATACGACCCCACTATAGAGGATTCCTACCGGAAGCAG 129
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 116 TyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisPro 135
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 130 GTGGTCATTTGATGGGAGACGTGCTGTGGACATCTCTGGATACCGCGCGCAGGAGGAG 189
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 136 PheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSer 155
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 190 TACAGCGCATCGCGAACCAAGTACATGCGCACCGCGGAGGGCTTCCTGTGTGTTTGGC 249
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 156 LeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGlnIleLeuAspThr 175
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 250 ATCAACACCAACCAAGTCTTTTGGAGACATCCACAGTACAGGAGCAGATC----- 300
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 176 LysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeuValIleCysGly 195
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 301 -----AAACGGTGAAGGACTCGGATGACGTGCCATGTGTGGTGGGG 345
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 196 AsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIleGluGlnVal 215
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 346 AACAAAGTGTGACCTG---GCTGCACGCACTGTGGAACTCTCGGAGGCTCAGGACCTCGCC 402
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 216 GlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLysAsnSerSerLeu 235
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 403 CGAAGC-----TACGGCATCCCTACATCGAGACCTCGGCCCAAGACCGGAGGAGTG 456
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 236 AspGlnMetPheArgAlaLeu-----PheAlaMetAlaLysLeu--- 248
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 457 GAGGATGCTTCTACAGTGTGGTGGCTGAGATCCCGCAGCACCAAGCTCGGAAGCTGAAC 516
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 249 ---ProSerGluMetSerProAspLeuHisArgLysValSerValGlnTyrCysAspVal 267
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 517 CTCTCTGATGAGATGGCCCGG-CTGCAT-----GAGCTCAAGTGTGTGCTCTC 566
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 268 Leu 268
   |||
Db 567 CTG 569

```

RESULT 11

US-09-765-298A-25
Sequence 25, Application US/09765298A
Patent No. US20020137017A1

GENERAL INFORMATION:

APPLICANT: ARONHEIM, AMI
TITLE OF INVENTION: METHOD FOR DETECTION PROTEIN-PROTEIN INTERACTIONS AND A KIT THERE
FILE REFERENCE: 108387.01
CURRENT APPLICATION NUMBER: US/09/765,298A
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: IL 125456
PRIOR FILING DATE: 1998-07-22
PRIOR APPLICATION NUMBER: IL 128017
PRIOR FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1

SEQ ID NO 25
LENGTH: 551
TYPE: DNA
ORGANISM: Homo sapiens
US-09-765-298A-25

Alignment Scores:

Pred. No.: 4, 77e-16 Length: 551
Score: 275.50 Matches: 67
Percent Similarity: 53.48% Conservativity: 33
Best Local Similarity: 35.83% Mismatches: 68
Query Match: 15.92% Indels: 19
DB: 10 Gaps: 5

US-09-709-103-3F1 (1-332) x US-09-765-298A-25 (1-551)

```

QY 76 TyrArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIleValSerArgPhe 95
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 4 TATAAGCTGGTGGTGGCGCGCGGTGGGCAAGAGTGGCTGACCATCCAGCTG 63
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 96 LeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPheHisArgLysPhe 115
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 64 ATCCAGAACCATTTTGTGGACCAATACGACCCCACTATAGAGGATTCCTACCGGAAGCAG 123
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 116 TyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisPro 135
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 124 GTGGTCATTTGATGGGAGACGTGCTGTGGACATCTCTGGATACCGCGCGCAGGAGGAG 183
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 136 PheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSer 155
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 184 TACAGCGCATCGCGAACCAAGTACATGCGCACCGCGGAGGGCTTCCTGTGTGTTTGGC 243
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 156 LeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGlnIleLeuAspThr 175
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 244 ATCAACACCAACCAAGTCTTTTGGAGGACATCCACAGTACAGGAGCAGATC----- 294
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 176 LysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeuValIleCysGly 195
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 295 -----AAACGGTGAAGGACTCGGATGACGTGCCATGTGTGTGTTGGG 339
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 196 AsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIleGluGlnVal 215
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 340 AACAAAGTGTGACCTG---GCTGCACGCACTGTGGAACTCTCGGAGGCTCAGGACCTCGCC 396
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 216 GlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLysAsnSerSerLeu 235
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 397 CGAAGC-----TACGGCATCCCTACATCGAGACCTCGGCCAAGACCGGAGGAGTG 450
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 236 AspGlnMetPheArgAlaLeu-----PheAlaMetAlaLysLeu--- 248
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 451 GAGGATGCTTCTACACGCTGTGGTGGTGGATCCGCGAGCACACAGCTGCGGAAGCTGAAC 510
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 249 ---ProSerGluMetSerPro 254
   |||
Db 511 CTCTCTGATGAGATGGGCCCC 531

```

RESULT 12

US-09-765-298A-27
Sequence 27, Application US/09765298A
Patent No. US20020137017A1

GENERAL INFORMATION:

APPLICANT: ARONHEIM, AMI
TITLE OF INVENTION: METHOD FOR DETECTION PROTEIN-PROTEIN INTERACTIONS AND A KIT THERE
FILE REFERENCE: 108387.01
CURRENT APPLICATION NUMBER: US/09/765,298A
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: IL 125456
PRIOR FILING DATE: 1998-07-22
PRIOR APPLICATION NUMBER: IL 128017
PRIOR FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27

Tue Dec 31 15:27:55 2002

us-09-709-103-3f1.p2n.rnpb

Page 10

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1

RESULTS
AAZ36892
ID AAZ36892 standard; cDNA; 846 BP.

XX
AC

XX
DT 13-MAR-2000 (first entry)

XX
DE
CDNA encoding an actuator

CDNA encoding an activator of G protein signalling (AGS) protein.

Activator of G protein signalling

KW
KW

GTP hydrolysis: G protein activation; G protein signalling; AGS; ras-related G protein; GTP hydrolysis: G protein activation; G protein signalling; AGS; ras-related G protein;

KW G protein-coupled signal transduction; pheromone response pathway;

cellular signal transduction; ss

XXXXXX

Homo sapiens.

Key	Location/Qualifiers
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FH	
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18-NOV-1999 . 666T

07-MAY-1960

07-MAY-1999; 99WO-US10151.

08-MAY-1998. 0811C-0004040

00 MAY 1998; 98US-0084842.
07-OCT-1998: 98US-010335E.

0, 001 1996, 9805-0103355.

(CADU-) CADUS PHARM CORP.
Cismowski M, Duzic E;
WPI: 2000-072337/06.
P-PSDB; AAV53921.
A new activator of G protein signalling used to treat disorders
characterized by an aberrant AGS protein activity -
Claim 3; Fig 3A; 162pp; English.
The present sequence encodes an activator of G protein signalling (AGS)
protein. The cDNA sequence was isolated from a human liver cDNA
library. The AGS protein exhibits homology to ras-related G proteins,
and contains alterations in conserved amino acids consistent with a
deficiency in GTP hydrolysis activity. AGS stimulates G protein
activity, G protein-coupled signal transduction and the pheromone
response pathway in a receptor-independent manner. The AGS protein
also shows G-gamma selectivity, as measured by growth assays in
yeast expressing various mammalian G-gamma constructs, and
tissue-specific expression, as measured by Northern blot analysis.
The AGS protein can be used to screen for compounds that modulate
cellular signal transduction. The protein is used to treat disorders
characterized by an aberrant AGS protein activity or AGS nucleic acid
expression.
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Matches 846; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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CC yeast expressing various mammalian G-gamma constructs, and
 CC tissue-specific expression, as measured by Northern blot analysis.
 CC The AGS protein can be used to screen for compounds that modulate
 CC cellular signal transduction. The protein is used to treat disorders
 CC characterized by an aberrant AGS protein activity or AGS nucleic acid
 CC expression.
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RESULT 3

AAZ36893

ID AAZ36893 standard; cDNA; 1801 BP.

XX AAZ36893;

DT 13-MAR-2000 (first entry)

XX cDNA encoding an activator of G protein signalling (AGS) protein.
 KW Activator of G protein signalling; AGS; ras-related G protein;
 KW GTP hydrolysis; G protein activity; pheromone response pathway;
 KW G protein-coupled signal transduction; G-gamma selectivity;
 KW cellular signal transduction; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
 XX 5'UTR 7..153
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 FT /product= "activator of G protein signalling (AGS)
 FT 3'UTR 1000..1801
 FT /*tag= c

XX WO9958670-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-US10151.

XX 08-MAY-1998; 98US-0084842.

XX 07-OCT-1998; 98US-0103355.

XX (CADU-) CADUS PHARM CORP.

XX Cismowski M, Duzic E;

XX WPI; 2000-072337/06.

XX P-PSDB; AAY53921.

XX A new activator of G protein signalling used to treat disorders
 XX characterized by an aberrant AGS protein activity -

XX Claim 3; Page 133-135; 162pp; English.

XX The present sequence encodes an activator of G protein signalling (AGS)
 XX protein. The cDNA sequence was isolated from a human liver cDNA
 XX library. The AGS protein exhibits homology to ras-related G proteins,
 XX and contains alterations in conserved amino acids consistent with a
 XX deficiency in GTP hydrolysis activity. AGS stimulates G protein
 XX activity, G protein-coupled signal transduction and the pheromone
 XX response pathway in a receptor-independent manner. The AGS protein
 XX also shows G-gamma selectivity, as measured by growth assays in
 XX yeast expressing various mammalian G-gamma constructs, and
 XX tissue-specific expression, as measured by Northern blot analysis.
 XX The AGS protein can be used to screen for compounds that modulate
 XX cellular signal transduction. The protein is used to treat disorders
 XX characterized by an aberrant AGS protein activity or AGS nucleic acid
 XX expression.

XX Sequence 1801 BP; 437 A; 561 C; 500 G; 303 T; 0 other;

XX Query Match 100.0%; Score 846; DB 21; Length 1801;

XX Best Local Similarity 100.0%; Pred. No. 1.7e-141;

XX Matches 846; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 154 ATGAACACTGGCGGATCATCAAGAGATGTGCCGCGACCTCGGAGCTGAGTATCCCG 213

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QY	181	C	A	C	C	G	A	G	T	T	C	A	T	C	C	A	T	C	C	G	C	G	A	G	T	T	A	C	C	A	G	T	T	A	C	C	A	G	T	T	A	C	C	A	G	C	T	C		240								
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QY	241	G	G	C	A	C	C	A	C	C	G	T	T	C	C	C	G	C	C	A	T	G	G	C	C	T	T	C	C	A	T	T	C	C	A	T	T	C	C	A	T	T	C	C	A	T		300										
Db	394	G	G	C	A	C	C	C	C	G	T	T	C	C	C	G	C	C	A	T	G	G	C	C	T	T	C	C	A	T	T	C	C	A	T	T	C	C	A	T	T	C	C	A	T		453											
QY	301	C	T	G	G	T	T	C	A	G	T	C	T	G	G	A	A	C	C	G	C	A	T	T	C	G	A	G	A	G	T	T	C	G	A	G	A	G	T	T	C	G	A	G	C	A		360										
Db	454	C	T	G	G	T	T	C	A	G	T	C	T	G	G	A	A	C	C	G	C	A	T	T	C	G	A	G	A	G	T	T	C	G	A	G	A	G	T	T	C	G	A	G	C	A		513										
QY	361	A	T	C	T	C	G	A	C	A	A	G	T	T	T	G	C	T	C	A	A	G	A	A	C	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A		420									
Db	514	A	T	C	T	C	G	A	C	A	A	G	T	T	T	G	C	T	C	A	A	G	A	A	C	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A		573										
QY	421	G	T	C	A	T	T	G	C	G	G	C	A	A	C	A	A	G	G	T	G	A	C	C	C	A	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C		480										
Db	574	G	T	C	A	T	T	G	C	G	G	C	A	A	C	A	A	G	G	T	G	A	C	C	C	A	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C		633										
QY	481	G	A	G	C	A	G	T	G	G	C	G	A	C	A	C	C	C	C	C	C	C	C	C	A	G	C	T	C	G	G	C	T	A	C	T	T	C	G	A	G	A	T	C	G	G	C		540									
Db	634	G	A	G	C	A	G	T	G	G	C	G	A	C	A	C	C	C																																								

XX	WO9950288-A2.	
PN		
XX	07-OCT-1999.	
XX		
XX	30-MAR-1999; 99WO-US06993.	
XX		
XX	31-MAR-1998; 98US-0053374.	
PR		
XX	(AMGE-) AMGEN INC.	
XX		
XX	Yen K;	
PI		
XX	WPI: 1999-601322/51.	
DR	P-PSDB; AAY42693.	
DR		
XX	kd312 polypeptides useful for treating diseases and disorders	
PT	associated with alterations in cell proliferation and cell death	-
XX		
XX	Claim 1; Fig 8; 85pp; English.	
PS		
XX	The invention provides nucleic acid molecules encoding human and rat	
CC	kd312 polypeptides. The kd312 polypeptides can be expressed by standard	
CC	recombinant methodology. The kd312 sequences, and the antibodies against	
CC	the proteins may be used to treat or diagnose the presence or progression	
CC	of various diseases, e.g. cancer, immunodeficiency disorders (e.g. AIDS),	
CC	stroke, heart attack, head trauma, and neurodegenerative diseases (e.g.	
CC	Parkinson's disease and Alzheimer's disease). The present sequence	
CC	represents the human kd312 cDNA sequence.	
XX		
XX	Sequence 1841 BP; 398 A; 605 C; 530 G; 308 T; 0 other;	
SO		

Db 795 AACAGCAGCTGGACAGATGTCGCGCTCTTCGCGATGGCAAGCTGCCAGCGAG 854
 QY 601 ATGAGCCAGACCTGCACGCAAGGTCTCGTGTGAGTACTGCGAGCTGCTGCACAAGAG 660
 Db 855 ATGAGCCAGACCTGCACGCAAGGTCTCGTGTGAGTACTGCGAGCTGCTGCACAAGAG 914
 QY 661 GCGCTGCGGAACAAGAACTGCTGCGGCGCGGCGAGCGCGCGCGCGCGCGCGCGCG 720
 Db 915 GCGCTGCGGAACAAGAACTGCTGCGGCGCGGCGAGCGCGCGCGCGCGCGCGCGCG 974
 QY 721 GAGCGCTTTGGCATGCTGCGCAACCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
 Db 975 GAGCGCTTTGGCATGCTGCGCAACCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1034
 QY 781 TACATCCGGAAGAGCG 840
 Db 1035 TACATCCGGAAGAGCG 1094
 QY 841 AGCTAG 846
 Db 1095 AGCTAG 1100

RESULT 5
 AAA49177
 ID AAA49177 standard; cDNA; 1776 BP.
 XX
 AC AAA49177;
 XX
 DT 03-NOV-2000 (first entry)
 XX
 DE cDNA encoding human GTPase associated protein-7.

XX Guanidine nucleotide binding protein; GTP-binding protein; G-protein;
 KW GTPase; GTPase associated protein; GTPase; cell proliferation;
 KW autoimmunity; inflammatory; immune system disorder; cancer; AIDS;
 KW acquired immune deficiency syndrome; asthma; atherosclerosis;
 KW arthritis; systemic lupus erythematosus; psoriasis; human; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT CDS
 FT 180..1025
 FT /*tag= a
 FT /product= GTPAP7
 XX
 PN WO200031263-A2.
 XX
 PD 02-JUN-2000.
 XX
 XX 23-NOV-1999; 99WO-US28013.
 XX
 PR 23-NOV-1998; 98US-0109592.
 PR 04-FEB-1999; 99US-0118610.
 PR 06-APR-1999; 99US-0127990.
 XX
 FA (INCY-) INCYTE PHARM INC.
 XX
 PI Hillman JL, Tang YT, Bandman O, Lal P, Yue H, Lu DAM, Baughn MR;
 PI Yang J, Azimzai Y;
 XX
 WI: 2000-400073/34.
 DR P-PSDB; AAY99655.
 XX
 XX Human GTPase associated proteins, polynucleotides, and antibodies,
 PT useful for diagnosing, preventing and treating various diseases such as
 PT atherosclerosis, cancer, acquired immune deficiency syndrome (AIDS),
 PT asthma, and autoimmune diseases -
 XX
 PS Claim 9; Page 125-126; 144pp; English.
 XX
 XX Human cDNA libraries from various tissues were screened for GTPase

Not Nucleotide binding protein

CC associated proteins (GTPAP). The present sequence is cDNA encoding
 CC human GTPAP-7. This sequence was derived from a cDNA library of the
 CC brain tumour tissue from the parietal lobe of a female.
 CC This protein is expressed in reproductive, nervous and
 CC gastrointestinal tissue. The GTPAP protein may be used to define
 CC agonists and antagonists of GTPAP activity and to generate antibodies
 CC to GTPAP. This means the GTPAP proteins may be useful for treatment or
 CC prevention of diseases associated with GTPAP such as cell proliferation
 CC disorders, autoimmune disorders, inflammatory disorders, immune system
 CC disorders, cancer, AIDS, asthma, atherosclerosis, arthritis, systemic
 CC lupus erythematosus and psoriasis.
 XX
 SQ Sequence 1776 BP; 430 A; 565 C; 490 G; 291 T; 0 other;

Query Match 99.8%; Score 844.4; DB 21; Length 1776;
 Best Local Similarity 99.9%; Pred. No. 3.2e-141;
 Matches 845; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAACTGCGCGCGATGATCAAGAGATGTGCCGAGGACTTCGGAGCTGAGTATCCCG 60
 Db 180 ATGAACTGCGCGCGATGATCAAGAGATGTGCCGAGGACTTCGGAGCTGAGTATCCCG 239
 QY 61 GCCAAGAACTGCTATCGCATGTCTCTCGGCTCTCCAAAGTGGGCAAGACGCCCATC 120
 Db 240 GCCAAGAACTGCTATCGCATGTCTCTCGGCTCTCCAAAGTGGGCAAGACGCCCATC 299
 QY 121 GTGTGGGCTTCTCACCAGCGCGCTTCGAGGAGCGCTTACAGCTCGACATCTCGACACGTC 180
 Db 300 GTGTGGGCTTCTCACCAGCGCGCTTCGAGGAGCGCTTACAGCTCGACATCTCGACACGTC 359
 QY 181 CACCGCAAGTCTTACTCCATCCGCGGAGGTCTACAGCTCGACATCTCGACACGTC 240
 Db 360 CACCGCAAGTCTTACTCCATCCGCGGAGGTCTACAGCTCGACATCTCGACACGTC 419
 QY 241 GCGAACACCGCTTCCCGCGCATGCGGCGCTCTCCATCTCACAGGAGAGCTTTTCATC 300
 Db 420 GCGAACACCGCTTCCCGCGCATGCGGCGCTCTCCATCTCACAGGAGAGCTTTTCATC 479
 QY 301 CTGTGTTTCAGTCTGACACCGCGCTCTTCGAGGAGGTGACGCGCTCAGGACGAG 360
 Db 480 CTGTGTTTCAGTCTGACACCGCGCTCTTCGAGGAGGTGACGCGCTCAGGACGAG 539
 QY 361 ATCTCTGACACCAAGTCTTGGCTCAAGAAACAAACCAAGGAGAGCTGGAGTGCCTCG 420
 Db 540 ATCTCTGACACCAAGTCTTGGCTCAAGAAACAAACCAAGGAGAGCTGGAGTGCCTCG 599
 QY 421 GTATCTCTGCGCAACAAGGTGACCGGCTTCTTACCGGAGGTGGACACGCGAGATC 480
 Db 600 GTATCTCTGCGCAACAAGGTGACCGGCTTCTTACCGGAGGTGGACACGCGAGATC 659
 QY 481 GAGCAGCTGTGGCGGAGCGACCGCGCTTCTTACCGGAGGTGGACACGCGAGATC 540
 Db 660 GAGCAGCTGTGGCGGAGCGACCGCGCTTCTTACCGGAGGTGGACACGCGAGATC 719
 QY 541 AACAGCAGCTTGGACACAGATGTTCCCGCGCTCTTCCCATGAGTTCGGCGCAAGAAG 600
 Db 720 AACAGCAGCTTGGACACAGATGTTCCCGCGCTCTTCCCATGAGTTCGGCGCAAGAAG 779
 QY 601 ATGAGCCAGACCTGCACCGCAAGGTCTCGGTGACGCTTCTGAGATCTCGGCGCAAGAAG 660
 Db 780 ATGAGCCAGACCTGCACCGCAAGGTCTCGGTGACGCTTCTGAGATCTCGGCGCAAGAAG 839
 QY 661 GCGCTGCGGAACAAGAGTGTCTGCGGCGCGGAGCGCGCGCGCGCGCGCGCGCGCG 720
 Db 840 GCGCTGCGGAACAAGAGTGTCTGCGGCGCGGAGCGCGCGCGCGCGCGCGCGCGCG 899
 QY 721 GAGCGCTTTGGCATGCTGCGCAACCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
 Db 900 GAGCGCTTTGGCATGCTGCGCAACCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCG 959
 QY 781 TACATCCGGAAGAGCG 840
 Db 960 TACATCCGGAAGAGCG 1019

Abstract

QY	1	ATGAAC	TGGCCG	GATGATCA	AGAGATGT	CGCCAG	CGACTCG	GAGTAT	CCCG	60
DB	303	ATGAAC	TGGCCG	GATGATCA	AGAGATGT	CGCCAG	CGACTCT	GAGTAT	CCCG	362
QY	61	GCCAA	GAAC	TGCTAT	CGCATGG	TATCCT	CGGTGT	CCAAAG	TGGGCA	120
DB	363	GCCAA	GAAC	TGCTAT	CGCATGG	TATCCT	CGGTGT	CCAAAG	TGGGCA	422
QY	121	GTGTG	CGGTTCT	CAC	CGGCGCT	TCGAGG	AGGCTAC	ACGCTT	ACCATCG	180
DB	423	GTGTG	CGGTTCT	CAC	CGGCGCT	TCGAGG	AGGCTT	ACACCC	TACCTTGA	482
QY	181	CACCG	CAAGT	TTTACT	CGATCC	CGCGGAG	GGTCTAC	CAGCTCG	ACATCCT	240
DB	483	CACCG	CAAGT	TTTACT	CGATCC	CGCGGAG	GGTCTAC	CAGCTCG	ACATCCT	542
QY	241	GGCA	ACCAC	CGGTTCC	CGCGCAT	CGCGGCG	CTCTCC	ATCCTC	AC	284
DB	543	GGCA	ATCAT	CCGTTT	CCCGCAT	CGCGGCG	CTCTAT	CTCTAC	AGTGTAG	602
QY	285	-----	-----	-----	-----	-----	-----	-----	-----	284
DB	603	GACAG	GACCG	TGGGG	AGGGAA	CTGCG	GGGAG	GGATG	GGCGGTGT	662
QY	285	-----	-----	-----	-----	-----	-----	-----	-----	284
DB	663	GCTGT	GCTGT	CTCTC	TCTCTC	GTCTTGG	CAGCTG	CCCTC	ACCTTCC	722
QY	285	-AGG	AGC	GTTT	TATCCT	TGTTT	AGTCTG	GACAA	CCCGG	343
DB	723	TAGG	AGC	GTTT	TATCCT	TGTTT	AGTCTG	GACAA	CCCGG	782
QY	344	AGCG	GCTC	AGGC	AGCAG	ATCCT	CGAC	ACA	AGTCTT	403
DB	783	AAAG	GCTCA	AAC	AGCAG	ATCCT	TAGAC	ACA	AGTCTG	842
QY	404	ACGT	TGG	ACGT	GCCCTG	GTGTC	ATCT	CGCA	CAAGG	463
DB	843	ATGT	TGG	ACGT	GCCCTG	GTGTC	ATCT	CGCA	CAAGG	902
QY	464	TGG	ACC	AGC	CGAG	ATCG	AGCTG	TGTGG	CGAC	523
DB	903	TGG	ACC	AGC	CGAG	ATCG	AGCTG	TGTGG	CGAC	962
QY	524	AGAT	CTCG	CGCA	AGAC	AGAC	CGCCTG	GGAC	AGATG	583
DB	963	AGAT	CTCG	CGCA	AGAC	AGAC	CGCCTG	GGAC	AGATG	1022
QY	584	CAA	AGCT	CGCC	AGCG	AGATG	AGCC	AGAC	CTGCA	643
DB	1023	CAA	AGCT	CGCC	AGCG	AGATG	AGCC	AGAC	CTGCA	1082
QY	644	ACGT	GCTGC	ACA	AGAG	CGCCT	CGCGA	CA	AGCTG	703
DB	1083	ACGT	GCTGC	ACA	AGAG	CGCCT	CGCGA	CA	AGCTG	1139
QY	704	GGG	CGG	CGAC	CGCG	AGCG	CCCTTT	TGG	ATCGT	763
DB	1140	GTG	GGG	CGAC	CGCG	AGATG	CCCTTT	TGG	ATCGT	1199
QY	764	TAC	AC	AGC	AGC	CTCAT	GTAC	TCG	CGAG	823
DB	1200	TGC	AT	AGG	AGC	CTCAT	GTAC	TCG	CGAG	1259
QY	824	AGG	AGC	GCTG	CGT	CAT	CAG	CTAG	846	
DB	1260	AGG	AGC	GCTG	CGT	CAT	CAG	CTAG	1282	

RESULT 9

AAZ36913

ID AAZ36913 standard; DNA: 837 BP.

polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis; psoriasis; gene; ss.

Mus musculus.

WO200210217-A2.

07-FEB-2002.

01-AUG-2001; 2001WO-US24031.

02-AUG-2000; 2000US-222599P.

11-AUG-2000; 2000US-224360P.

11-APR-2001; 2001US-282850P.

(UWJO) UNIV JOHNS HOPKINS.

St Croix B, Kinzler KW, Vogelstein B;

WPI; 2002-291856/33.

P-PSDB; ABB90781.

An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth -

Disclosure; Page 294-295; 331pp; English.

The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein selected from ABB90732, ABB90740, ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumor growth, polycystic kidney disease, subjects bearing a vascularised tumour, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789) are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers (PEM) ABL91903-ABL91995.

Sequence 3020 BP; 690 A; 848 C; 780 G; 702 T; 0 other;

Query Match 42.3%; Score 358; DB 24; Length 3020; Best Local Similarity 66.2%; Pred. No. 6.2e-55; Matches 548; Conservative 0; Mismatches 250; Indels 30; Gaps 1;

13 GCGATGATCAAGAGATGTCGCCGAGGACTCGGACTGAGTATCCCGCCCAAGAACTGC 72
 373 GCCATGATGAAGACCTTGTCCAGTGGGAACTGCACACTCAATGTGCTCTAAGAACTCC 432
 73 TATCGATGTCATCTCGCTCGTCCAGGTGGGCAAGACGCGCCATCGTGTGCGGCTTC 132
 433 TACCGATGTCGTCGTCGTCGCTCCGAGTGGGCAAGAGCTCCATTCCTCCGCTTC 492
 133 CTCACCGGCGCTTCGAGGAGCGCTACACGCTACCATGAGGACTTCACCGCAGTTC 192
 493 CTCATGCGCCCTTTGAGGACCACTACACGCTATCGAGGACTTCATCGCAGGTTG 552
 193 TACTTCATCCCGCGGAGGTCTACACGCTCGACATCTTCGACAGTCCGCGCAACACCGC 252
 553 TACAACTCCACGGGAGATGATGACGCTGATATCTTGACACCTTGACACCAACCCCA 612
 253 TTCGCCGCTATCGGCGCTCTCCATCTCACAGGAGACGCTTTTCATCTGTTGTTCA 312
 613 TTCCTGCTATCGGCGGCTCTCCATCTCACAGGAGATGCTTTCATCTGTTGTTCA 672
 313 CTGACACACCGGACTCTTCGAGGAGGTGCGCGCTCAGGAGGAGTCTTCGACAC 372
 673 CTGGATAGCGGGAGTCTCTTTGATGAGGTCAAGCGCTTCCAGAAACAGATCTTGGAGT 732
 373 AAGTCTTCTCAAGAAACAAACCAAGGAGAACTGGACGTGCGCCCTGGTCTATCTGCGGC 432

733 AAGTCTGCTGCTGAAGATAAACAAGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 792
 433 AACAGAGGTGACCGGAGCTTCTACCGGAGGTGGACCGAGAGATCCAGCAGCTGTTG 492
 793 AACAGAGATGACACACAGTGAAGTGTGCGGCGAGTCCCTGCCATGGAGGCTGAGCTG 852
 493 GGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 552
 853 GTGCTGCTGATGAAGAACTGCGCTATTTTCAGGTTGTCAAGGAGGAGGAGGAGGAG 912
 553 GACAGAGTTCGCGGCTTTCGCGCATGCGCAAGCTGCCAGCGAGATGAGCCGAGAC 612
 913 AACAGAGATGTTCTATGTGCTTTCAGCATGCGCAAGCTGCCAGTCCCTGCCATGAGT 972
 613 CTGACACGCAAGGCTCTCGGTGCTGAGTGTGCTGAGATCTCGGCGCAGGAGGAGGAG 672
 973 CTGACACATAGATCTCGGTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGT 1022
 673 AAGAGAGTGTGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 732
 1023 -----CTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1062
 733 ATCTGTCGACCTTCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 792
 1063 ATGCTGCTCACCCTTTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1122
 793 AAGGCGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 840
 1123 AAGTCTTACGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1170

RESULT 14

AAS90571 ID AAS90571 standard; cDNA; 951 BP.

XX AAS90571;

XX 13-FEB-2002 (first entry)

XX DNA encoding novel human diagnostic protein #26375.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX P-PSDB; ABB26384.

XX New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -

XX Claim 1; SEQ ID No 26375; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome

	317	Conservative	0	Mismatches	87	Indels	1	Gaps
441	TGACCGGACTTCTACCGCGAGGTGACCGCGAGATCGACACCTGGTGGCGACGA	500						
620	TAAACCGGACTTCTACCGGGAATTAACCAACGCGAAATCGAACAACTAATAAAGACGA	561						

Mon Dec 30 09:16:48 2002

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QY 501 CCCCCAGCGCTGGCCCTACTTCGAGATCTGGCCAAAGAAACAGCAGCCTGGACCAGAT 560
Db 560 CCCCCAGCGCTACGCTACTTCGAATCTGGACCAAAAAAACAACACCTAAACCAAT 501
QY 561 GTTCGGCGCGCTCTTCGCCATGGCCAGCTGCCAGCGGAGATGAGCCAGACCTGCACCG 620
Db 500 ATTCCGGCGCTCTTCGCCATAACCAACTACCCAACTACCAAGAAATAAACCCAAACCTACACCG 441
QY 621 CAAGGTCTCGGTGCTACTTCGACGCTGCTGCACAAAGAGCGCTGCGGAACAAGAGCT 680
Db 440 CAAATCTCGATACANTACTACGCTACTACACAAACAAACGCTACGAAACAAACAACT 381
QY 681 GCTCGGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 740
Db 380 ACTACGAACCGACAACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 322
QY 741 ACCCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 800
Db 321 ACCCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 262
QY 801 CGCCGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 845
Db 261 CGCCGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 217

```

Search completed: December 28, 2002, 02:59:52
Job time : 185.866 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 28, 2002, 02:47:28 ; Search time 1119.58 Seconds
(without alignments)
12237.926 Million cell updates/sec

Title: US-09-709-103-1

Perfect score: 846

Sequence: 1 atgaactgcgcgcatgat.....agcgtgcgtcatcagctag 846

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hic:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_hic:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: gb_gss:*
- 18: em_gss_hum:*
- 19: em_gss_inv:*
- 20: em_gss_pln:*
- 21: em_gss_vrt:*
- 22: em_gss_fun:*
- 23: em_gss_mam:*
- 24: em_gss_mus:*
- 25: em_gss_oth:*
- 26: em_gss_pro:*
- 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	695.8	82.2	1035	14	BM919341
2	669.8	79.2	962	13	BM543472
3	664.8	78.6	965	9	AL533318
4	661.8	78.2	742	10	AW028127
5	650.4	76.9	958	14	BQ719566
6	641	75.8	1103	14	BM920514

7	612.6	72.4	1053	14	BM921737
8	586	69.3	1023	13	BM543630
9	580	68.6	1032	14	BQ067637
10	540.8	63.9	758	13	BI553776
11	536.2	63.4	814	13	BI596688
12	521.4	61.6	1137	14	BM921656
13	521.4	61.6	1160	14	BM805574
14	519.6	61.4	831	13	BI596637
15	513.6	60.7	655	12	BG711792
16	513	60.6	649	12	BG085090
17	506	59.8	506	13	BM311047
18	481	56.9	699	12	BG706012
19	470	55.6	700	13	BI596509
20	469	55.4	699	12	BG709229
21	448	53.0	674	13	BI601563
22	446	52.7	617	13	BI393669
23	439	51.9	726	12	BF613135
24	438.8	51.9	675	13	BI545172
25	433.4	51.2	666	13	BI549939
26	427.8	50.6	644	13	BG969048
27	426.4	50.4	689	10	BM632699
28	417.6	49.4	589	13	BM426066
29	415.8	49.1	648	10	BM636889
30	401.6	47.5	571	13	BI682922
31	401	47.4	1006	14	BQ073742
32	399	47.2	947	14	BQ954076
33	389.6	46.1	904	14	BQ947936
34	386.4	45.7	1438	14	BM807669
35	384.2	45.4	888	13	BI754083
36	374.2	44.2	640	13	BJ490945
37	365.6	43.2	505	13	BI391213
38	362.8	42.9	509	10	AW915326
39	359	42.4	1332	13	BM460899
40	358	42.3	1300	11	AK015898
41	354	41.8	456	12	BF555582
42	351	41.5	556	12	BG654362
43	349.6	41.3	710	13	BJ526038
44	342	40.4	1404	13	BM548645
45	341	40.3	531	13	BI823596

ALIGNMENTS

RESULT 1	BM919341	BM919341	1035 bp	linear	EST 12-MAR-2002
LOCUS	AGNCOURT_6715681	NIH_MGC_120	Homo sapiens	cdna clone	IMAGE:5748585
DEFINITION	5', mRNA sequence.				
ACCESSION	BM919341				
VERSION	BM919341.1	GI:19369720			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
TITLE	1 (bases 1 to 1035)				
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/				
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)				
	Unpublished (1999)				
	Contact: Robert Strausberg, Ph.D.				
	Email: cgapbs-femail.nih.gov				
	Tissue Procurement: Life Technologies, Inc.				
	CDNA Library Preparation: Life Technologies, Inc.				
	DNA sequencing by: The I.M.G.E. Consortium (LLNL)				
	Clone distribution by: Agencourt Bioscience Corporation				
	found through the I.M.G.E. Consortium/LLNL at:				
	http://image.llnl.gov				
	Plate: LLAM12776				
	High quality sequence stop: 658.				
	Location/Qualifiers				
	1. .1035				

FEATURES
source

18 GGCAGCCTTTGG---CATCGTGGACCTTCGCGCGCGGC 757


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Db 524 CTGGTGTTCAGTCTGGACAAACCGCGACTCTTCGAGGAGGTGTCAGCGGCTCAGGACGAG 583
QY 361 ATCTCTGACACCAAGTCTTGCCTCAAGAACAAACCAAGGAGAGACGTGGAGCTGCCCTTG 420
Db 584 ATCTCTGACACCAAGTCTTGCCTCAAGAACAAACCAAGGAGAGACGTGGAGCTGCCCTTG 643
QY 421 GTCATCTGGGGCAACCAAGGTGACCGCGACTTCTACCGGAGGTGGACACGCGGAGATC 480
Db 644 GTCATCTGGGGCAACCAAGGTGACCGCGACTTCTACCGGAGGTGGACACGCGGAGATC 703
QY 481 GAGCAGTGTGGGGGAGACACCGCGCTGCGCTTCTACCGGAGGTGGACACGCGGAGATC 540
Db 704 GAGCAGTGTGGGGGAGACACCGCGCTGCGCTTCTACCGGAGGTGGACACGCGGAGATC 763
QY 541 AACACAGCCCTGGGACGAGTCTCCGCGCGCTTCTGCGCATGTCGCGGAGTGGACACGCGGAG 600
Db 764 AACACAGCCCTGGGACGAGTCTCCGCGCGCTTCTGCGCATGTCGCGGAGTGGACACGCGGAG 823
QY 601 ATGAGCCGACACCTGCACCCGCAAGGTCTCGGTGCACTGCGGAGTGGACACGCGGAGATC 660
Db 824 ATGAGCCGACACCTGCACCCGCAAGGTCTCGGTGCACTGCGGAGTGGACACGCGGAGATC 883
QY 661 GCGCTGC-GGAACAAGAGTGTCTGCGGCGCG 692
Db 884 GCGCTGCGGACAGAAACCTGCTGCGGCGCG 916

RESULT 4
AL533318 965 bp mRNA linear EST 13-FEB-2001
LOCUS AL533318 LFI_FL015_Brn1 Homo sapiens cDNA clone CS0DN003YJ19 5
DEFINITION Prime, mRNA sequence.
ACCESSION AL533318
VERSION AL533318.1 GI:12796811
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
1..965
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DN003YJ19"
/clone_lib="LFI_FL015_Brn1"
/sex="male"
/tissue_type="Adult brain"
/notes="Vector: pCMVSPORT 6; Site:1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was constructed by Life Technologies.
Contact : Feng Liang Life Technologies, a division of
Invitrogen 9800 Medical Center Drive Rockville, Maryland
20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 189 a 352 c 273 g 144 t 7 others
ORIGIN
Query Match 78.6%; Score 664.8; DB 9; Length 965;
Best Local Similarity 95.5%; Pred. No. 1.2e-120;
Matches 720; Conservative 7; Mismatches 19; Indels 8; Gaps 4;

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QY 1 ATGAAGTGGCGCGATGATCAAGAAGATGTGCCGAGGAGCTCGGAGCTGAGTATCCCG 60
Db 191 ATGAAGTGGCGCGATGATCAAGAAGATGTGCCGAGGAGCTCGGAGCTGAGTATCCCG 250
QY 61 GCCAAGAACTGCTATCGCATGCTATCCTCGCTGCTCAAGGTGGCAAGCGCCATC 120
Db 251 GCCAAGAACTGCTATCGCATGCTATCCTCGCTGCTCAAGGTGGCAAGCGCCATC 310
QY 121 GTGTGCGGCTTCTCACCAGCGGCTTCGAGGAGGCTTACAGCCCTACCATCGAGACTTC 180
Db 311 GTGTGCGGCTTCTCACCAGCGGCTTCGAGGAGGCTTACAGCCCTACCATCGAGACTTC 370
QY 181 CACCGCAAGTCTTACTCCATCCGCGGAGGCTTACAGCTCGACATCTCGACAGTTC 240
Db 371 CACCGCAAGTCTTACTCCATCCGCGGAGGCTTACAGCTCGACATCTCGACAGTTC 430
QY 241 GGCAACACCCGCTTCCCGGCAATGCGGCGCTTCCATCTCAGAGAGAGCTTTTCATC 300
Db 431 GGCAACACCCGCTTCCCGGCAATGCGGCGCTTCCATCTCAGAGAGAGCTTTTCATC 489
QY 301 CTGGTGTTCAGTCTGGCAACCGGAGTCTTCGAGGAGGTGCGAGGCTCGAGGAGCAG 360
Db 490 CTGGTGTTCAGTCTGGCAACCGGAGTCTTCGAGGAGGTGCGAGGCTCGAGGAGCAG 549
QY 361 ATCTCTCGACACCAAGTCTTGCCTCAAGAACAAACCAAGGAGAACTGGACGTGCCCTG 420
Db 550 ATCTCTCGACACCAAGTCTTGCCTCAAGAACAAACCAAGGAGAACTGGACGTGCCCTG 609
QY 421 GTCATCTCGGCAACAAAGGTGACCGGAGTCTTACCGGAGGTGACCGAGGAGATC 480
Db 610 GTCATCTCGGCAACAAAGGTGACCGGAGTCTTACCGGAGGTGACCGAGGAGATC 669
QY 481 GAGCAGTGTGGGCGAGGAGACCCCGCTGCGCTTCTCGAGATCTCGGCAAGAG 540
Db 670 GAGCAGTGTGGGCGAGGAGACCCCGCTGCGCTTCTCGAGATCTCGGCAAGAG 729
QY 541 AACAGCAGCTTGGACCAAGATGTTCCGCGGCTTTCGCGATCGCCCAAGTGGCCAGGAG 600
Db 730 AACAGCAGCTTGGACCAAGATGTTCCGCGGCTTTCGCGATCGCCCAAGTGGCCAGGAG 789
QY 601 ATGAGCCGACACCTGCACCGCAAGGTCTCGGTGCACTGCGAGTCTGCTGCAAGAG 660
Db 790 ATGAGCCGACACCTGCACCGCAAGGTCTCGGTGCACTGCGAGTCTGCTGCAAGAG 848
QY 661 GCGCTCGGAAACAAAGTCTGCGGCGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCG 720
Db 849 GCGCTCGGAAACAA-AARCTGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 902
QY 721 GAGCGCTTTGGCATGTCGGACACCTTTCGCGGCGGCGGCGGCGGCGGCGGCGGCG 754
Db 903 GCGAGCTTTTGGCATGTCGGACACCTTTCGCGGCGGCGGCGGCGGCGGCGGCGGCG 936

RESULT 4
AL533318 742 bp mRNA linear EST 27-OCT-1999
LOCUS W26c07.xl NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2530668 3.
DEFINITION similar to TR:O35626 O35626 RAS, DEXAMETHASONE-INDUCED 1 ;, mRNA
sequence.
ACCESSION AL533318
VERSION AL533318.1 GI:5886883
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov

```


Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 www.blo.llnl.gov/bbrp/image/image.html
 Seq primer: -40UP from Gibco
 High quality sequence stop: 445.

FEATURES

source
 1. 742
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2530668"
 /clone_lib="NCI_CGAP_Kid11"
 /lab_host="DH10B"
 /note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 132376-132391, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo."
 BASE COUNT 149 a 260 c 208 g 122 t 3 others

Query Match 78.2%; Score 661.8; DB 10; Length 742;
 Best Local Similarity 97.3%; Pred. No. 4.4e-120;
 Matches 672; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
 QY 1 ATGAACCTGGCGGATGATCAAGAGATGTGCCGAGCGACTCGGAGTGTATCCCG 60
 Db 35 ATGAACCTGGCGGATGATCAAGAGATGTGCCGAGCGACTCGGAGTGTATCCCG 94
 QY 61 GCCAAGACTGCTATCGATGCTATCTCTGGCTCTCAAGTGGGCAAGCGGCATC 120
 Db 95 GCCAAGACTGCTATCGATGCTATCTCTGGCTCTCAAGTGGGCAAGCGGCATC 154
 QY 121 GTGTGGGCTTCTTCCATCCGCGGCTTGAGGAGCGCTTACAGCCTACCTGAGGACTTC 180
 Db 155 GTGTGGGCTTCTTCCATCCGCGGCTTGAGGAGCGCTTACAGCCTACCTGAGGACTTC 214
 QY 181 CACCGCAAGTCTTACTCCATCCGCGGAGTGTCTACAGCTCGACATCTCTCGACAGTCC 240
 Db 215 CACCGCAAGTCTTACTCCATCCGCGGAGTGTCTACAGCTCGACATCTCTCGACAGTCC 274
 QY 241 GGCACACACCGGTTCCCGGCTATCGGCGCTCTCCATCTCTCAGGAGACGTTTTCATC 300
 Db 275 GGCACACACCGGTTCCCGGCTATCGGCGCTCTCCATCTCTCAGGAGACGTTTTCATC 334
 QY 301 CTGGTGTTCAGTCTGGACACCGGACTCTCTCGAGAGGTGTCAGCGGCTCAGGAGCAG 360
 Db 335 CTGGTGTTCAGTCTGGACACCGGACTCTCTCGAGAGGTGTCAGCGGCTCAGGAGCAG 394
 QY 361 ATCTCGACACCAAGTCTTGGCTCAAGAACCAAAACCAAGAGAGACGTGGAGCTGCCCTG 420
 Db 395 ATCTCGACACCAAGTCTTGGCTCAAGAACCAAAACCAAGAGAGACGTGGAGCTGCCCTG 454
 QY 421 GTCATCTGGGGCAACAGGGTACCGGACTCTTACCGGAGGTGGACACGCGGAGATC 480
 Db 455 GTCATCTGGGGCAACAGGGTACCGGACTCTTACCGGAGGTGGACACGCGGAGATC 514
 QY 481 GAGCAGCTGTGGGCGACGACGCCAGCGCTCGGCTCTACTTGGAGATCTCGGCCAAGAG 540
 Db 515 GAGCAGCTGTGGGCGACGACGCCAGCGCTCGGCTCTACTTGGAGATCTCGGCCAAGAG 574
 QY 541 AACAGCAGCTGGACGAGATGTTCCCGGCTCTTCGCGATGCGCAAGCTGCCAGCGAG 600
 Db 575 AACAGCAGCTGGACGAGATGTTCCCGGCTCTTCGCGATGCGCAAGCTGCCAGCGAG 634

QY 601 ATGAGCCAGACCTGCACCGCAAGGTTCTGGTGCAGTACTGCGAGCTGTGCACAGAAG 660
 Db 635 ATGAGCCAGACCTGCACCGCAAGGTTCTGGTGCAGTACTGCGAGCTGTGCACAGAAG 694
 QY 661 GCGCTGCGGAACAGAGAGTGTGCGGGCGG 691
 Db 695 GCGCTGCGGAACAGAGAGTGTGCGGGTCCG 725

RESULT 5

BQ719566 958 bp mRNA linear EST 16-JUL-2002
 LOCUS BQ719566
 DEFINITION AGENCOURT_8305191 Lupski_sympathetic_trunk Homo sapiens cDNA clone
 IMAGE:6193170 5', mRNA sequence.
 ACCESSION BQ719566
 VERSION BQ719566.1 GI:21858463
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 958)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue procurement: Dr. James R. Lupski
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM13596 row: f column: 19
 High quality sequence stop: 514.
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 /db_xref="taxon:9606"
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 /sex="male"
 /tissue_type="sympathetic trunk"
 /dev_stage="adult, 16 yr"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCACGCGTCCG-3' and 5'-GACTAGTCTAGATCGGAGCGGCGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life Technologies."

FEATURES

source
 1. 958
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6193170"
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 /sex="male"
 /tissue_type="sympathetic trunk"
 /dev_stage="adult, 16 yr"
 /lab_host="DH10B"
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BASE COUNT 185 a 339 c 275 g 159 t

Query Match 76.9%; Score 650.4; DB 14; Length 958;
 Best Local Similarity 95.0%; Pred. No. 7.8e-118;
 Matches 684; Conservative 0; Mismatches 31; Indels 5; Gaps 1;
 QY 43 TCGGAGCTGAGTATCCGGCCCAAGAACTGCTATCGCATGGTTCATCTCGGCTCGTCCAAG 102
 Db 1 TCGGAGCTGAGTATCCGGCCCAAGAACTGCTATCGCATGGTTCATCTCGGCTCGTCCAAG 60
 QY 103 GTGGGCAAGACGGCCATCGTGTGGCGCTTCTTACCGCGCGCTCGAGGACGCTACACG 162
 Db 61 GTGGGCAAGACGGCCATCGTGTGGCGCTTCTTACCGCGCGCTCGAGGACGCTACACG 120
 QY 163 CCTACCATGAGGACTTCCACCGCAGTCTTACTCATCCGCGGCGAGGTCTTACCAGCTC 222


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Db 121 CCTACATCGAGGACTTCACCGCAAGTTCTACTCTCATCCGCGGAGGTCTACAGCTC 180
QY 223 GACATCTCGACAGCTCCGCGCAACACCGTTCCCGCGCATCGCGGCTCTCATCTC 282
Db 181 GACATCTCGACAGCTCCGCGCAACACCGTTCCCGCGCATCGCGGCTCTCATCTC 240
QY 283 ACAGGAGAGGTTTTCATCTGCTGTGTAGTCTGGCAACCCGACTCTCTCGAGGAGTG 342
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QY 343 CAGCGGCTCAGGACAGATCTCGACACCAAGTCTTGCCTCAGAACCAACCAAGGAG 402
Db 301 CAGCGGCTCAGGACAGATCTCGACACCAAGTCTTGCCTCAGAACCAACCAAGGAG 360
QY 403 AACGTGGAGCTCCCGCTTGTCTATCTGGCGCAACCAAGGTTGACCGGACTTCTACCGGAG 462
Db 361 AACGTGGAGCTCCCGCTTGTCTATCTGGCGCAACCAAGGTTGACCGGACTTCTACCGGAG 420
QY 463 GTGGACACGCGGAGATCGAGCAGCTGTGGGCGACACCCCGAGCGCTCGGCTACTTC 522
Db 421 GTGGACACGCGGAGATCGAGCAGCTGTGGGCGACACCCCGAGCGCTCGGCTACTTC 480
QY 523 GAGATCTCGGCAAGACAGCAGCTGTGGACAGATGTTCCGCGGCTCTTTCGCCATG 582
Db 481 GAGATCTCGGCAAGACAGCAGCTGTGGACAGATGTTCCGCGGCTCTTTCGCCATG 540
QY 583 GCCAAGTCCCGGAGATGAGCCAGACCTGCACCGCAAGTCTTCGCTGAGTACTGC 642
Db 541 GCCAAGTCCCGGAGATGAGCCAGACCTGCACCGCAAGTCTTCGCTGAGTACTGC 600
QY 643 GAGCTGTGCACAAAGAGGCGTTCGCGCAACCAAGGTTGACCGGACTTCTACCGGAG 660
Db 601 GAGCTGTGCACAAAGAGGCGTTCGCGCAACCAAGGTTGACCGGACTTCTACCGGAG 620
QY 698 GCGGCGGCGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 757
Db 661 GCGGCGGCGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720

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RESULT 6
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LOCUS BM920514 1103 bp mRNA linear EST 12-MAR-2002
DEFINITION AGENCOURT_6709473 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5750507
5', mRNA sequence.
ACCESSION BM920514
VERSION BM920514.1 GI:19370893
KEYWORDS EST.
SOURCE Human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: Agencourt Bioscience Corporation
Found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12781 row: j column: 12
High quality sequence stop: 676.
Location/Qualifiers
1. .1103
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5750507"
/clone_lib="NIH_MGC_122"
FEATURES
source

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/lab_host="DH10B"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."
BASE COUNT 230 a 402 c 314 g 156 t
ORIGIN 1 others

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Query Match 75.8%; Score 641; DB 14; Length 1103;
Best Local Similarity 90.7%; Pred. No. 5.5e-116;
Matches 764; Conservative 0; Mismatches 61; Indels 17; Gaps 7;
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Db 201 ATGAAGTGGCGGCGGATGATCAAGAGATGTGCCGAGGACTCGGAGCTGAGTATCCCG 260
QY 61 GCCAAGAACTGCTATCCGATGTCATCTCGGCTCTGTCGAGGTGGGCAAGCGGCATC 120
Db 261 GCCAAGAACTGCTATCCGATGTCATCTCGGCTCTGTCGAGGTGGGCAAGCGGCATC 320
QY 121 GTGTGCGGCTTCTTACCGCGCGCTTTCGAGGAGCGCTTACACGCTACCATCGAGGACTTC 180
Db 321 GTGTGCGGCTTCTTACCGCGCGCTTTCGAGGAGCGCTTACACGCTACCATCGAGGACTTC 380
QY 181 CACGCAAGTCTTACTCCATCCGCGGAGGTTACAGCTCGACATCTCGACACGTC 240
Db 381 CACGCAAGTCTTACTCCATCCGCGGAGGTTACAGCTCGACATCTCGACACGTC 440
QY 241 GGCACACACCGTTCCCGGCGCATTCGAGGAGGTTGCGGCTTCCATCTCAGAGGAGCTTTTCATC 300
Db 441 GGCACACACCGTTCCCGGCGCATTCGAGGAGGTTGCGGCTTCCATCTCAGAGGAGCTTTTCATC 500
QY 301 CTGGTCTTCAGTCTGGACAAACCGGACTTCTTCGAGGAGGTTGCGGCTTCCAGCAGCAG 360
Db 501 CTGGTCTTCAGTCTGGACAAACCGGACTTCTTCGAGGAGGTTGCGGCTTCCAGCAGCAG 560
QY 361 ATCTCTGCACCAAGTCTTTCGCTCAAGAACAAACCAAGGAGGAGGAGGAGGAGGAG 420
Db 561 ATCTCTGCACCAAGTCTTTCGCTCAAGAACAAACCAAGGAGGAGGAGGAGGAGGAG 620
QY 421 GTATCTCTGCGCAACCAAGGTTGACCGGCGCTTACCGGAGGTTGACCGGAGGAGGAG 480
Db 621 GTATCTCTGCGCAACCAAGGTTGACCGGCGCTTACCGGAGGTTGACCGGAGGAGGAG 680
QY 481 GAGCAGCTGGTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
Db 681 GAGCAGCTGGTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 740
QY 541 AACAGCAGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 599
Db 741 AA-AGCAGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 799
QY 600 GATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 659
Db 800 GATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 859
QY 660 GCGGC-TGCGGCAACAA-----GCTGCTGCGGCGGCGGAGGAGGAGGAGGAGGAG 711
Db 860 AGGCTTGGCGAACAAGAAAGCTGTTGGGCGCGGCAACCGCGGCGGCGGCGGCGGCA 919
QY 712 GACCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 968
Db 920 ACCGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 979
QY 769 AGCG-ACCTCATGTATCGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 824
Db 980 AGGGAACCTTATGGAAATCCCGCAAAAGCAACCGCGGCGGAGGAGGAGGAGGAGGAG 1039

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[illegible]

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RESULT 8
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LOCUS      BM543630
DEFINITION Agencourt_6492527 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5726764
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ACCESSION  BM543630
VERSION     BM543630.1 GI:18774186
KEYWORDS   EST.
SOURCE      human.
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1023)
             NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS     National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE       Unpublished (1999)
JOURNAL
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgabs@mail.nih.gov
              Tissue Procurement: Invitrogen
              CDNA Library Preparation: Life Technologies, Inc.
              CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLAM12719 row: m column: 05
              High quality sequence stop: 637.
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                    /clone="IMAGE:5726764"
                    /clone_lib="NIH_MGC_124"
                    /tissue_type="hippocampus"
                    /lab_host="DH10B"
                    /note="Organ: brain; vector: pCMV-SPORT6; site_1: EcoRV
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/db_xref="taxon:9606"
/clone="IMAGE:5753301"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
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source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: This is a NIH MGC library."
BASE COUNT  215 a 390 c 297 g 150 t 1 others
ORIGIN
Query Match          72.4%; Score 612.6; DB 14; Length 1053;
Best Local Similarity 92.0%; Pred. No. 2.1e-110;
Matches 669; Conservative 0; Mismatches 54; Indels 4; Gaps 2;
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(destroyed); Site_2: NotI; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012.*

BASE COUNT 196 a 378 c 281 g 168 t
ORIGIN

Query Match 69.3%; Score 586; DB 13; Length 1023;
Best Local Similarity 97.9%; Pred. No. 3.4e-105;
Matches 615; Conservative 0; Mismatches 10; Indels 3; Gaps 2;

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QY 1 ATGAAGACTGGCGGATCATCAAGAGATGTGCCGAGGACGCTCGAGCTGAGTATCCCG 60
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Db 149 ATGAAGACTGGCGGATCATCAAGAGATGTGCCGAGGACGCTCGAGCTGAGTATCCCG 208
QY 61 GCCAAGAACTGCTATCGCATGTTCATCTCGGCTCTCCAGGTGGGCAAGAGGCGCATC 120
   |||
Db 209 GCCAAGAACTGCTATCGCATGTTCATCTCGGCTCTCCAGGTGGGCAAGAGGCGCATC 268
QY 121 GTGTGGCGCTTCTTCCAGGCGGCTTGGAGGCGCTACACGCCCTACCATCGAGGACTTC 180
   |||
Db 269 GTGTGGCGCTTCTTCCAGGCGGCTTGGAGGCGCTACACGCCCTACCATCGAGGACTTC 328
QY 181 CACCGCAAGTTTACTTCCATCCCGGCGAGGCTTACCAGCTCGACATCTCGACACGTC 240
   |||
Db 329 CACCGCAAGTTTACTTCCATCCCGGCGAGGCTTACCAGCTCGACATCTCGACACGTC 388
QY 241 GGCACACACCGTTCGCCGCGATGCGGCGCTTCCATCTCCACAGGAGAGCTTTTCATC 300
   |||
Db 389 GGCACACACCGTTCGCCGCGATGCGGCGCTTCCATCTCCACAGGAGAGCTTTTCATC 448
QY 301 CTGGTGTTCAGTCTGACAAACCGGAGCTCTTCGAGGAGGTGCGAGGCTCAGCGACAG 360
   |||
Db 449 CTGGTGTTCAGTCTGACAAACCGGAGCTCTTCGAGGAGGTGCGAGGCTCAGCGACAG 508
QY 361 ATCTCGACACCAAGTCTTGGCTCTCAAGAACAAACCAAGGAGAACTGGAGCTGCCCTG 420
   |||
Db 509 ATCTCGACACCAAGTCTTGGCTCTCAAGAACAAACCAAGGAGAACTGGAGCTGCCCTG 568
QY 421 GTCATCTGGGCAACAAAGGTTGACCGGACTTCTTACCGGAGGTGGACAGCGGAGATC 480
   |||
Db 569 GTCATCTGGGCAACAAAGGTTGACCGGACTTCTTACCGGAGGTGGACAGCGGAGATC 628
QY 481 GAGCAGCTGGTGGGCGAGACCCCGAGCGCTTACTTCCAGATCTCGGCAAGAAAG 540
   |||
Db 629 GAGCAGCTGGTGGGCGAGACCCCGAGCGCTTACTTCCAGATCTCGGCAAGAAAG 688
QY 541 AACAGCAGCT--GACACAGATGTTCCGCGGCTTTCGCCATGGCC--AAGCTGCCAGC 597
   |||
Db 689 AACAGCAGCTGGGACAGATGTTCCGCGGCTTTCGCCATGGCCAAAGCTGCCCGCG 748
QY 598 GAGATGAGCCAGACCTGACCCGCAAG 625
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Db 749 GAGATGAGCCAGACCTGACCCGCAAG 776

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RESULT 9
BQ067637
LOCUS BQ067637 1032 bp mRNA linear EST 02-APR-2002
DEFINITION AGENCOURT_6759053 NIH_MGC_115 Homo sapiens cdna clone IMAGE:5755214
5', mRNA sequence.

ACCESSION BQ067637
VERSION BQ067637.1 GI:19896683
KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1032)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/.

TITLE JOURNAL COMMENT

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaps@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)
CDNA Library Arrayed by: Agencourt Bioscience Corporation
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12793 row: n column: 15
High quality sequence stop: 602.

FEATURES source

Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5755214"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"

/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH-MGC Library."

BASE COUNT 210 a 375 c 298 g 148 t 1 others
ORIGIN

Query Match 68.6%; Score 580; DB 14; Length 1032;
Best Local Similarity 91.6%; Pred. No. 5.1e-104;
Matches 683; Conservative 0; Mismatches 50; Indels 13; Gaps 6;

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QY 1 ATGAAGACTGGCGGATCATCAAGAGATGTGCCGAGGACGCTCGAGCTGAGTATCCCG 60
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Db 201 ATGAAGACTGGCGGATCATCAAGAGATGTGCCGAGGACGCTCGAGCTGAGTATCCCG 260
QY 61 GCCAAGAACTGCTATCGCATGTTCATCTCGGCTCTCCAGGTGGGCAAGAGGCGCATC 120
   |||
Db 261 GCCAAGAACTGCTATCGCATGTTCATCTCGGCTCTCCAGGTGGGCAAGAGGCGCATC 320
QY 121 GTGTGGCGCTTCTTCCAGGCGGCTTGGAGGCGCTACACGCCCTACCATCGAGGACTTC 180
   |||
Db 321 GTGTGGCGCTTCTTCCAGGCGGCTTGGAGGCGCTACACGCCCTACCATCGAGGACTTC 380
QY 181 CACCGCAAGTTTACTTCCATCCCGGCGAGGCTTACCAGCTCGACATCTCGACACGTC 240
   |||
Db 381 CACCGCAAGTTTACTTCCATCCCGGCGAGGCTTACCAGCTCGACATCTCGACACGTC 440
QY 241 GGCACACACCGTTCGCCGCGATGCGGCGCTTCCATCTCCACAGGAGAGCTTTTCATC 300
   |||
Db 441 GGCACACACCGTTCGCCGCGATGCGGCGCTTCCATCTCCACAGGAGAGCTTTTCATC 500
QY 301 CTGGTGTTCAGTCTGACAAACCGGAGCTTTCGAGGAGGTGCGAGGCTCAGCGACAG 360
   |||
Db 501 CTGGTGTTCAGTCTGACAAACCGGAGCTTTCGAGGAGGTGCGAGGCTCAGCGACAG 560
QY 361 ATCTCTGACACCAAGTCTTGGCTCTCAAGAACAAACCAAGGAGAACTGGAGCTGCCCTG 420
   |||
Db 561 ATCTCTGACACCAAGTCTTGGCTCTCAAGAACAAACCAAGGAGAACTGGAGCTGCCCTG 620
QY 421 GTCATCTGGGCAACAAAGGTTGACCGGACTTCTACCGGAGGTGGACAGCGGAGATC 480
   |||
Db 621 GTCATCTGGGCAACAAAGGTTGACCGGACTTCTACCGGAGGTGGACAGCGGAGATC 680
QY 481 GAGCAGCTGGTGGGCGAGACCCCGAGCGCTTCTTCCAGATCTCGGCAAGAAAG 540
   |||
Db 681 GAGCAGCTGGTGGGCGAGACCCCGAGCGCTTCTTCCAGATCTCGGCAAGAAAG 740

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Mon Dec 30 09:16:52 2002

352 AGGAGCAGATCTCGACACCAAGTCTTGCTCAAGAACAAACAA -GGAGAGCTGA 410
 66 AGGAGCAGATCTCGACACCAAGTCTTGCTCAAGAACAAACAA -GGAGAGCTGA 125
 411 CGTCCCTCGTCAATCGCGGCAACAGGTGACCGGAGTCTTACCGGAGGTGACCA 470
 126 CGTCCCTCGTCAATCGCGGCAACAGGTGACCGGAGTCTTACCGGAGGTGACCA 185
 471 GCGGAGATCGACAGCTGGTGGGCGACGACCCAGCGCTGCGCTTACCTTCGAGATCTC 530
 186 GCGGAGATCGACAGCTGGTGGGCGACGACCCAGCGCTGCGCTTACCTTCGAGATCTC 245
 531 GCGGAGATCGACAGCTGGTGGGCGACGACCCAGCGCTGCGCTTACCTTCGAGATCTC 590
 246 GCGGAGATCGACAGCTGGTGGGCGACGACCCAGCGCTGCGCTTACCTTCGAGATCTC 305
 591 GCGGAGATCGACAGCTGGTGGGCGACGACCCAGCGCTGCGCTTACCTTCGAGATCTC 650
 306 GCGGAGATCGACAGCTGGTGGGCGACGACCCAGCGCTGCGCTTACCTTCGAGATCTC 365
 651 GCGGAGATCGACAGCTGGTGGGCGACGACCCAGCGCTGCGCTTACCTTCGAGATCTC 710
 366 GCGGAGATCGACAGCTGGTGGGCGACGACCCAGCGCTGCGCTTACCTTCGAGATCTC 425
 711 GCGGAGATCGACAGCTGGTGGGCGACGACCCAGCGCTGCGCTTACCTTCGAGATCTC 770
 426 GCGGAGATCGACAGCTGGTGGGCGACGACCCAGCGCTGCGCTTACCTTCGAGATCTC 485
 771 GCGGAGATCGACAGCTGGTGGGCGACGACCCAGCGCTGCGCTTACCTTCGAGATCTC 830
 486 GCGGAGATCGACAGCTGGTGGGCGACGACCCAGCGCTGCGCTTACCTTCGAGATCTC 545
 831 CTGCGTCATCAGCTAG 846
 546 CTGCGTCATCAGCTAG 561

RESULT 11
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 LOCUS 603243262F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5285894 5',
 DEFINITION mRNA sequence.
 ACCESSION BI596688
 VERSION BI596688.1 GI:15489627
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 814)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaaps-remail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM1722 row: k column: 15
 High quality sequence stop: 803.
 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:5285894"
 /clone_lib="NIH_MGC_96"
 /tissue_type="hypothalamus"
 /lab_host="DH10B"

FEATURES

source

541 AACAGCAGCTGG-ACAGATGTTCCGCGCTCTTCG-CCATGGCCAAAGCTGCCAG-C 597
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 598 GAGATGAG-CCAGACCTGACACC-CAAGGTCTCGTGTGAGT-----ACTGCCAGCT 647
 801 GAGATGAGCCAGACCTGACACC-CAAGGTCTCGTGTGAGT-----ACTGCCAGCT 660
 648 GCTGCACGAAGAGCGCTGCGGCAACAGAGCTCTCGGCGCGGCGGCGCGCGG 707
 861 ACAAAAAGGCGCTGCGGCAACAAACCTTCTCGGCGCGGCGGCGGCGGCGG 920
 708 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 733
 921 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 946

RESULT 10
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 LOCUS 603190722F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5262101 5',
 DEFINITION mRNA sequence.
 ACCESSION BI553776
 VERSION BI553776.1 GI:15441088
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 758)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaaps-remail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM1660 row: 1 column: 06
 High quality sequence stop: 738.
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 1. .758
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); Oligo-dr primed using primer 5'-gtttttttttttttttt-3',
 size-selected for average insert size 2.5 kb and
 normalized to ROT 5. This is a primary library enriched
 for full-length clones and constructed using the
 Cap-trapper method (Carninci, in preparation). Library
 constructed by M. Brownstein (NIH/NHGRI, National
 Institutes of Health). Note: this is a NIH_MGC Library."

FEATURES

source

BASE COUNT 155 a 252 c 249 g 102 t
 ORIGIN
 Query Match 63.9%; Score 540.8; DB 13; Length 758;
 Best Local Similarity 99.5%; Pred. No. 2.4e-96;
 Matches 553; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 292 GTTTCATCTGTTGTTCACTCGGACACCGGCGGCGGCGGCGGCGGCGGCTC 351
 6 GTTTCATCTGTTGTTCACTCGGACACCGGCGGCGGCGGCGGCGGCGGCTC 65

BASE COUNT 160 a 310 c 225 g 119 t
ORIGIN
/note="Organ: brain; Vector: pBluescriptR (modified
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g); Oligo-dT primed using primer 5'-gtttttttttttttttttt-3',
size-selected for average insert size 2.3 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIMH/NEHRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
160 a 310 c 225 g 119 t

Db	760	AAACAGCATCCCTGGACCCCAATGTTCCGGGGCTCTCTCCCTCGCCCAACCTGCCAG	819
Qy	598	GAGATGAGC	606
Db	820	CGGAGAAGC	828
RESULT 13			
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AGENCY	AGENCY	NIH_MGC_124	Homo sapiens
DEFINITION	5', mRNA	sequence	
ACCESSION	BM805574		
VERSION	BM805574.1	GI:19122397	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	NIH-MGC	http://mgi.nci.nih.gov/.	
TITLE	1 (bases 1 to 1160)		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-remail.nih.gov		
	Tissue Procurement: Invitrogen		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:		
	http://image.llnl.gov		
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BASE COUNT	207 a	473 c	279 g
ORIGIN	201 t		
Query Match	61.68;	Score 521;	DB 14; Length 1160;
Best Local Similarity	97.18;	Pred. No. 1.9e-92;	
Matches	541; Conservative	0; Mismatches	15; Indels
			1; Gaps
Qy	1	ATGAAGTGGCGGCGATCAAGAAGATGTGCCCGGAGCTCGGAGCTGAGTATCCCG	60
Db	197	ATGAAGTGGCGGCGATCAAGAAGATGTGCCCGGAGCTCGGAGCTGAGTATCCCG	256
Qy	61	GCAAGAACTGTATCGATGTCATCTCGGCTCGTCCAGGTGGGCAAGCGGCCATC	120
Db	257	GCAAGAACTGTATCGATGTCATCTCGGCTCGTCCAGGTGGGCAAGCGGCCATC	316
Qy	121	GTCTCGGCTCTCTACCGCGGCTTCGAGGAGCGCTACAGCGCTACCGTACGAGACTC	180
Db	317	GTCTCGGCTCTCTACCGCGGCTTCGAGGAGCGCTACAGCGCTACCGTACGAGACTC	376
Qy	181	CACCGCAAGTTTACTTCCATCCGCGGAGGTCTACGAGCTCGACATCTCGACAGTCC	240
Db	377	CACCGCAAGTTTACTTCCATCCGCGGAGGTCTACGAGCTCGACATCTCGACAGTCC	436
Qy	241	GGCAACACCGTTCCCGCATGCGCGCTCTCCATCTCACAGGAGACGCTTTTCATC	300
Db	437	GGCAACACCGTTCCCGCATGCGCGCTCTCCATCTCACAGGAGACGCTTTTCATC	496
Qy	301	CTGGTGTTCAGTCTGGACAAACCGGAGCTCTCGAGGAGGTGCGAGCGCTCAGGAGCAG	360
Db	497	CTGGTGTTCAGTCTGGACAAACCGGAGCTCTCGAGGAGGTGCGAGCGCTCAGGAGCAG	556
Qy	361	ATCTCTGACACCGAGTCTGCTCAAGAAACAAACCAAGGAGAACTGGACGTCGCCCTG	420
Db	557	ATCTCTGACACCGAGTCTGCTCAAGAAACAAACCAAGGAGAACTGGACGTCGCCCTG	616
Qy	421	GTCTATCTGCGGCAACAAAGGTGACCGGAGTCTTACCGCG-AGTGGACGAGCGAGAT	479
Db	617	GCCATCTGCGGCAACAAAGGTGACCGGAGTCTTACCGCGAGGTGGACGAGCGAGAT	676
Qy	480	CGAGCAGTGTGGGCGGAGACCGCCAGCGCTGCGCTACTTCGAGATCTCGGCCAAGAA	539
Db	677	CGAGCAGTGTGGGCGGAGACCGCCAGCGCTGCGCTACTTCGAGATCTCGGCCAAGAA	736
Qy	540	GAACAGCAGCGCTGGACC	556
Db	737	AAACACCCCTGGGAC	753
RESULT 14			
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LOCUS	603243203F1	NIH_MGC_96	Homo sapiens
DEFINITION	mRNA sequence.		
ACCESSION	BM805637		
VERSION	BM805637.1	GI:15489576	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	NIH-MGC	http://mgi.nci.nih.gov/.	
TITLE	1 (bases 1 to 831)		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-remail.nih.gov		
	Tissue Procurement: Miklos Palkovits, M.D., Ph.D.		
	cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiki and Piero Carninci (RIKEN)		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:		
	http://image.llnl.gov		
	Plate: LLAM11722	row: e	column: 01
	High quality sequence stop: 777.		
	High quality sequence start: 777.		
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	/tissue_type="hypothalamus"		
	/lab_host="DH10B"		
	/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTATTTTATTTN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NHGRI), National Institutes of Health). Note: this is a NIH_MGC Library."		
BASE COUNT	167 a	311 c	233 g
ORIGIN	120 t		

Query Match	61.4%;	Score 519.6;	DB 13;	Length 831;
Best Local Similarity	96.7%;	Pred. No. 3.5e-92;		
Matches 584;	Conservative 0;	Mismatches 14;	Indels 6;	Gaps 5
QY	12	CGCGCATCATCAAGAAGATGCGCCGAGCAGCTCGGAGCTGAGTATCCGGCGCAAGAACTG	71	
Db	230	CGCGATGATCAAGAAGATGCGCGAGGAGCTCGGAGCTGAGTATCCGGCGCAAGAACTG	289	
QY	72	CTATCGCATGGTTCATCTCTGGGTCGTCTCCAAAGTGGCGCAAGACGCCATCTGTGTGCGGCTT	131	
Db	290	CTATCGCATGGTTCATCTCTGGGTCGTCTCCAAAGTGGCGCAAGACGCCATCTGTGTGCGGCTT	349	
QY	132	CTCTACCGGGCGGCTTCGAGGAGCGCTACACGGCTACCATCGAGGACTTCCACCGCAAGTT	191	
Db	350	CTCTACCGGGCGGCTTCGAGGAGCGCTACACGGCTACCATCGAGGACTTCCACCGCAAGTT	409	
QY	192	CTACTCCATCCGGCGGAGGTCTACAGCTCGACATCTCGACAGCTCGCGCAACCAACCC	251	
Db	410	CTACTCCATCCGGCGGAGGTCTACAGCTCGACATCTCGACAGCTCGCGCAACCAACCC	469	
QY	252	GTTCGCCGCCATCGCGCGGCTTCCATCCTCACAGGAGAGGTTTCATCTGGTGTTCAG	311	
Db	470	GTTCGCCGCCATCGCGCGGCTTCCATCCTCACAGGAGAGGTTTCATCTGGTGTTCAG	529	
QY	312	TCTGGACAAACCGCGACTCTCTTCGAGGAGGTGCACGGCTCAGGCGAGCATCTCCACAC	371	
Db	530	TCTGGACAAACCGCGACTCTCTTCGAGGAGGTGCACGGCTCAGGCGAGCATCTCCACAC	589	
QY	372	CAAGTCTTGCTCAAGAACAAACCAAGGAGAGCTGAGCTGCCCTGTCTATCTGCGG	431	
Db	590	CAAGTCTTGCTCAAGAACAAACCAAGGAGAGCTGAGCTGCCCTGTCTATCTGCGG	649	
QY	432	CAACAAGGCTGACCGGACTTCTACCGGA--GTGGACGACGCCGA--GATCGAGCAGT	488	
Db	650	CAACAAGGCTGACCGGACTTCTACCGGAGGTTGGACGCGCAAGAAATCGAGCAGT	709	
QY	489	GTGGGGGACGACCCCGAGCGCTCGCGCTACTTCGAGATCTCGGCCAAGAAACAGCAG	548	
Db	710	GTGGGGCGACGA-CCCCAGCGCTGGCCTACTTCGGAGATCTCGG--CAAGAAGACAGCAG	767	
QY	549	CTTGACACAGATGTTTCGGCGGCTTTCGCCATGGCCAGCTGCCAGCGAGATGAGCCC	608	
Db	768	CTTGACACAGATGTTTCGGGGGCTTCTTCGCCAAGGCCAAGCTG--CCAGCGAGATGAGCCC	826	
QY	609	AGAC	612	
Db	827	AGAC	830	

RESULT 15
BG711792
LOCUS
DEFINITION
 BG711792 655 bp mRNA linear EST 08-MAY-2001
 pg11n.pk009.i15 Normalized Liver Library Gallus gallus cDNA clone
 pg11n.pk009.i15 5' similar to gb|AAF43090.1|AF239157.1 (AF239157)
 Dextral1 [Rattus norvegicus]G, mRNA sequence.
ACCESSION BG711792
VERSION
KEYWORDS
SOURCE
 BG711792.1 GI:14005742
 EST
 chicken.
ORGANISM
 Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 655)
REFERENCE
 Burnside,J., Morgan,R.W. and Cogburn,L.A.
AUTHORS Chicken ESTs from a normalized liver library
TITLE
 Unpublished (2001)
JOURNAL
 Contact: Joan Burnside
COMMENT
 Molecular Endocrinology
 University of Delaware
 40 Townsend Hall, Newark, DE 19717, USA
 Tel: 302 831-1345

Fax: 302-831-3411
 Email: joan@udel.edu, www.chickest.udel.edu.
 Location/Qualifiers
 1. .655
 /organism="Gallus gallus"
 /db_xref="taxon:9031"
 /clone_pgln.pk009.115"
 /clone_lib="Normalized Liver Library"
 /sex="Male and Female"
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 /lab_host="E.coli EMD108"
 /note="Vector: pCMVSPORT 6"
 BASE COUNT 145 a 206 c 184 g 104 t 16 others
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 Best Local Similarity 88.3%; Pred. No. 5e-91;
 Matches 560; Conservative 0; Mismatches 73; Indels 1; Gaps 1;
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 Db 614 GATGAGCCCAAGTGCACCGCANNNNNNNNNN 647

Search completed: December 28, 2002, 05:50:39
Job time : 1127.58 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 28, 2002, 02:13:37 ; Search time 4571.56 Seconds
(without alignments)
11465.267 Million cell updates/sec

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Perfect score: 1801

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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40: em.htgo.mus:*

41: em.htgo.other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	1673.4	92.9	1746	9	AF177335	AF177335 Homo sapi
4	1460	81.1	4990	9	AF222979	AF222979 Homo sapi
5	1458.4	81.0	183334	9	AC020558	AC020558 Homo sapi
6	1431.2	79.5	5141	9	AF262018	AF262018 Homo sapi
7	1430.2	79.4	58882	2	AC073621	AC073621 Homo sapi
8	1389.8	77.2	183598	2	AC090608	AC090608 Homo sapi
9	1137	63.1	1187	9	AF153192	AF153192 Homo sapi
10	940.4	52.2	979	9	AF172846	AF172846 Homo sapi
11	846	47.0	846	9	AF498923	AF498923 Homo sapi
12	764.8	42.5	1612	10	BC034166	BC034166 Mus muscu
13	764.2	42.4	1623	10	AF009246	AF009246 Mus muscu
14	746.8	41.5	1616	10	AF239157	AF239157 Rattus no
15	592.2	32.9	179124	10	AL603710	AL603710 Mouse DNA
16	468.2	26.0	162504	2	AC122995	AC122995 Rattus no
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25	352.6	19.6	414	6	AX336237	AX336237 Sequence
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ALIGNMENTS

RESULT 1
AF069506

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AF069506

Homo sapiens

cds.

AF069506

GI:4959037

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1740)

Cismowski, M.J., Takesono, A., Ma, C., Lizano, J.S., Xie, X.,

Fuernkranz, H., Lanier, S.M. and Duzic, E.

1740 bp mRNA linear PRI 10-JAN-2000
Homo sapiens activator of G protein signaling (AGS1) mRNA, complete

Mon Dec 30 09:17:15 2002

us-09-709-103-3.rge

TITLE Genetic screens in yeast to identify mammalian nonreceptor modulators of G-protein signaling
JOURNAL Nat. Biotechnol. 17 (9), 878-883 (1999)
MEDLINE 99403338
PUBMED 10471929
REFERENCE 2 (bases 1 to 1740)
AUTHORS Cismowski, M.J., Fuernkranz, H., Ma, C., Spruyt, M., Xie, X., Lanier, S.M. and Duzic, E.
TITLE Direct Submission
JOURNAL Submitted (01-JUN-1998) Receptor Pharmacology/Biochemistry, Cadus Pharmaceutical Corporation, 777 Old Saw Mill River Rd., Tarrytown, NY 10591, USA

FEATURES
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LOCUS

DEFINITION Homo sapiens clone SPI942 unknown mRNA.

ACCESSION AF177335

VERSION AF177335.1 GI:10503968

KEYWORDS

SOURCE Homo sapiens.

ORGANISM Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 1746)

Gu, J. R., Wan, D. F., Zhao, X. T., Zhou, X. M., Jiang, H. Q., Zhang, P. P., Qin, W. X., Huang, Y., Qiu, X. K., Qian, L. F., He, L. P., Li, H. N., Yu, Y., Yu, J. and Han, L. H.

Novel human cDNA clone with function of inhibiting cancer cell growth

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1746)

Gu, J. R., Wan, D. F., Zhao, X. T., Zhou, X. M., Jiang, H. Q., Zhang, P. P., Qin, W. X., Huang, Y., Qiu, X. K., Qian, L. F., He, L. P., Li, H. N., Yu, Y., Yu, J. and Han, L. H.

Direct Submission

Submitted (06-AUG-1999) National Laboratory For Oncogenes & Related Genes, Shanghai Cancer Institute, 25/Ln 2200 Xie Tu Road, Shanghai 200032, P.R. China

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 Db 1546 ACATGTGAGTGAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1605
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 Db 1606 CGGTGTCACATGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 1665
 QY 1625 GTCTTTAAAGTATTGCTTTATTTGTTTAAATATACATAAATAAATAAATAAATAAATAA 1684
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RESULT 4
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 LOCUS AF222979 4990 bp DNA linear PRI 02-JAN-2001
 DEFINITION Homo sapiens activator of G-protein signaling gene, complete cds.
 ACCESSION AF222979
 VERSION AF222979.1 GI:12004991
 KEYWORDS
 SOURCE Homo sapiens.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 4990)
 AUTHORS Cismowski, M.J., Xie, X. and Duzic, E.
 TITLE Genomic sequence of the human ras-related G-protein activator AGS1
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 4990)
 AUTHORS Cismowski, M.J., Xie, X. and Duzic, E.
 TITLE Direct Submission
 JOURNAL Submitted (10-JAN-2000) OSI Pharmaceuticals, 777 Old Saw Mill River
 Road, Yonkers, NY 10591, USA
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 EQLVDDPQRCAYFEISAKNSLSDQMFALFAMAKLPSEMPDLHRKVSQYCYDLH
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 BASE COUNT 1049 a 1507 c 1509 g 925 t
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 Best Local Similarity 88.8%; Pred. No. 9.2e-183;
 Matches 1681; Conservative 0; Mismatches 0; Indels 211; Gaps 1;
 QY 7 CCGAGCGAGCGCGGAGCGCCCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 66
 Db 2756 CCGAGCGAGCGCGGAGCGCCCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 66
 QY 67 GCTCACCGCGCGTGCACCG 126
 Db 2816 GCTCACCGCGCGTGCACCG 126
 QY 127 CGCCCGCGCGTGCAGCG 2875
 Db 2876 CGCCCGCGCGTGCAGCG 186
 QY 187 CCGAGCGACTCGGAGCTGAGTATCCCGGCAAGAACTGCTATCGCATGCTATCGCGCGCG 2935
 Db 2936 CCGAGCGACTCGGAGCTGAGTATCCCGGCAAGAACTGCTATCGCATGCTATCGCGCGCG 246
 QY 247 TCGTCAAGTGGGCAAGACG 2995
 Db 2996 TCGTCAAGTGGGCAAGACG 306
 QY 307 GCCTACACCGCTTACCATCGAGACTTCCACCGCAAGTCTTACTCCATCCGCGCGCGCGCG 3055
 Db 3056 GCCTACACCGCTTACCATCGAGACTTCCACCGCAAGTCTTACTCCATCCGCGCGCGCGCG 366
 QY 367 TACCAAGCTCGACATCCTCGACACGTCGCGCAACACCGCGTTCCTCCCGCGCGCGCGCG 3115
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 QY 427 TCCATCCTTAC - 437
 Db 3176 TCCATCCTTACAGGCTGAGCG 3235


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Best Local Similarity 88.8%; Pred. No. 1.9e-182;
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DB 2167 GCTCACCCTCGGCGGCGGCGGAGCGGAGCCCTCAGCGCTCTCTGCCCTTCTCGGCCCGG 2108
QY 127 GCGCGCGCTCGGCGGCGGCTGCGCCATGAAGTGGCCGCGATGATCAAGAGATGTC 186
DB 2107 GCGCGCGCTCGGCGGCGGCTGCGCCATGAAGTGGCCGCGATGATCAAGAGATGTC 2048
QY 187 CCGAGCGAGCTCGGAGCTGAGTATCCGCGCAAGAACTGCTATCGCATGCTCCTCGGC 246
DB 2047 CCGAGCGAGCTCGGAGCTGAGTATCCGCGCAAGAACTGCTATCGCATGCTCCTCGGC 1988
QY 247 TCGTCCAAAGTGGGCAAGACGCGCATCGTTCGCGCTTCTCAGCGGCGCTTCGAGGAC 306
DB 1987 TCGTCCAAAGTGGGCAAGACGCGCATCGTTCGCGCTTCTCAGCGGCGCTTCGAGGAC 1928
QY 307 GCTCAGCGCTACCATGAGAGCTTCCACCGCAAGTCTACTCCATCCGCGCGGAGGTC 366
DB 1927 GCTCAGCGCTACCATGAGAGCTTCCACCGCAAGTCTACTCCATCCGCGCGGAGGTC 1868
QY 367 TACCAGCTCGACATCCTCGACAGCTTCCGGCAACCAACCGCTTCCCGGCTCAGCGCGCTC 426
DB 1867 TACCAGCTCGACATCCTCGACAGCTTCCGGCAACCAACCGCTTCCCGGCTCAGCGCGCTC 1808
QY 427 TCGATCCTAC----- 437
DB 1807 TCGATCCTACAGGTGAGCGCGGCGCGGCGAGGTGCGGGAGGAGGCGGCGGCAACCT 1748
QY 438 ----- 437
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QY 438 ----- 437
DB 1687 CTTAGAGAGCTAGCGCGCGCGCGGCGCTCAAAAGTCAGCCCGACTTGTCCCTGGCG 1628
QY 438 -----AGGAGAGCTTTTCATCCT 455
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QY 456 GGTGTTAGTCTGGAACAACGGGAGCTTCTCGAGAGGTGCGAGCGCTCAGGAGCAGAT 515
DB 1567 GGTGTTAGTCTGGAACAACGGGAGCTTCTCGAGAGGTGCGAGCGCTCAGGAGCAGAT 1508
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DB 1507 CCGCAGCAGCAAGCTTGGCTCAAGAAACAAACCAAGGAGAGCTGGAGCTGCGCCCTGGT 1448
QY 576 CATCTCGGCAACAAGGTTGACCGGAGCTTCTACCGCGAGGTGGACCGCGGAGATCGA 635
DB 1447 CATCTCGGCAACAAGGTTGACCGGAGCTTCTACCGCGAGGTGGACCGCGGAGATCGA 1388
QY 636 GCAGCTGGTGGGAGACACCGCCGAGCGCTGCGCTACTTTCGAGATCTCGGCCCAAGAGAA 695
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QY 696 CAGCAGCTGGAGCCAGATGTTCCGCGCGCTTTCGCCATGGCCAAAGCTGCCAGGAGAT 755
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QY 756 GAGCCAGAGCTCCAGCCGAGGTCTCGTGCAGTACTGCGAGCTGCTGCAACAAGAGC 815
DB 1267 GAGCCAGAGCTCCAGCCGAGGTCTCGTGCAGTACTGCGAGCTGCTGCAACAAGAGC 1208
QY 816 GCTGCGGACCAAGAAGCTGCTGCGGCGCGGAGCGGCGGCGGCGGCGGCGGCGG 875
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DB 1027 CTAGGAGCCCGCGCGCTGGCGACACACCTTAAGGAGGACCTTTTGTAAAGTCAATC 968
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RESULT 6
AF262018
LOCUS
DEFINITION Homo sapiens dexamethasone-induced ras-related protein 1 (DEXRAS1)

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 DB 601 ATGAGCCAGACCTGCACCGCAAGTCTCGTCTAGTCTGCGACGTCTGCAAGAAG 660
 QY 814 GCGCTGGGGAACAAGAGTCTGCTGGGCGCGGACGCGGCGCGCGCGCGCGCGCG 873
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 QY 934 TACATCCGCGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 993
 DB 781 TACATCCGCGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
 QY 994 AGCTAGAGAGCG 1053
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 QY 1054 TCCACG 1113
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 QY 1114 CGATCCG 1172
 DB 960 CGATCCG 1018
 QY 1173 CGGAGGAG 1232
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RESULT 10
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 LOCUS Homo sapiens ras-related protein (DEXRAS1) mRNA, complete cds.
 DEFINITION AF172846
 VERSION AF172846.1 GI:6014488
 KEYWORDS
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 979)
 AUTHORS Tu, Y. and Wu, C.
 TITLE Cloning, expression and characterization of a novel human
 Ras-related protein that is regulated by glucocorticoid hormone
 JOURNAL Biochim. Biophys. Acta 1489 (2-3), 452-456 (1999)
 MEDLINE 20135605
 PUBMED 10673050
 REFERENCE 2 (bases 1 to 979)
 AUTHORS Tu, Y. and Wu, C.
 TITLE Direct Submission
 JOURNAL Submitted (27-JUL-1999) Department of Cell Biology, University of
 Alabama at Birmingham, 1670 University Blvd., Birmingham, AL 35294,
 USA

FEATURES
 source location/Qualifiers
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 Best Local Similarity 99.5%; Pred. No. 1.8e-114;
 Matches 975; Conservative 0; Mismatches 1; Indels 4; Gaps 3;
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 QY 150 CCCAATGAAGTGGCG 209
 DB 60 CCCAATGAAGTGGCG 119
 QY 210 CCGCGCGCAAGAGCTCTTCGATGATGATGATGATGATGATGATGATGATGATGAT 269
 DB 120 CCGCGCGCAAGAGCTCTTCGATGATGATGATGATGATGATGATGATGATGATGAT 179
 QY 270 CATCTGTCG 329
 DB 180 CATCTGTCG 239
 QY 330 CTTCCACGCGAGTCT 389
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 QY 390 GTCCGCGCAACACCG 449
 DB 300 GTCCGCGCAACACCG 359
 QY 450 CATCTGTCG 509
 DB 360 CATCTGTCG 419
 QY 420 GCGATGTCG 479
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 QY 570 CTTGTCATCTGCG 629
 DB 480 CTTGTCATCTGCG 539
 QY 630 GATGAGACGAGTGTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 689
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 QY 1047 AGTCAATCCAGCGCGCGCG 1066
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RESULT 11

AF498923

LOCUS

DEFINITION Homo sapiens activator of G protein signaling (RASD1) mRNA, PRI 01-MAY-2002

ACCESSION

AF498923

VERSION AF498923.1 GI:20379021

KEYWORDS

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 846)
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

AUTHORS Puhl, H.L., Ikeda, S.R. and Aronstam, R.S.

JOURNAL Submitted (05-APR-2002) CDNA Resource Center, Guthrie Research

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 QY 514 ATCTTGACACCAAGTCTTCTCTCAAGAACCAACCAAGAACCAAGAACCAAG 573
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 QY 814 GCGCTGGGGAACAAGAGCTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 873
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 QY 874 GAGCGCTTGGCATGCTGGACCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 933
 Db 721 GAGCGCTTGGCATGCTGGACCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 780
 QY 934 TACATCCGCGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 993
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 QY 994 AGCTTAC 999
 Db 841 AGCTTAC 846

RESULT 12
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 LOCUS
 DEFINITION Mus musculus, RAS, dexamethasone-induced 1, clone MGC:36188
 ACCESSION BC034166
 VERSION BC034166.1 GI:21706874
 KEYWORDS MGC.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1612)
 AUTHORS Strausberg, R.
 JOURNAL Submitted (02-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 REMARK NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
 CONTACT: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 CDNA Library Preparation: Life Technologies, Inc.

Query Match 47.0%; Score 846; DB 9; Length 846;
 Best Local Similarity 100.0%; Pred. No. 4, 6e-102;
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/INL at: <http://image.inl.gov>
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6677672.

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ORIGIN

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Query Match	42.5%;	Score 764.8;	DB 10;	Length 1612;
Best Local Similarity	72.8%;	Pred. No. 2.3e-91;		
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DEFINITION AF009246
ACCESSION AF009246
VERSION AF009246.1 GI:2253712
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SOURCE Mus musculus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 1623)
AUTHORS Kempainen,R.J. and Behrend,E.N.
TITLE Dexamethasone rapidly induces a novel ras superfamily
JOURNAL member-related gene in Atr-20 cells
MEDLINE J. Biol. Chem. 273 (6), 3129-3131 (1998)
PUBMED 9452419
REFERENCE 2 (bases 1 to 1623)
AUTHORS Kempainen,R.J. and Behrend,E.N.
TITLE Direct Submission
JOURNAL Submitted (18-JUN-1997) Physiology & Pharmacology, Auburn
University College of Veterinary Medicine, 213 Greene Hall, Auburn,
AL 36849, USA

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BASE COUNT 412 a 437 c 417 g 357 t
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Best Local Similarity 71.9%; Pred. No. 2.7e-91;
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 ACCESSION AF239157 GI:7230767
 VERSION AF239157.1 GI:7230767
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 Rattus.
 1 (bases 1 to 1616)
 Fang, M., Jaffrey, S.R., Sawa, A., Ye, K., Luo, X. and Snyder, S.H.
 Dextrasi, a G protein specifically coupled to neuronal nitric oxide
 synthase via CAPON
 Neuron 28 (1), 183-193 (2000)
 JOURNAL MEDLINE 20537828
 PUBMED 11086993
 2 (bases 1 to 1616)
 Fang, M., Jaffrey, S.R., Sawa, A., Ye, K. and Snyder, S.H.
 Direct Submission
 Submitted (24-FEB-2000) Neuroscience, Johns Hopkins University, 725
 N. Wolfe St, Baltimore, MD 21205, USA
 JOURNAL N. Wolfe St, Baltimore, MD 21205, USA
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RESULT 2
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ID AAZ36914 standard; DNA; 1740 BP.
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AC AAZ36914;
XX
XX 13-MAR-2000 (first entry)
XX
DE DNA encoding an activator of G protein signalling (AGS) protein.
XX
KW Activator of G protein signalling; AGS; ras-related G protein;
KW GTP hydrolysis; G protein activity; pheromone response pathway;
KW G protein-coupled signal transduction; G-gamma selectivity;
KW cellular signal transduction; ss.
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OS Homo sapiens.
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FH Key 145.991
FT CDS /*tag= a
FT /product= "activator of G protein signalling (AGS)
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PR 08-MAY-1998; 98US-0084842.
PR 07-OCT-1998; 98US-0103355.
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PA (CADU-) CADUS PHARM CORP.
XX
PI Cismowski M, Duzic E;
PI
DR WPI: 2000-072337/06.
DR P-PDB; AAY33924.
XX
PT A new activator of G protein signalling used to treat disorders
PT characterized by an aberrant AGS protein activity -
XX
PS Disclosure: Page 146-148; 162pp: English.
XX
XX

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The present sequence encodes an activator of G protein signalling (AGS) protein. The cDNA sequence was isolated from a human liver cDNA library. The AGS protein exhibits homology to ras-related G proteins, and contains alterations in conserved amino acids consistent with a deficiency in GTP hydrolysis activity. AGS stimulates G protein activity, G protein-coupled signal transduction and the pheromone response pathway in a receptor-independent manner. The AGS protein also shows G-gamma selectivity, as measured by growth assays in yeast expressing various mammalian G-gamma constructs, and tissue-specific expression, as measured by Northern blot analysis. The AGS protein can be used to screen for compounds that modulate cellular signal transduction. The protein is used to treat disorders characterized by an aberrant AGS protein activity or AGS nucleic acid

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CC expression.
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Db	1201	CCCCACCCCGGGTCCCATTTGAGGGCCGCGACCCCATTAATTTGGAGAGCGAGGGCCCA	1260
Qy	1269	GCCGAGGGGTGATTTATCTTCTCAAGAGCCTTAAGAGTGAGCCGCGGGGTGGGGAGGATG	1328
Db	1261	GCGGAGGGGTGATTTATCTTCTCAAGAGCCTTAAGAGTGAGCGCGGGGTGGGGAGGATG	1320
Qy	1329	TGAAGTTATCCAGCCTCTGCTAGGCTTCAAGAAACCCGTATGCCGCTTGAAGGTCCAGGA	1388
Db	1321	TGAAGTTATCCAGCCTCTGCTAGGCTTCAAGAAACCCGTATGCCGCTTGAAGGTCCAGGA	1380
Qy	1389	CCCAAGGGGACTTATCTTGCTGTGATCCGGGGTGGCTGTGACAGCCGGTAGAGCCTGTG	1448
Db	1381	CCCAAGGGGACTTATCTTGCTGTGATCCGGGGTGGCTGTGACAGCCGGTAGAGCCTGTG	1440
Qy	1449	CCCTCCCGAAACTAAGCGGGGGGGCGGTGCTCAATATCATAGCCAACTGTTTACAT	1508
Db	1441	CCCTCCCGAAACTAAGCGGGGGGGCGGTGCTCAATATCATAGCCAACTGTTTACAT	1500
Qy	1509	GTCAGTGAACCTGTGACAAAGGAACACAAACAAACCTTGACCTTTAAACGTATGTCGGT	1568
Db	1501	GTCAGTGAACCTGTGACAAAGGAACACAAACAAACCTTGACCTTTAAACGTATGTCGGT	1560
Qy	1569	GTCACATGAGACAGAACAAACCTTACCAGAGGTATTATCTGTGTGTGTGAGGTCT	1628
Db	1561	GTCACATGAGACAGAACAAACCTTACCAGAGGTATTATCTGTGTGTGTGAGGTCT	1620
Qy	1629	TTAAAGTATGCTTATTTGCTTTTATTAATATCAATTAATAAATTTAAATGGAATA	1688
Db	1621	TTAAAGTATGCTTATTTGCTTTTATTAATATCAATTAATAAATTTAAATGGAATA	1680
Qy	1689	AA	1748
Db	1681	AA	1740
RESULT 3			
ID	AAA49177	AAA49177	
XX	AAA49177	standard; cDNA: 1776 BP.	
XX	03-NOV-2000	(first entry)	
XX	cDNA encoding human GTPase associated protein-7.		
XX	Guanine nucleotide binding protein; GTP-binding protein; G-protein;		
XX	GTPase; GTPase associated protein; GTPAP; cell proliferation;		
XX	autoimmune; inflammatory; immune system disorder; cancer; AIDS;		
XX	acquired immune deficiency syndrome; asthma; atherosclerosis;		
XX	arthritis; systemic lupus erythematosus; psoriasis; human; ss.		
OS	Homo sapiens.		
PH	key	location/Qualifiers	
FT	CDS	180..1025	
FT		/*tag= a	

FT	/product= GTPAP7
PN	WO200031263-A2.
PD	02-JUN-2000.
PX	
PF	23-NOV-1999; 99WO-US28013.
PX	
PR	23-NOV-1998; 98US-0109592.
PR	04-FEB-1999; 99US-0118610.
PR	06-APR-1999; 99US-0127990.
PX	
PA	(INCY-) INCYTE PHARM INC.
PX	
PI	Hillman JL, Tang YT, Bandman O, Lal P, Yue H, Lu DM, Baughn MR;
PI	Tang J, Azimzai Y;
PX	
DR	WPI: 2000-400073/34.
PX	P-PsDB; AAY9655.
PX	
PT	Human GTPase associated proteins, polynucleotides, and antibodies,
PT	useful for diagnosing, preventing and treating various diseases such as
PT	atherosclerosis, cancer, acquired immune deficiency syndrome (AIDS),
PT	asthma, and autoimmune diseases -
PS	Claim 9; page 125-126; 14pp; English.
PX	
CC	Human cDNA libraries from various tissues were screened for GTPase
CC	associated proteins (GTPAP). The present sequence is cDNA encoding
CC	human GTPAP-7. This sequence was derived from a cDNA library of the
CC	brain tumour tissue from the parietal lobe of a female.
CC	This protein is expressed in reproductive, nervous and
CC	gastrointestinal tissue. The GTPAP proteins may be used to define
CC	agonists and antagonists of GTPAP activity and to generate antibodies
CC	to GTPAP. This means the GTPAP proteins may be useful for treatment or
CC	prevention of diseases associated with GTPAP such as cell proliferation
CC	disorders, autoimmune disorders, inflammatory disorders, immune system
CC	disorders, cancer, AIDS, asthma, atherosclerosis, arthritis, systemic
CC	lupus erythematosus and psoriasis.
XX	
SQ	Sequence 1776 BP; 430 A; 565 C; 490 G; 291 T; 0 other:
Query Match	96.2%; Score 1732.4; DB 21; Length 1776;
Best Local Similarity	99.7%; Pred. No. 6, 8e-229;
Matches 1736; Conservative	0; Mismatches 6; Indels 0; Gaps 0.
OY	7 CGAGGGGAGCGCGAGCCCCCAAGGCCGAGCGGCCACGCAGAGAAGCCTTCAGCC 66
DB	
33	CGAGGCCAACCGGAGGCCCAAGCCGAGCGGCCACGAGAGAGCCTTCCAGCC 92
OY	67 GGTACACCCTCGTGCCACCCAGCAGACCTCAGCGCTCTCTGCTCTTGCGGCCG 126
DB	
93	GCTACACCCCGGTGGCCACCCAGCAGACCTCAGCGCTCTCTGCTCTTGCGGCCG 152
OY	127 CGCCGCCCTTCGCGGCCCTCTGCTCCCATATGAATCTGGCGCGATGATCAAAGATGTC 186
DB	
153	CGCCGCCCTTCGCGGCCCTCTGCTCCCATATGAATCTGGCGCGATGATCAAAGATGTC 212
OY	187 CCGAGCACCTCGGAGCTGATATCCGGCCAAAGTAAGTATGATGATGTCATCTCGCG 246
DB	
213	CCGAGCACCTCGGAGCTGATATCCGGCCAAAGTAAGTATGATGATGTCATCTCGCG 272
OY	247 TCCTCAAGGTGGGCAAGAGCGCCATCTGTCTCGGCTCTCTACCGCGCGCTTCGAGAG 306
DB	
273	TCCTCAAGGTGGGCAAGAGCGCCATCTGTCTCGGCTCTCTACCGCGCGCTTCGAGAG 332
OY	307 GCCTACACGGCTACTCATCGAGGATTCTCACCGGAAGTTACATCATCCGCGCGAGATC 366
DB	
333	GCCTACACGGCTACTCATCGAGGATTCTCACCGCGGAAGTTACTTCTCATCTCGCGCGAGATC 392
OY	367 TACAGGTTCGACATCTCTCGACAGCTCCGGCAACACCCGTTCCCGCGCATGCGGCTC 426
DB	
393	TACAGGTTCGACATCTCTCGACAGCTCCGGCAACACCCGTTCCCGCGCATGCGGCTC 452

xx kd312 polypeptides useful for treating diseases and disorders
 pt associated with alterations in cell proliferation and cell death
 xx
 ps Claim 1; Fig 5; 85bp; English.

xx The invention provides nucleic acid molecules encoding human and rat
 cc kd312 polypeptides. The kd312 polypeptides can be expressed by standard
 cc recombinant methodology. The kd312 sequences, and the antibodies against
 cc the proteins may be used to treat or diagnose the presence or progression
 cc of various diseases, e.g. cancer, immunodeficiency disorders (e.g. AIDS),
 cc stroke, heart attack, head trauma, and neurodegenerative diseases (e.g.
 cc Parkinson's disease and Alzheimer's disease). The present sequence
 xx represents the human kd312 genomic DNA sequence.

xx Sequence 3986 BP; 856 A; 1226 C; 1172 G; 732 T; 0 other;

Query Match 80.9%; Score 1456.8; DB 20; Length 3986;
 Best Local Similarity 88.7%; Pred. No. 3.8e-191;
 Matches 1679; Conservative 0; Mismatches 2; Indels 211; Gaps 1;

Qy 7 CCGAGCGAGCCGCGAGCCCGAGCCCGCGCCAGCCCGAGAGAGCCCTCCAGCC 66
 Db 627 CCGAGCGAGCCGCGAGCCCGAGCCCGCGCCAGCCCGAGAGAGCCCTCCAGCC 686
 Qy 67 GCTACCCCGCGGTGCACCCCGAGGACCTCAGCCGCTCTGCTCTGCTCTGCTCTG 126
 Db 687 GCTACCCCGCGGTGCACCCCGAGGACCTCAGCCGCTCTGCTCTGCTCTGCTCTG 746
 Qy 127 CGCCCGCCCTGCGCGCCCTCTGCGCAATGAAATGAGCGCGATGATCAAGAAATGTC 186
 Db 747 CGCCCGCCCTGCGCGCCCTCTGCGCAATGAAATGAGCGCGATGATCAAGAAATGTC 806
 Qy 187 CCGAGCGAGCTGAGAGCTGATATCCCGCGCAAAATCTGATGCGATGCTCTGCGC 246
 Db 807 CCGAGCGAGCTGAGAGCTGATATCCCGCGCAAAATCTGATGCGATGCTCTGCGC 866
 Qy 247 TCGTCAAGTGGGCAAGAGCGCATGCTGCTGCTCTGCTCTGCTCTGCTCTGCTCA 306
 Db 867 TCGTCAAGTGGGCAAGAGCGCATGCTGCTGCTCTGCTCTGCTCTGCTCTGCTCA 926
 Qy 307 GCTACAGCGCTACATCGAGGACTTCACCGCAAGTTTACTTCATCCGCGGAGATC 366
 Db 927 GCTACAGCGCTACATCGAGGACTTCACCGCAAGTTTACTTCATCCGCGGAGATC 986
 Qy 367 TACCACTGCAATCCGCGAGCTGCGGCAACCAACCCCTTCCCGGCAATGCGGCGCTC 426
 Db 987 TACCACTGCAATCCGCGAGCTGCGGCAACCAACCCCTTCCCGGCAATGCGGCGCTC 1046
 Qy 427 TCCATCTCTAC----- 437
 Db 1047 TCCATCTCTACAGGTAGCCGGGGCGCGGCAAGTGGCGGAGGAAGGCGGGAGCCCT 1106
 Qy 438 ----- 437
 Db 1107 CGGCGAGGGCGCCCGCGAGCCCGGTCCGCTGCTGCGCGCGAGTAGTGGCGTTCGCG 1166
 Qy 438 ----- 437
 Db 1167 CTTAGAGAGGTAGCGCGCGCGCGCGGCTCAAAAGTCAAGCCGCTGTCCTCCGCGCG 1226
 Qy 438 ----- 437
 Db 1227 GCCACCCCTACCT 1286
 Qy 456 GGTGTTCAGTCTGAGCAACCGGAGCTCTGAGAGAGTGAAGGGCTCAGGCGAGAGAT 515
 Db 1287 GGTGTTCAGTCTGAGCAACCGGAGCTCTGAGAGAGTGAAGGGCTCAGGCGAGAGAT 1346
 Qy 516 CCTCGACCAAGTCTTGGCTTCAAGAACAAACCAAGAGAGTGAAGTGGCGCGCTGCT 575
 Db 1347 CCTCGACCAAGTCTTGGCTTCAAGAACAAACCAAGAGAGTGAAGTGGCGCGCTGCT 1406

Qy 576 CATCTGCGGCAACAGGGTGAACCGGACTTCTACCGGAGGTGAGCCAGCGAGATCGA 635
 Db 1407 CATCTGCGGCAACAGGGTGAACCGGACTTCTACCGGAGGTGAGCCAGCGAGATCGA 1466
 Qy 636 GCAGCTGTGGGCGACGACCGCCAGCGCTGCGCTACTCTGAGATCTGCGCCAAAGAA 695
 Db 1467 GCAGCTGTGGGCGACGACCGCCAGCGCTGCGCTACTCTGAGATCTGCGCCAAAGAA 1526
 Qy 696 CAGCAGCTTGCACCAAGATGTTCCGCGCTCTGCGCATGAGCCAAAGTGGCCAGCAGAT 755
 Db 1527 CAGCAGCTTGCACCAAGATGTTCCGCGCTCTGCGCATGAGCCAAAGTGGCCAGCAGAT 1586
 Qy 756 GAGCCAGACCTGACCGCAAGTCTGCGTCAAGTATCTGAGAGTGTGTCACAAAGAGC 815
 Db 1587 GAGCCAGACCTGACCGCAAGTCTGCGTCAAGTATCTGAGAGTGTGTCACAAAGAGC 1646
 Qy 816 GCTGCGCAACAAAGAGTCTGCGGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCA 875
 Db 1647 GCTGCGCAACAAAGAGTCTGCGGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCA 1706
 Qy 876 GCGCTTGGCAATCGTGGCACCCCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 935
 Db 1707 GCGCTTGGCAATCGTGGCACCCCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1766
 Qy 936 CATCGCGAGAGGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 995
 Db 1767 CATCGCGAGAGGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1826
 Qy 996 CTAGAGAGCG 1055
 Db 1827 CTAGAGAGCG 1886
 Qy 1056 CAAGCGCGCGGTTGGCG 1115
 Db 1887 CAAGCGCGCGGTTGGCG 1946
 Qy 1116 ATCCG 1175
 Db 1947 ATCCG 2006
 Qy 1176 AAGGAAGAGAGAGGCGCAAGAGTGGGACTATTCGCCACCCCGCGTCCCGCAATGAGCC 1235
 Db 2007 AAGGAAGAGAGAGGCGCAAGAGTGGGACTATTCGCCACCCCGCGTCCCGCAATGAGCC 2066
 Qy 1236 CGCACCCCGCATTAATTTGGGAGCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1295
 Db 2067 CGCACCCCGCATTAATTTGGGAGCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2126
 Qy 1296 ACCTAAGAGTGAAGCGCGGCGTGGGAGGAGTGTGAAGTTATCAAGCTCTGCTAGCTT 1355
 Db 2127 ACCTAAGAGTGAAGCGCGGCGTGGGAGGAGTGTGAAGTTATCAAGCTCTGCTAGCTT 2186
 Qy 1356 CAAGAAACCGTCAATGCGCGCTTGAAGGTGAGAGACCCAGCGGCGATTAATCTGTCTGAT 1415
 Db 2187 CAAGAAACCGTCAATGCGCGCTTGAAGGTGAGAGACCCAGCGGCGATTAATCTGTCTGAT 2246
 Qy 1416 TCCGGGTGCTGTGACAGCGGCTAGAGCTTGCCTCCCGCAAACTAAGCGGCGGCGGT 1475
 Db 2247 TCCGGGTGCTGTGACAGCGGCTAGAGCTTGCCTCCCGCAAACTAAGCGGCGGCGGT 2306
 Qy 1476 GGGTCAATCATAGCAATGACTTGTATCATGTGAGTGAATGCAAGCAAGAGACACA 1535
 Db 2307 GGGTCAATCATAGCAATGACTTGTATCATGTGAGTGAATGCAAGCAAGAGACACA 2366
 Qy 1536 AAACAAACCTTCACTTAAACGATAGTCCGCTGTCACATGAGACAGCAAAACCTTA 1595
 Db 2367 AAACAAACCTTCACTTAAACGATAGTCCGCTGTCACATGAGACAGCAAAACCTTA 2426
 Qy 1596 CCCAGTGTATTACTGT 1655
 Db 2427 CCCAGTGTATTACTGT 2486
 Qy 1656 TAATATACAAATAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1687

PN W0950288-A2.
 XX 07-OCT-1999.
 PD 30-MAR-1999; 99WO-US06993.
 XX 31-MAR-1998; 98US-0053374.
 PR (AMGE-) AMGEN INC.
 PA
 PI Yen K:
 DR WPI: 1999-601322/51.
 P-PSDB: AAY42694.
 XX
 XX k312 polypeptides useful for treating diseases and disorders
 associated with alterations in cell proliferation and cell death
 PS Claim 2; Fig 9; 85pp; English.
 CC The invention provides nucleic acid molecules encoding human and rat
 CC k312 polypeptides. The k312 polypeptides can be expressed by standard
 CC recombinant methodology. The k312 sequences, and the antibodies against
 CC the proteins may be used to treat or diagnose the presence or progression
 CC of various diseases, e.g. cancer, immunodeficiency disorders (e.g. AIDS),
 CC stroke, heart attack, head trauma, and neurodegenerative diseases (e.g.
 CC Parkinson's disease and Alzheimer's disease). The present sequence
 CC represents the rat k312 cDNA sequence.
 XX
 SQ Sequence 1689 BP; 417 A; 462 C; 434 G; 376 T; 0 other;
 Query Match 42.2%; Score 760.4; DB 20; Length 1689;
 Best Local Similarity 72.3%; Pred. No. 8.4e-96;
 Matches 1222; Conservative 0; Mismatches 366; Indels 102; Gaps 14;

Db 560 CGGTAAACAAAGGGAGCCGGGACTTACCGCGAAGTGGACAGCGGGAGATGAGCAGCT 619
 Qy 642 GGTGGGAGAGACCCCGAGGGCTGCTACTTCCGATCTCGGCCAAGAGACAGAG 701
 Db 620 GGTGGGAGAGACCCCGAGGGCTGCTACTTCCGATCTCGGCCAAGAGATGAGCAG 679
 Qy 702 CTTGGACAGATGTTCCGCGGCTCTTCCGATGAGCCAGAGCTCCGAGAGATGAGCC 761
 Db 680 CTTGGACAGATGTTCCGCGGCTCTTCCGATGAGCCAGAGCTCCGAGAGATGAGCC 739
 Qy 762 AGACCTGACAGAGAGTCTCGGTCGACGATCTGACGAGCTGTCACAAAGAGCGCTGG 821
 Db 740 TGACTTGCACCGAAGAGTGTCTGTGACTGTGACGCTGTGACAAAGAGCGCTGGAG 799
 Qy 822 GAACAAAGAGCTCTGCGGCGGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 881
 Db 800 GAACAAAGAGCTCTTGTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 856
 Qy 882 TGGCATCTGTCGACACCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 941
 Db 857 TGGCATCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 916
 Qy 942 CGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1001
 Db 917 TGAAGAAACAGTGTGACGAGCGGCTAAGGCAAGAGAGCGGCTGTGATCAGTTAGGA 976
 Qy 1002 GCCCGCGCGGCTGGCGGACACAACTAAGAGAGACCTTTTGTGTT---AAGTCAATGCA 1057
 Db 977 GCCCGAGGCTGAGTGCAGGACACAACTGAGAGACCTTTTGTGTTCAAAAGTCAATGCG 1036
 Qy 1058 ACGGCGCG-----GTGGCGCCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1107
 Db 1037 TTTCCAGGCTTAACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1096
 Qy 1108 TCCCGGCGATTC-GCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1166
 Db 1097 TCCCGTGAAGACCGAGCGCTGTGACAGAGAGATGTGCGCAAGAGAGTAAAGTAAAGTAT 1156
 Qy 1167 CTGCTCCGAGAGAAAG 1226
 Db 1157 CTGCTGTGAGAGAGAA--GAACTAGCTAAGACTGGAGACTT----- 1195
 Qy 1227 ATTGAGCGCGCGCGCCATCCCATTAATTGGGAGCGAGGCGGCGGCGGCGGCGGCGG 1286
 Db 1196 -----CGCTCCGATTCGTGGGATGCGAGAGCGGCGGAGGAGTGAATTC 1242
 Qy 1287 TTTCTAAAGACCTAAGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1346
 Db 1243 TTTTCTCAGAGACTTGTAGAGTG-----TGTAAGGGCTTCGGCTCT 1286
 Qy 1347 GCTAGGCTTCAAGAAACCGTCAATGCGCGCTGAGGCGGAGAGAGAGAGAGAGAGAGAG 1406
 Db 1287 G--AACTTCAAGTAACTGTGGGCTTCTGTGGGCGGAGAGAGAGAGAGAGAGAGAGAG 1344
 Qy 1407 GTCTGTGATTCGGGCTTGTGTCGACGCGGTAG-----AGCTTGGCTTCGGGAA 1458
 Db 1345 GTCTGTGATTC--GTGTGTGTCGACGCGGTGTGACGACCTGTGTCTTCAAGAACTGGAA 1403
 Qy 1459 ACTAAGCGGCGGCGGCGGCTGCAATCATATAGCAAGTACTGTTTACATGTGAGTGA 1518
 Db 1404 ACTTGGGCTCGAGGTGGGCTTCAATCATATAGCAAGCACTGTTTACATGTGTGTGT 1463
 Qy 1519 CTGCACAAAG 1578
 Db 1464 GTGTATTAATCCAAAG 1523
 Qy 1579 ACAG 1638
 Db 1524 ACGTACATTAAG 1565
 Qy 1639 TGTCTTATTTTGTTTTAT 1698
 Db 1566 --CTTATTAATTTTATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1623

Db	1085	TCGCGCCAGAGTGGCCACCACCGAGGCCGGAAGCTCTGTGGGGCA---CGAAGATGCG	1141
QY	667	GCCTACTTTCGAGATCTCGGCCAAGAAAGACAGCAGGCTTGAGCCAGATGTTCGGCGCGTC	726
Db	1142	GCGCTACTTCGAGGTGTGCGCCCAAGAAAGAACACCAAGTGGACGAGATGTTCTACTGCTC	1201
QY	727	TTTCGCANTGGCCAAAGCTGCGCCACGCGAGATGTAGCCACAGCTGCACCGCAAGGTCTCGGTG	786
Db	1202	TTTCAGCATGGCCAAAGCTGCCACACAGAGATGAGCCCCCGCTCTCATATCGCAAGATCTCGGTG	1261
QY	787	CAGTACTGCGACGTCGTGCGCAAGAAAGGGCGTTCGGAAACAAGACTGCTGGGGGCGCGC	846
Db	1262	CAGTACGGTATACGCTCTTCACGCCACGAGCC-----C	1291
QY	847	AGCGCGCGCGCGCGCGCGAGCCCGCGGCGAGCGCTTTGGCATCTGTGACACCTTCGCGCGC	906
Db	1292	TTTCGATCGTCGCGCGCGCGTCAAGAGATGGAAGCGCTATGGCATGTGTCGCGCTTCGCGCGC	1351
QY	907	CGGCGCAGGCTTACACAGCGACCTCATGTACATCCGAGAGAGGCCAGCGCGCGCACGCCAG	966
Db	1352	CGGCGCAGGCTTCAACAGTGTACCTCAAGTACATCAAGGCCAAGTCTCTTCGGAAGGCCAG	1411
QY	967	GCCAGAGCAAGAGAGCGCTCGTCAATC	993
Db	1412	GCCCGTGAAGGAGCAAGTGCACCAATC	1438

RESULT 11
AAZ36913

AAZ36913

AC AAZ36913;

DT 13-MAR-2000 (first entry)
YY

DE DNA encoding a homologue of activator of G protein signalling AGS1.
XX

MM G protein-coupled signal transduction; G-gamma subunit
NM G protein-coupled signal transduction; G-gamma subunit
KW G protein-coupled signal transduction; G-gamma subunit

cellular signal transduction; AGS1 homologue; ss.

XX
NS Homo sapiens

OS Homo sapiens

FH	Key	Location/Qualifiers
EM	and	1. 337

CD3
E1
E2T

```

/ catalog = a
/product = "AGSI homologue"
ET

```

XX
XX
PN

MOJ-0906670 AL
NN
XX

PD 18-NOV-1999.

XX 07-MAY-1966 0000

07-MAY-1999; 99WU-05101
XX

PR 08-MAY-1998; 98US-00

PR 07-OCT-1998; 98US-
XY

PA (CADU-) CADUS PHA

XX

PI cismowski M, Duzic E;
XY

WPI: 2000-072337/06

DR P-PSDB; AAY53923.

XX
PT

PT characterized by an aberrant AGS protein activity; a new activator of protein signaling used to treat disorders

homology to ras-related G proteins, and contains alterations in conserved amino acids consistent with a deficiency in GTP hydrolysis activity. AGS stimulates G protein activity, G protein-coupled signal transduction and the phenome response pathway in a receptor-independent manner. The AGS protein also shows G-gamma selectivity, as measured by growth assays in yeast expressing various mammalian G-gamma constructs, and tissue-specific expression, as measured by Northern blot analysis. The AGS protein can be used to screen for compounds that modulate cellular signal transduction. The protein is used to treat disorders characterized by an aberrant AGS protein activity or AGS nucleic acid expression.

Sequence 837 BP; 177 A; 272 C; 233 G; 155 T; 0 other.

Query Match	Score	DB	Length
22.68;	407.4;	21;	837;

Matches 594; Conservative 0; Mismatches 20;

QY 166 GCGATGATCAAGAAGATGTGCCCGAGCGACTTCGAGCTGAGTATCCCGGCGAACAACGC 33E

QY	166	GCAGTATCAAGAAAGTATGCCCCGAGCACTCGAGTGTATCCCGGCCAAGAACTGC	22
Db	34	GCCTATGTAAGACTTTTGTCCACGCGGGAATCGACGCTCATGTGTGCCCCCAAAATCA	93
QY	226	TATCGATGGTCATCCTCGGCTGTGTCCAAAGGTGGGCAAGCGGCATGTGTGCGGCTTC	285
Db	94	TACCGATGGTGGTGTGGGTGCTCTGTGGGTGGGCAAGAGCTCATGTGTCTGCTTC	153
QY	286	CTTACCGGGCCGCTTGAGAGCGCCTTACACGCTTACCATCGAGGACTTCCACCGCAATTTC	345
Db	154	CTCAATGGCCGCTTTTGAGGACCAATACACACCCACATCGAGGACTTCCACGTAAGTA	213
QY	346	TACTCATCCGGGGGAGGAGTGTACAGATGTGACATCTGTGACACGTCGCGCACACCCG	405
Db	214	TACAAATCCGGGGGAGATGTACCACTGTGACATCTGTGATTCCTGTGGCAACACCC	273
QY	406	TTTCCCCGCATCGCGCGCTCTCCATCTCAACAGAGAGCTTTTATCTCGGTGTTCAGT	465
Db	274	TTTCCCCGCATCGCGCGCTCTCCATCTCAACAGAGGAGTGTCTATCTGTGTTCAGC	333
QY	466	CTGGAACAACGGGAGTCTTGTGAGAGGTGCACGGCTCAAGCAGCAATCTTGACACC	535
Db	334	CTGGATTAACCGGGAATCTCTGTATGAAGTCAACCGCTTTCACAAACATCTTGAAGTTC	393
QY	526	AACTTTGCTCTTAAGAAACAAACCAAGAAAGAGTGGAGTCCGCTGGTATCTGGGCG	585
Db	394	AAGTCTGTGCTTAAGAAACAAACCAAGAGGCGCGGAGCTCCCATGTGTATCTGTGGC	453
QY	586	AACAAGGTGACC--GCGACTTCTACCGGAGGTGGACACCGCGAGATCGACAGCTG	642
Db	454	AACAAGAAACGACACAGGGGAGACTGTGCGCGCAGGTGCCACCAACCGAGCGGAGCTCTG	513
QY	643	GTGGGAGACAGACCCGCGGTGGGCTTACTTTCAGATATTCGGGCCAAGAACACAGAC	702
Db	514	GTGTGGGGGACG--AACAATGGGCTTACTTTCGAGGTGTGGCCCAAAACACCAAC	570
QY	703	CTGGACCAATGTTCCGCGGCTCTTTCGCCATGAGCCAAAGCTCCGACGAGATGAGCCCA	762
Db	571	GTGGACGAGATGTTCTACGTGCTCTTCAGATATGCGCAACAGCTGCACACGAGATAGCCCC	630
QY	763	GACCTGCACCCGCAAGGTCTGGGTGCAGTACTGCAGAGTGTCTGCACAAAGAGCGCTGGG	822
Db	631	GGCTCTGATCGCAAGATCTCCGTGCAGTACGGGTGAGCGCTTCAACCCGAGCC-----	683
QY	823	AACAAGAGCTGTGTGCGGGCGGACGGGGGCGGGCGGCGCACCGGGCGAGCGCTTT	882
Db	684	-----CTTCTGATGCGCGCGCTCAAGGAGATGACCGCTAT	720
QY	883	GGCATCTGTGCACCTTTCGGCGCGGACCCAGTACACAGCACTGATGATCATCCG	942
Db	721	GGCATGTCTTCGCTTTCGCGCGCGCCGCGCCAGCTCAACATGACCTCAATGATCAAG	780
QY	943	GAGAAAGCCACCGCGGCACCCAGGCGCAAGGCAAGAGAGCGCTCGTCAATC	993
Db	781	GCCAAGGCTCTTGGGGAAGGCGCGCCCTGTGAGAGGCAAGATGCACATCATC	831

RESULT 12

ABL92076 standard; cDNA; 2832 BP.

AC ABL92076;

DT 30-MAY-2002 (first entry)

DE Human Tumour Endothelial Marker polynucleotide SEQ ID NO 174.

Human; mouse; rat; TEM: tumour endothelial marker; NEM; PEM; cytosolic; normal endothelial marker; pan-endothelial marker; immunostimulant; antiangiogenic; tumour; neovascularisation; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis; psoriasis; gene; ss.

OS Homo sapiens.

PN WO200210217-A2.

PD 07-FEB-2002.

PF 01-AUG-2001; 2001WO-US24031.

PR 02-AUG-2000; 2000US-222599P.

PR 11-AUG-2000; 2000US-224360P.

PR 11-APR-2001; 2001US-282850P.

PA (UYJO) UNIV JOHNS HOPKINS.

PI St Croix B, Kinzler KW, Vogelstein B;

DR WPI: 2002-291856/33.

An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth -

Disclosure: Page 119-120: 331pp: English.

The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein selected from ABB90732, ABB90740, ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumor growth, neovascularisation in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789) are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers (PEM) ABL91903-ABL91995.

Sequence 2832 BP; 602 A; 891 C; 727 G; 612 T; 0 other;

Query Match 22 6%; Score 407.4; DB 24; Length 2832;

Best Local Similarity 71.5%; Pred. No. 1.8e-47;

Matches 594; Conservative 0; Mismatches 201; Indels 36; Gaps 3;

QY 166 GCGATGATCAAGATGTCGCCGAGGAGCTGAGTATCCCGCAAGAACTGC 225

DB 34 GCATGATGAAGCTTGTCCAGGAGGAGTGCACGCTGTCGCCCAAACTCA 93

QY 226 TATCGATGTCATCTCGGCTGTCCTCAAGTGGGCAAGAGCCGATCGTGGCTTC 285

DB 94 TACGCGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 153

QY 286 CTCACGCGCGCTTCGAGAGCGCTTACACGCTTACAGAGAGCTTCACCGCAAGTTC 345

DB 154 CTCATGCGCGCTTGGAGACCACTACACACCCACATCGAGAGCTTCACCGTAAGSTA 213

QY 346 TATCCATCCGCGGAGGAGTCTACAGCTGAGACATCTCGAGACGTCGCAACCCG 405

DB 214 TACAGATCCGCGGAGGAGGAGTCTACAGCTGAGACATCTCGAGACGTCGCAACCCG 273

QY 406 TTCGCCGCGAGTGGGCGGCTCTCCATCTTCACAGAGAGCTTTTCACTCTGTTCACT 465

DB 274 TTCGCCGCGAGTGGGCGGCTCTCCATCTTCACAGAGAGCTTTTCACTCTGTTCACT 333

QY 466 CTGAGACAGCGGAGTCTCTGAGAGGAGTGGAGGAGTGGAGGAGTGGAGGAGTGGAGG 525

DB 334 CTGAGATACCGGAGTCTCTGAGAGGAGTGGAGGAGTGGAGGAGTGGAGGAGTGGAGG 393

QY 526 AAGCTTTCCTCAAGAACAAACAGAGAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 585

DB 394 AAGCTTTCCTCAAGAACAAACAGAGAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 453

QY 586 AACAGGAGTAC---CGAGCTTCTACCGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 642

DB 454 AACAGGAGTAC---CGAGCTTCTACCGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 513

QY 643 GTGGGCGAGCAGCCCGAGGCTGAGCTTCTGAGATCTGAGCTGAGCTGAGCTGAGCTGAGCT 702

DB 514 GTGGGCGAGCAGCCCGAGGCTGAGCTTCTGAGATCTGAGCTGAGCTGAGCTGAGCTGAGCT 570

QY 703 CTGAGCAGATGTTCCGCGGCTCTTCCAGTGGCCAAAGTGGCCAAAGTGGCCAAAGTGGCCAA 762

DB 571 GTGAGCAGATGTTCTAGTGTCTCTGAGATGGCCAAAGTGGCCAAAGTGGCCAAAGTGGCCAA 630

QY 763 GACCTGACCGCAGGCTCTGAGTGTCTGAGTGTCTGAGTGTCTGAGTGTCTGAGTGTCTGAGT 822

DB 631 GACCTGACCGCAGGCTCTGAGTGTCTGAGTGTCTGAGTGTCTGAGTGTCTGAGTGTCTGAGT 683

QY 823 AACAAAGTGTCTGAGGCGGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 882

DB 684 -----CTTCTGATGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720

QY 883 GGCATGTCGACACCTTTCG 942

DB 721 GGCATGTCGACACCTTTCG 780

QY 943 GAGAGGCGCAGCG 993

DB 781 GCCAAGTCTCTTCCGGAAGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 831

RESULT 13

ABQ28320/C

ID ABQ28320 standard; DNA; 624 BP.

ABQ28320;

DT 12-JUL-2002 (first entry)

DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 14911.

Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;

KW drug; side effect; cancer; central nervous system; cardiovascular;

KW gastrointestinal; respiratory system; single nucleotide polymorphism;

SNP; cell differentiation; ds.

OS Homo sapiens.

PN WO200218632-A2.

PD 07-MAR-2002.

QY 01-SEP-2001; 2001WO-EP10074.

DB 01-SEP-2000; 2000DE-1043826.

PR 05-SEP-2000; 2000DE-1044543.

PA (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K, Guetig D;
 XX WPI: 2002-371829/40.
 XX
 XX Determining the degree of cytosine methylation in genomic DNA, useful
 XX for diagnosis and prognosis, comprises selective hybridization of
 XX amplicons from chemically treated DNA -
 XX
 XX Claim 12: 56pp + Sequence Listing; 56pp; German.

XX This invention describes a novel method for determining the degree of
 XX methylation of a particular cytosine in a motif 5'-CpG-3', present in a
 XX genomic sample of DNA. The sample is treated chemically to convert
 XX cytosine (C) but not methylated C, to uracil, then part of the genomic
 XX DNA that contains the target C is amplified to form a labeled amplicon.
 XX The amplicon is hybridised to two classes, each with at least one
 XX member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
 XX and the degree of hybridisation to both classes is determined from the
 XX label on the amplicon. From the ratio of labels hybridised to the two
 XX classes of oligomers, the degree of methylation is calculated. The method
 XX is used: (i) for diagnosis and/or prognosis of side effects of
 XX therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
 XX of the central nervous, cardiovascular, gastrointestinal and respiratory
 XX systems etc., particularly by detecting mutations or single nucleotide
 XX polymorphisms (SNP/s); and (ii) for differentiation of cell or tissue
 XX types and for investigating cell differentiation. The method allows the
 XX methylation status of many C residues to be determined simultaneously.
 XX AB013410-AB054121 represent genomic DNA sequences used to illustrate the
 XX method for determining the degree of cytosine methylation described in
 XX the disclosure of the invention.

XX Sequence 624 BP: 79 A; 68 C; 212 G; 265 T; 0 other;

XX Query Match 21.7%; Score 391.4; DB 24; Length 624;
 XX Best Local Similarity 77.9%; Pred. No. 2.8e-45;
 XX Matches 484; Conservative 0; Mismatches 136; Indels 1; Gaps 1;

QY 594 TGACGCGACTTCTTACCGAGGTGGACGAGCATCGAGCAGCTGGGGGAGCA 653
 DB 620 TAACCGCGACTTCTTACCGAGGTGGACGAGCATCGAGCAGCTGGGGGAGCA 651
 QY 654 CCCCCGCGCGCTTCTTACCGAGGTGGACGAGCATCGAGCAGCTGGGGGAGCA 713
 DB 560 CCCCCGCGCGCTTCTTACCGAGGTGGACGAGCATCGAGCAGCTGGGGGAGCA 501
 QY 714 GTTCCGCGCGCTTCTTACCGAGGTGGACGAGCATCGAGCAGCTGGGGGAGCA 773
 DB 500 ATTCCGCGCGCTTCTTACCGAGGTGGACGAGCATCGAGCAGCTGGGGGAGCA 441
 QY 774 CAAAGTCTCGGTGAGTACGAGTGTGACAGCAAGAGGCTGGGAGCAAGAGCT 833
 DB 440 CAAAGTCTCGGTGAGTACGAGTGTGACAGCAAGAGGCTGGGAGCAAGAGCT 381
 QY 834 GCTGGGGGCGCGCGCTTCTTACCGAGGTGGACGAGCATCGAGCAGCTGGGGGAGCA 893
 DB 380 ACTAGCAACCGAGCAAGAGGCTGTGACAGCAAGAGGCTGGGAGCAAGAGCT 322
 QY 894 ACCCTTTCGCGCGCGCTTCTTACCGAGGTGGACGAGCATCGAGCAGCTGGGGGAGCA 953
 DB 321 ACCCTTTCGCGCGCGCTTCTTACCGAGGTGGACGAGCATCGAGCAGCTGGGGGAGCA 262
 QY 954 GCGCGGCGCGCGCTTCTTACCGAGGTGGACGAGCATCGAGCAGCTGGGGGAGCA 1013
 DB 261 GCGCGGCGCGCGCTTCTTACCGAGGTGGACGAGCATCGAGCAGCTGGGGGAGCA 202
 QY 1014 TGGCGGCGCGCGCTTCTTACCGAGGTGGACGAGCATCGAGCAGCTGGGGGAGCA 1073
 DB 201 TAAAGCAACCGAGCAAGAGGCTGTGACAGCAAGAGGCTGGGAGCAAGAGCT 142
 QY 1074 CAGGCGCGCGCGCTTCTTACCGAGGTGGACGAGCATCGAGCAGCTGGGGGAGCA 1133
 DB 141 CAAAGCAACCGAGCAAGAGGCTGTGACAGCAAGAGGCTGGGAGCAAGAGCT 82

QY 1134 GGAGCGCGCGCTTCTTACCGAGGTGGACGAGCATCGAGCAGCTGGGGGAGCA 1193
 DB 81 AAAAGCGCGCGCTTCTTACCGAGGTGGACGAGCATCGAGCAGCTGGGGGAGCA 22
 QY 1194 AAGACTGGGACTATTCGCCAC 1214
 DB 21 AAAACTAAACTATTCGCCAC 1

RESULT 14

AB028321
 ID AB028321 standard; DNA: 624 BP.

XX AB028321:

DT 12-JUL-2002 (first entry)

XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 14912.

KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
 KW drug; side effect; cancer; central nervous system; cardiovascular;
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;
 KW SNP; cell differentiation; ds.

XX Homo sapiens.

XX WO200210632-A2.

XX 07-MAR-2002.

XX 01-SEP-2001; 2001WO-EP10074.

XX 01-SEP-2000; 2000DE-1043826.

XX 05-SEP-2000; 2000DE-1044543.

XX (EPIC-) EPIDENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K, Guetig D;

XX WPI: 2002-371829/40.

XX Determining the degree of cytosine methylation in genomic DNA, useful
 XX for diagnosis and prognosis, comprises selective hybridization of
 XX amplicons from chemically treated DNA -

XX Claim 12: 56pp + Sequence Listing; 56pp; German.

XX This invention describes a novel method for determining the degree of
 XX methylation of a particular cytosine in a motif 5'-CpG-3', present in a
 XX genomic sample of DNA. The sample is treated chemically to convert
 XX cytosine (C) but not methylated C, to uracil, then part of the genomic
 XX DNA that contains the target C is amplified to form a labeled amplicon.
 XX The amplicon is hybridised to two classes, each with at least one
 XX member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
 XX and the degree of hybridisation to both classes is determined from the
 XX label on the amplicon. From the ratio of labels hybridised to the two
 XX classes of oligomers, the degree of methylation is calculated. The method
 XX is used: (i) for diagnosis and/or prognosis of side effects of
 XX therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
 XX of the central nervous, cardiovascular, gastrointestinal and respiratory
 XX systems etc., particularly by detecting mutations or single nucleotide
 XX polymorphisms (SNP/s); and (ii) for differentiation of cell or tissue
 XX types and for investigating cell differentiation. The method allows the
 XX methylation status of many C residues to be determined simultaneously.
 XX AB013410-AB054121 represent genomic DNA sequences used to illustrate the
 XX method for determining the degree of cytosine methylation described in
 XX the disclosure of the invention.

XX Sequence 624 BP: 265 A; 212 C; 68 G; 79 T; 0 other;

XX Query Match 21.7%; Score 391.4; DB 24; Length 624;
 XX Best Local Similarity 77.9%; Pred. No. 2.8e-45;

Mon Dec 30 09:17:17 2002

us-09-709-103-3.rng

Page 17

Db 480 GTTTTAGTGGGAGCGCGCGCGATTGGCGTTTTTTTTTTCGGCGATTTCGTTTTACTA 539

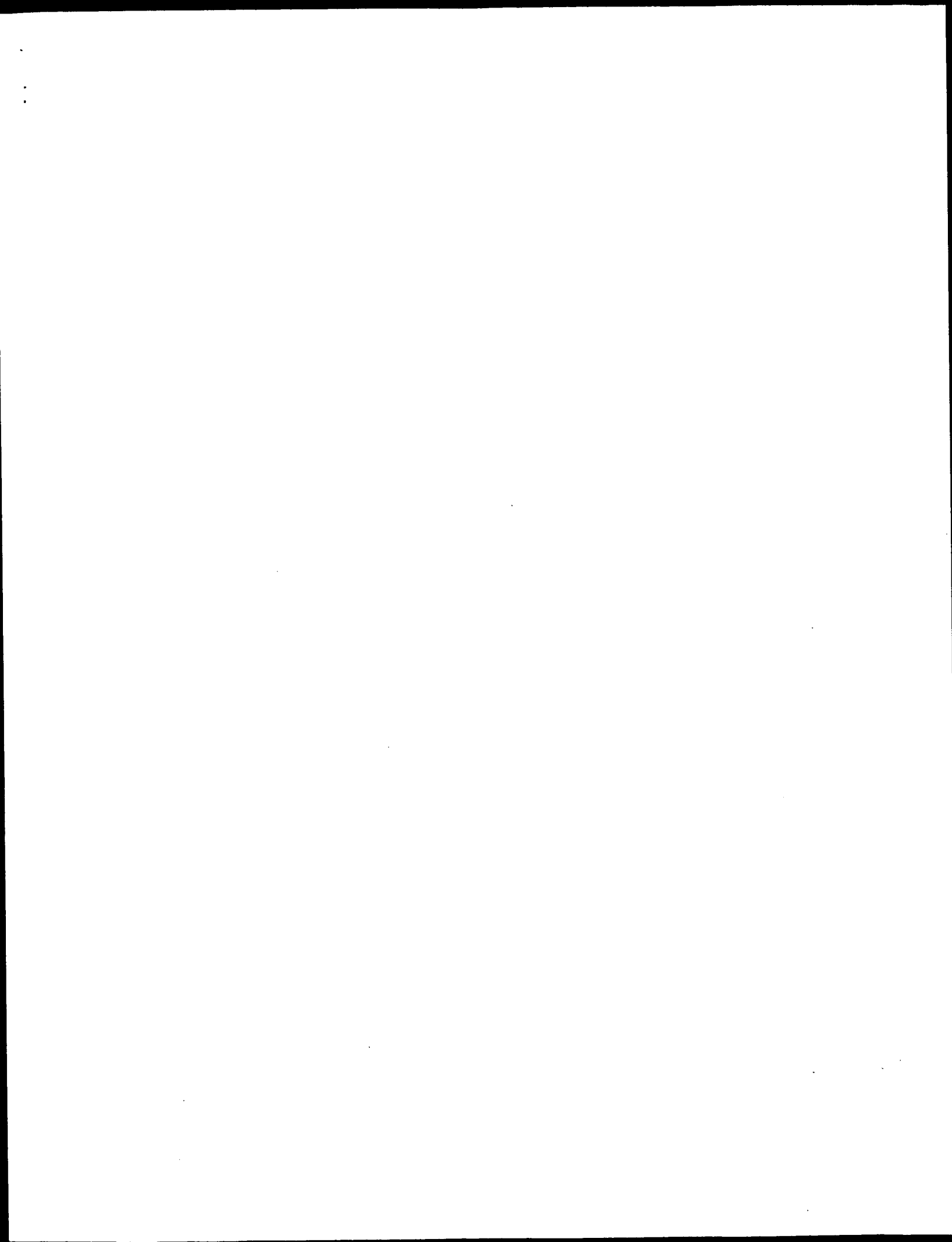
QY 1130 CTGGGGAGCGCCCTCAACCGAAGAGCGATCTCTGCTCCGGAAGAAAGAAAGC 1189

Db 540 TTGGGAGCGCTTTTAAATCGAAGAGCGCGTTATTTGTTCCGAAGAAAGAAAGC 599

QY 1190 GCCCAACACGCGGACTATT 1208

Db 600 GGTTAAGATTGGGATATT 618

Search completed: December 28, 2002, 03:00:10
Job time : 388.134 secs



Query Match	22.8%	Score 409.8	DB 10	Length 3082
Best Local Similarity	66.3%	Pred. No. 6.8e-54		
Matches 654	Conservative 0	Mismatches 297	Indels 36	Gaps 3
QY	10	AGCGGAGCCGGAGACCCCAAGCCGAGCCGCCAGCCCGAGAGAGACCCCTCCAGCCGT	69	
Db	52	AGCGGAGGGGAGAGATCCCGCGCAGTAGACCGGAGAGCCAGACAGACTGTGGAGGCTGC	111	
QY	70	CACCCGCGTGCACACCCGAGGAGCCTCAGCCGCTCTTGCCCTTCTCGGCCCGCGC	129	
Db	112	GCGGCTGGAGACGACGACGACGCTCCCGGAGCTCCCGGCGCTTCCAGGACACTCTGTAGAC	171	
QY	130	CCGCGCTCGCGGCCCTCTGCCCAATGAACATGGCGCGGATGATCAAGAAAGTGCOCG	189	
Db	172	CGTGCAGAGAGGCCCGGCCCGCATTTCCAGGCCCGAGAGCATGATGAAGACTTTGTCCAGC	231	
QY	190	AGGGAATCGGAGACTAGATATCCCGGCCAAGAATGCTATCGCATGTCATCTCGGCTCG	249	
Db	232	GGGAAATGCACCTCAAGTGTGCCCGCCAAAACATCAACGCAATGCTGCTGGGTGCC	291	
QY	250	TCCAAAGTGGGCAAGACGGCCATGCTGTCGGGCTTCTCACCGCGCTTCGAGAGCGCC	309	

Db	292	TCCTGGGTGGGCAAGAGCTCCATCTGCTGTCTCGCTTCCCTCAATAGGCGCGTTTAAAGACACG	351
Qy	310	TACACGCGCTACATCGAGGACTTTCACACCGCAAGTTCCTACTCCATCCCGGGCGAGGCTTAC	369
Db	352	TACACACCCACATCGAGGACTTTCACACCGTAAAGTATTAACAATCCGCGCGACATGTAC	411
Qy	370	CAGTGCACATCTCTGCACAGCTCCGGCAACACACGCTTCCCGCCCAATGGGCGGCTCTCC	429
Db	412	CAGTGCACATCTCTGGATACCTCTGGGAAACACACCTTTCGCCCATATGGGACAGCTGTCC	471
Qy	430	ATTCCTACAGAGAGACGTTTTTCATCTGGTTCAGTCTGGACACACCGCATCTCTTCAG	489
Db	472	ATTCCTACAGAGGATGTCTTCATCTGTGTGTGTCAGCTGGATTAACCGGAGTCTCTGCAT	531
Qy	490	GAGTGCACGCGGCTCAGGACAGACATCTCTGGACACACAGTCTTGCCCTCAAGAACAAACCC	549
Db	532	GAGGTCAAGCGCTTCAGAACACATCTTGAAGTCAAGTCTCTGCTTGAAAGAACAAAGACC	591
Qy	550	AAGGAGAACGTGTGACAGTACCCCTGTATCTGGCGCAACAAAGGGGTGACC--GCGACTTC	606
Db	592	AAGGAGGCGGCGGAGATCTCCCATGTGTATCTGTGTGCAACAAAGACACACGCGGAGCTG	651
Qy	607	TACCGCGAGTGTGACACAGCGCGGATGTGACAGCTGTGTGGGCGCACACACCCCGACGCTTG	666
Db	652	TGCCCCGAGGTGTGCCACACACAGAGCGGAGCTGTGTGTGTGTGGGCGA---CGAAGAACTCC	708
Qy	667	GCGTCACTTCGAGATCTGGGCGCAAGAACAGACGCTTGACACAGATGTTCGCCGCGCTTC	726
Db	709	GCGTCACTTCGAGATGTCTGGCGCAAGAACACCAACGCTGGACGAGATCTTCAAGTGTCTC	768
Qy	727	TTCGCGCATGTGCGCAAGCTGCCACGAGAGTGTGAGCCAGACTGTGACCGCAAGTCTCGGTG	786
Db	769	TTCACACTGTGGCCAAAGCTGCCACAGAGATGTGAGCCCGCCCTGTGTCGAAGATCTCGGTG	828
Qy	787	CAGTCACTGTGAGATGTCTGTGACAAAGAGGCGGTGTGGGAAACAAGAAAGTGTGTGGGCGCGC	846
Db	829	CAGTCACTGTGAGCGCTTCCACCCCAAGGCG-----C858	858
Qy	847	AGCGGCGGCGGCGGCGGCGGACCGCGGCGAGCGCTTGTGGCATCTGTGGCACCTTGTGCGCGC	906
Db	859	TTCGTGATCGCGCGCGGTCAAGAGAGATGTGACCGCTTATGCAATGATCTGTGCCCTTGTGCCCGC	918
Qy	907	CGGCGCAGGCTTACACAGGACCTCTATACATCCGCGGAAAGGCGACGCGCGGCGACG	966
Db	919	CGCGCCAGGCTCAACAGATGACTCTCAAGTACATCAAGGCCAAGGTCCTTTCGGGAAGGCCAG	978
Qy	967	GCCAAAGACAGAGAGCGGTGTGCTGTATC993	
Db	979	GCCCGTGAAGGAGCAAGTGCACATTC1005	
RESULT 2			
US-09-880-107-2890/c			
: Sequence 2890, Application US/09880107			
: Patent No. US20020142981A1			
: GENERAL INFORMATION:			
: APPLICANT: Horne, Darci T.			
: APPLICANT: Vockley, Joseph G.			
: APPLICANT: Scherf, Uwe			
: APPLICANT: Gene Logic, Inc.			
: TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer			
: FILE REFERENCE: 44921-5028-WO			
: CURRENT APPLICATION NUMBER: US/09/880,107			
: CURRENT FILING DATE: 2001-06-14			
: PRIOR APPLICATION NUMBER: US 60/211,379			
: PRIOR FILING DATE: 2000-06-14			
: PRIOR APPLICATION NUMBER: US 60/237,054			
: PRIOR FILING DATE: 2000-10-02			
: NUMBER OF SEQ ID NOS: 3950			
: SOFTWARE: PatentIn Ver. 2.1			
: SEQ ID NO 2890			
: LENGTH: 414			
: TYPE: DNA			

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? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: Genbank Accession No. US20020142981A1 R51831
? NAME/KEY: unsure
? LOCATION: (1)-(414)
? OTHER INFORMATION: n = a o r c o f g o r t
US-09-860-107-2890

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Query Match	19.6%;	Score 352.6;	DB 10;	Length 414;
Best Local Similarity	94.7%;	Pred. No. 2.1e-45;		
Matches 392;	Conservative	0;	Mismatches 18;	Indels 4;
				Gaps 3;

QY	1284	ATCTTTCMAAAGACCTAAGTGTG - AACGGGGGTGGGGAGGATGTG - AAGTATATCCG	1341
Db	414	AACCTTCMAAACAATTAAAGTAAACCAACGGGTGGGGAGGATGTGTAAGTTAACCA	355
QY	1342	CCTCGTAGAGCTTCAGAAGAACCGTCAATGCC - GCTTGAAGGGTCAGGACCCAGGGGCA	1399
Db	354	CCTCGTAGAGCCTCAAGAAACCGTATATGCCGCTTGAAGGGTCAGGACCCAGGGGCA	295
QY	1400	TTATCTTGTCTGTGATTTCCGGGTTCCTGTGTACAGCCGGTAGAGCCTCTGCCCTCCGAAA	1459
Db	294	TTATCTTGTCTGTGATTTCCGGGTTCCTGTGTGTACAGCCGGTAGAGCCTCTGCCCTCCGAAA	235
QY	1460	CTAAGCGGGGGGGCGGTGGGTCAATATCAATACCAAGTGAACCTGTTACATGTGAGTGAAC	1519
Db	234	CTAAGCGGGGGGGCGGTGGGTCAATATCAATACCAAGTGAACCTGTTACATGTGAGTGAAC	175
QY	1520	TGCACAAAGGAACAACAACAACCTTGCACTTTAAGCGGTAGTCCGGTGCACATGGA	1579
Db	174	TGCACAAAGGAACAACAACAACCTTGCACTTTAAGCGGTAGTCCGGTGCACATGGA	115
QY	1580	CACGAACAACAACCTTACCACGTTTATATCTGTGTGTGTGATAGTCTTTTAAAGTTATT	1639
Db	114	CACGAANAACAACCTTACCACGTTTATATCTGTGTGTGTGATAGTCTTTTAAAGTTATT	55
QY	1640	GCTTTATTTGGTTTTTAAATTAACAATAAAATTAATTTAAATGGAAAAAATAA 1693	
Db	54	GCTTTATTTGGTTTTTAAATTAACAATAAAATTAATTTAAATGGAAAAAATAA 1	

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RESULT 3
US-09-960-352-10273
; Sequence 10273, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengping
; APPLICANT: Byatt, John C.
; APPLICANT: Mathalaagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 10273
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3),(23),(31)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 44-LIB3058-050-Q1-K1-C8
US-09-960-352-10273

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Query Match	17.0%	Score 305.8;	DB 10;	Length 405;
Best local Similarity	87.3%	Pred. No. 2.5e-38;		
Matches 345;	Conservative	0;	Mismatches 49;	Indels 1;
			Gaps	1;
QY	94	CCCTACGCGGCTCTCTGCCCTTCTCTCGGCGCGCGGCC-6GCGTCTGGCGGCGGCGCTTGGCCC	152	

Query Match	Similarity	13.3%	Score 240.2	DB 10	Length 11221
Best Local	Similarity	68.7%	Pred. No. 3.7e-28		
Matches	392	Conservative	0	Mismatches 143	Indels 36
				Gaps	3
QY	426	CTCTCATCTCTACAGAGACGTTTTCATCCTGGTGTTCAGTCTGGACAACGCGACTCTT	485		
Db	7680	CTCTCTCCCTGGAGGGGATGTCCTTCATCTGTGATGTTTCAGCTGGATTAACCGGGAGTCTT	7739		
QY	486	CGAGGAGGTGCAGCGGCTCAGCGACACATCCTGTGCACCAAGCTTGCTCTGAAGAACAA	545		
Db	7740	CGATGAGGTTCAGGCCCTTCAGAACCAATCTGTGAGGTCAAGTCTGCTGGAAGAACAA	7799		
QY	546	AACCAAGGAACGTGGACGTGCCCTTGTCATCTGCGGCACCAAGGTTACG---	602		
Db	7800	GACCAAGGAGGCGGCGGAGCTGCCATGTGTCATCTGTGGCAACAAAGAACACACGCGCA	7859		
QY	603	CTTCTACCCGAGGTGGAGCCAGCGGCAATGACGACACTGTTGGGCGACGACCCCAAGCG	662		
Db	7860	GGTGTGCCGCCAGGTGCCACACCGAGAGCCGCACTCTGTGTGCGGCGA---CGAGAA	7916		
QY	663	CTGCGCTACTTCGAGATCTCGGCCAAGAAAGAACAGAGCTGTGACCAAGATGTTTCGCGC	722		
Db	7917	CTGCGCTACTTCGAGGTGTGCGCCAAAGAACACCAACAGTGGACGAGATGTTTCTACCT	7976		
QY	723	GGTCTTGCGCATGGCGCAAGCTGCCAAGGAGATAGAGCCAGACTGCACCGCAAGTCTTC	782		

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RESULT 5
US-09-864-761-21643
: Sequence 21643, Application US/09864761
: Patent No. US20020046763A1
: GENERAL INFORMATION:
: APPLICANT: Penn, Sharon G.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Wensheng
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
: FILE REFERENCE: Aemolca-X-1
: CURRENT APPLICATION NUMBER: US/09/864,761
: CURRENT FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 60/180,312
: PRIOR FILING DATE: 2000-02-04
: PRIOR APPLICATION NUMBER: US 60/207,456
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: US 09/632,366
: PRIOR FILING DATE: 2000-08-03
: PRIOR APPLICATION NUMBER: GB 24263,6
: PRIOR FILING DATE: 2000-10-04
: PRIOR APPLICATION NUMBER: US 60/236,359
: PRIOR FILING DATE: 2000-09-27
: PRIOR APPLICATION NUMBER: PCT/US01/00666
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00667
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00664
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00669
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00665
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00668
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00663
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00662
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00661
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00670
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: US 60/234,687
: PRIOR FILING DATE: 2000-09-21
: PRIOR APPLICATION NUMBER: US 09/608,408
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: US 09/774,203
: PRIOR FILING DATE: 2001-01-29
: NUMBER OF SEQ ID NOS: 49117
: SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
: SEQ ID NO 21643
: LENGTH: 368

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Db 305 AAAAGTCCCGTCTCTGG 325

RESULT 8

US-09-765-298A-25

Sequence 25, Application US/09765298A

Patent No. US20020137017A1

GENERAL INFORMATION:

APPLICANT: ARONHEIM, AMI

TITLE OF INVENTION: METHOD FOR DETECTION PROTEIN-PROTEIN INTERACTIONS AND A KIT THERE

FILE REFERENCE: 108387.01

CURRENT APPLICATION NUMBER: US/09/765, 298A

PRIOR FILING DATE: 2001-01-22

PRIOR FILING DATE: 1998-07-22

PRIOR FILING DATE: 1999-01-12

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn version 3.1

SEQ ID NO 25

LENGTH: 351

TYPE: DNA

ORGANISM: Homo sapiens

US-09-765-298A-25

Query Match

Best Local Similarity 57.4%; Score 92.6; DB 10; Length 551;

Matches 167; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

Db 226 TATGCGATGTCATCTCGGCTGCTCCAGGTGGGCAAGCGGCATCGTGTGCGCTTC 285

Db 4 TATTAAGCTGTGTGTGGGGCGGCGGTGTGGGCAAGGTGGGCGTACACCATTCAGCTG 63

QY 286 CTCACGCGCGCTTCGAGAGCGCTTACACGCTTACATCGAGACTTCCACCGCAAGTTC 345

Db 64 ATCAGAACCATTTTGTGAGAGATAGACCCCTATAGAGATTCTTACCGAAGCAG 123

QY 346 TATCCCGCATCGCGCGCTTCGAGAGCGTTCACGCTTCTCGACACGTCGCGCAACCGC 405

Db 124 GTGCTCATTTGATGTGGGAGAGCTGCTGTGGACATCTGTGATACCGCGCCAGAGAG 183

QY 406 TTCGCCGATGCGCGCTTCGAGAGCGTTCACGAGAGAGAGAGAGAGAGAGAGAGAG 465

Db 184 TACAGCGCCATCGCGGACCGATACGATCGACGCGGAGGAGGCTTCGTGTGTGGCC 243

QY 466 CTGAGCAACCGCGCTTCGAGAGCGTTCGAGAGAGAGAGAGAGAGAGAGAGAGATC 516

Db 244 ATCAACAACCAAGCTTTTGTGAGAGATCACCAGTACAGAGAGAGAGATC 294

RESULT 9

US-10-104-484-1

Sequence 1, Application US/10104484

Patent No. US2002015056A1

GENERAL INFORMATION:

APPLICANT: Guan, Kun-Lian

APPLICANT: Stewart, Scott

TITLE OF INVENTION: METHOD OF INHIBITING CANCEROUS CELL PROLIFERATION USING RAS MUTAN

FILE REFERENCE: UMICH-0010

CURRENT APPLICATION NUMBER: US/10/104, 484

PRIOR FILING DATE: 2002-03-25

PRIOR FILING DATE: 2001-03-23

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 570

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Nucleotide sequence of the GDP-bound Ras mutant, RasN17N69.

US-10-104-484-1

Query Match

Best Local Similarity 57.4%; Score 92.6; DB 12; Length 570;

Matches 167; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

Db 226 TATGCGATGTCATCTCGGCTGCTCCAGGTGGGCAAGCGGCATCGTGTGCGCTTC 285

Db 10 TATTAAGCTGTGTGTGGGGCGGCGGTGTGGGCAAGGTGGGCGTACACCATTCAGCTG 69

QY 286 CTCACGCGCGCTTCGAGAGCGCTTACACGCTTACATCGAGACTTCCACCGCAAGTTC 345

Db 70 ATCAGAACCATTTTGTGAGAGATAGACCCCTATAGAGATTCTTACCGAAGCAG 129

QY 346 TATCCCGCATCGCGCGCTTCGAGAGCGTTCACGCTTCTCGACACGTCGCGCAACCGC 405

Db 130 GTGCTCATTTGATGTGGGAGAGCTGCTGTGGACATCTGTGATACCGCGCCAGAGAG 189

QY 406 TTCGCCGATGCGCGCTTCGAGAGCGTTCACGAGAGAGAGAGAGAGAGAGAGAGAG 465

Db 190 TACAGCGCCATCGCGGACCGATACGATCGACCGGAGAGGCTTCGTGTGTGGCC 249

QY 466 CTGAGCAACCGCGCTTCGAGAGCGTTCGAGAGAGAGAGAGAGAGAGAGAGAGATC 516

Db 250 ATCAACAACCAAGCTTTTGTGAGAGATCACCAGTACAGAGAGAGATC 300

RESULT 10

US-10-104-484-3

Sequence 3, Application US/10104484

Patent No. US2002015056A1

GENERAL INFORMATION:

APPLICANT: Guan, Kun-Lian

APPLICANT: Stewart, Scott

TITLE OF INVENTION: METHOD OF INHIBITING CANCEROUS CELL PROLIFERATION USING RAS MU

FILE REFERENCE: UMICH-0010

CURRENT APPLICATION NUMBER: US/10/104, 484

PRIOR FILING DATE: 2002-03-25

PRIOR FILING DATE: 2001-03-23

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3

LENGTH: 570

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Nucleotide sequence of the wild type Ras mutant, RasN17N69.

US-10-104-484-3

Query Match

Best Local Similarity 57.4%; Score 92.6; DB 12; Length 570;

Matches 167; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

Db 226 TATGCGATGTCATCTCGGCTGCTCCAGGTGGGCAAGCGGCATCGTGTGCGCTTC 285

Db 10 TATTAAGCTGTGTGTGGGGCGGCGGTGTGGGCAAGGTGGGCGTACACCATTCAGCTG 69

QY 286 CTCACGCGCGCTTCGAGAGCGCTTACACGCTTACATCGAGACTTCCACCGCAAGTTC 345

Db 70 ATCAGAACCATTTTGTGAGAGATAGACCCCTATAGAGATTCTTACCGAAGCAG 129

QY 346 TATCCCGCATCGCGCGCTTCGAGAGCGTTCACGCTTCTCGACACGTCGCGCAACCGC 405

Db 130 GTGCTCATTTGATGTGGGAGAGCTGCTGTGGACATCTGTGATACCGCGCCAGAGAG 189

QY 406 TTCGCCGATGCGCGCTTCGAGAGCGTTCACGAGAGAGAGAGAGAGAGAGAGAGAG 465

Db 190 TACAGCGCCATCGCGGACCGATACGATCGACCGGAGAGGCTTCGTGTGTGGCC 249

QY 466 CTGAGCAACCGCGCTTCGAGAGCGTTCGAGAGAGAGAGAGAGAGAGAGAGAGATC 516

ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 04-LIB3058-049-01-K1-A11
US-09-960-352-836

Query Match
Best Local Similarity 4.9%; Score 88.8; DB 10; Length 373;
Matches 117; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1596 CCCAGGTGTTTACCTGCTGTGAGCTCTTAAAGTATTCCTTATTTGTTT 1655
DB 173 CCCCGTTTTTTTGTGTTTATTTTATTTTATTTTATTTTGTCCCTTTA 114

QY 1656 TAATATACATTAATAATTAATGAAAAAATTTTAAAAAATTTTAAAAA 1715
DB 113 AAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAA 54

QY 1716 AAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAA 1759
DB 53 AAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAA 10

RESULT 15

US-09-925-301-223
Sequence 223, Application US/09925301
Patent No. US2002005208A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA106

CURRENT APPLICATION NUMBER: US/09/925,301

PRIOR FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05882

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: 60/124,270

NUMBER OF SEQ ID NOS: 1694

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 223

LENGTH: 2921

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1609)

OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: misc_feature

LOCATION: (2915)

OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: misc_feature

LOCATION: (2921)

OTHER INFORMATION: n equals a,t,g, or c

US-09-925-301-223

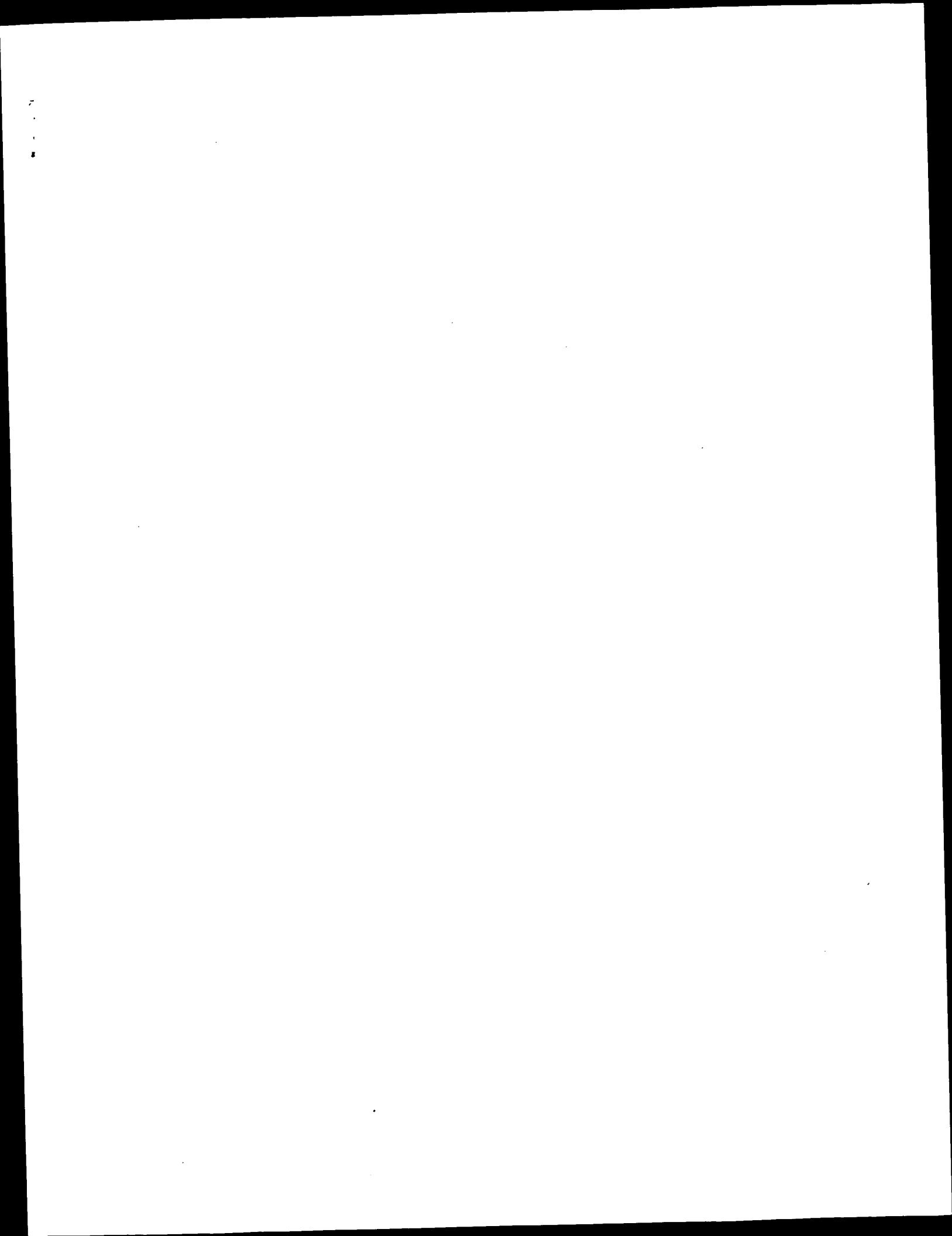
Query Match
Best Local Similarity 4.9%; Score 88.8; DB 10; Length 2921;
Matches 114; Conservative 1; Mismatches 43; Indels 0; Gaps 0;

QY 1591 CCTTACCCAGGTGTTTACTGTGTGTGAGCTCTTAAAGTATTCCTTATTTG 1650
DB 2712 CCTTGCATAAATGCTAAAGTGTGAGTGTGGAATTAATCAATTAATCAATTTG 2771

QY 1651 TTTTATATATACATTAATAATTAATTAATTAATTAATTAATTAATTAAT 1710
DB 2772 AAGTGTGMAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2831

QY 1711 AAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAA 1748
DB 2832 AAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAA 2869

Search completed: December 28, 2002, 05:56:08
Job time: 130.059 secs



was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com"

BASE COUNT 168 a 280 c 276 g 200 t 3 others
ORIGIN

Query Match 49.48; Score 889; DB 9; Length 927;
Best Local Similarity 98.88; Pred. No. 5,1e-99;
Matches 914; Conservative 2; Mismatches 7; Indels 2; Gaps 2;

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DB 927 TCTTGGCCATGGCCAAAGTCCCAAGCAGATGAGCCACAGCCTGACCCGCAAGGTCGCG 868
QY 785 TGCAGTACTGCGAGCTGCTGCACAAAGAGCGCTGCCGAACAAAGAGCTGCTGGGGCCG 844
    |||||||
DB 867 TGCAGTACTGCGAGCTGCTGCACAAAGAGCGCTGCCGAACAAAGAGCTGCTGGGGCCG 808
QY 845 GCAGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 904
    |||||||
DB 807 GCAGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 748
QY 905 GCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 964
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DB 747 GCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 688
QY 965 AGGCCAAGGACAAAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1023
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DB 687 AGGCCAAGGACAAAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 628
QY 1024 ACCTAAGGAGGACCTTTTGTGTTAAGTCAATCAAGGCGCGGTGCGCCGCGCGGGA 1083
    |||||||
DB 627 ACCTAAGGAGGACCTTTTGTGTTAAGTCAATCAAGGCGCGGTGCGCCGCGCGGGA 568
QY 1084 GCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1143
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DB 567 GCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 508
QY 1144 CTGAACCGGAGGAGCGGTGCTGCTCCGGAAGGAAGAAAGCGGCGCAAGACTGGGA 1203
    |||||||
DB 507 CTGAACCGGAGGAGCGGTGCTGCTCCGGAAGGAAGAAAGCGGCGCAAGACTGGGA 448
QY 1204 CTATTCCCGACCCCGGTCGCCCATTTGAGGCGCGCCACCCCATTAATCTTTGGAGCGAGG 1263
    |||||||
DB 447 CTATTCCCGACCCCGGTCGCCCATTTGAGGCGCGCCACCCCATTAATCTTTGGAGCGAGG 388
QY 1264 GCGGAGCGGAGGGGTGATTTATCTTCTCAAGAGCTAAGAGGAGCGGGGGGGGGAG 1323
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DB 387 GCGGAGCGGAGGGGTGATTTATCTTCTCAAGAGCTAAGAGGAGCGGGGGGGGGAG 328
QY 1324 GGATGTGAAGTATTCAGAGCTCTGCTAGGCTTCAAGAAACGCTCATGCGCGTTGAGGGT 1383
    |||||||
DB 327 GGATGTGAAGTATTCAGAGCTCTGCTAGGCTTCAAGAAACGCTCATGCGCGTTGAGGGT 268
QY 1384 CAGGAGCCACGSGGGGCTTATCTTGTGTGATTCGGGGTGTGTGACAGCCGGTAGAGC 1443
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DB 267 CAGGAGCCACGSGGGGCTTATCTTGTGTGATTCGGGGTGTGTGACAGCCGGTAGAGC 208
QY 1444 CTTCTGCGCCCTCCGAAACTAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1503
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DB 207 CTTCTGCGCCCTCCGAAACTAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 148
QY 1504 TACATGTGAGTGAAGTGAACAAGGAACACAAACAAACTTGAACCTTTAAGCGTAGATT 1563
    |||||||
DB 147 TACATGTGAGTGAAGTGAACAAGGAACACAAACAAACTTGAACCTTTAAGCGTAGATT 88
QY 1564 CCGGTGTCAACATGACACGAACAAACCTTACCAAGGTGTTATATCTGTGTGTGTA 1623

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DB 87 CCGGTGTCAACATGACACGAACAAACCTTACCAAGGTGTTATATCTGTGTGTA- 29
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QY 1624 GGTCTTAAAGTATTCCTTATTT 1648
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DB 28 GGTCTTAAAGTATTCCTTATTT 4

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RESULT 2

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LOCUS AGENCOUNT 6715681 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5748585
DEFINITION 5', mRNA sequence.
ACCESSION BM919341
VERSION BM919341.1 GI:19369720
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1035)
NIH-MGC http://mgs.nci.nih.gov/
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)
UNPUBLISHED (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA library prepared by: The I.M.A.G.E. Consortium (ULNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ULNL at:
http://image.llnl.gov
Plate: LLM12776 row: j column: 10
High quality sequence stop: 658.
Location/Qualifiers

FEATURES

source

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/db_xref="taxon:9606"
/clone="IMAGE:5748585"
/clone_lib="NIH_MGC_120"
/lab_host="DH10B"
/note="Organ: pooled pancreas and spleen. Vector:
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source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb. insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH-MGC Library."

BASE COUNT 209 a 386 c 293 g 146 t 1 others
ORIGIN

Query Match 46.88; Score 842.8; DB 14; Length 1035;
Best Local Similarity 96.98; Pred. No. 1,9e-93;
Matches 882; Conservative 0; Mismatches 22; Indels 6; Gaps 2;

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QY 7 CCGAGCGGAGCGGAGCGCCCAAGCGCGGCGCCAGCGCCAGAGAGAGCCCTCCAGCC 66
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DB 40 CCGAGCGGAGCGGAGCGCCCAAGCGCGGCGCCAGCGCCAGAGAGAGAGAGAGAGTGC 99
QY 67 GCTCACCCTCGGCTGCACCCAGCGAGCCCTCAGCGCTCTGCGCCCTTCTCTGCGCCCG 126
    |||||||
DB 100 GCTCACCCTCGGCTGCACCCAGCGAGCCCTCAGCGCTCTGCGCCCTTCTCTGCGCCCG 159
QY 127 CGCGCGCTCTGCGCGCCCTGCGCAATGAAGTGGCGCGGAGTGAAGAGATGTGC 186
    |||||||
DB 160 CGCGCGCTCTGCGCGCCCTGCGCAATGAAGTGGCGCGGAGTGAAGAGATGTGC 219
QY 187 CCGAGCGAGTGGAGTATCCCGGCAAGAACTGCTATGCGATGCTATCTCGGC 246
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DB 220 CCGAGCGAGTGGAGTATCCCGGCAAGAACTGCTATGCGATGCTATCTCGGC 279

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OY 247 TCGTCCAGGTGGGCAAGACGGCCATGTCGCGCTTCTCACCAGCGCGCTTCAGAGC 306
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Db 280 TCGTCCAGGTGGGCAAGACGGCCATGTCGCGCTTCTCACCAGCGCGCTTCAGAGC 339
OY 307 GCCTACAGCCTTACCATGAGACTTCCACCGCAGTCTCTCATCCGGGGGAGGTC 366
    |||||||
Db 340 GCCTACAGCCTTACCATGAGACTTCCACCGCAGTCTCTCATCCGGGGGAGGTC 399
OY 367 TACAGCTGACATCTCTGACACGTCCGGCAACACCCGTTCCCGCATCGCGGCTC 426
    |||||||
Db 400 TACAGCTGACATCTCTGACACGTCCGGCAACACCCGTTCCCGCATCGCGGCTC 459
OY 427 TCCATCTCAGAGAGAGTTCCTGTCCTGCTTCACTGACACACCGGACTCTTC 486
    |||||||
Db 460 TCCATCTCAGAGAGAGTTCCTGTCCTGCTTCACTGACACACCGGACTCTTC 519
OY 487 GAGGAGGTGACAGCGCTCAGCAGACAGATCTCGACACCAAGTCTGCTCAGAACAA 546
    |||||||
Db 520 GAGGAGGTGACAGCGCTCAGCAGACAGATCTCGACACCAAGTCTGCTCAGAACAA 579
OY 547 ACCAAGGAGAACGTGAGAGTCCCTGCTCCTGTCATCTGCGCAACAAGGGTGAACGCTTC 606
    |||||||
Db 580 ACCAAGGAGAACGTGAGAGTCCCTGCTCCTGTCATCTGCGCAACAAGGGTGAACGCTTC 639
OY 607 TACCGGAGGTGACACGAGATGAGAGATGAGAGTGTGGGCGACACCGCGCTGC 666
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Db 640 TACCGGAGGTGACACGAGATGAGAGATGAGAGTGTGGGCGACACCGCGCTGC 699
OY 667 GCCTACTCGAGATCTCGGCGCCAGAGAACAGCAGCTGAGACAGATGTCGCGGCTC 726
    |||||||
Db 700 GCCTACTCGAGATCTCGGCGCCAGAGAACAGCAGCTGAGACAGATGTCGCGGCTC 759
OY 727 TTGCGCATGGGCGACAGTCCCGACGAGATGAGCCAGACCTGCAACCGCAAGTCTCGGTC 786
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Db 760 TTGCGCATGGGCGACAGTCCCGACGAGATGAGCCAGACCTGCAACCGCAAGTCTCGGTC 819
OY 787 CAGTACTGCGACGTGTGCAACAAGAGCGCTGCGGAAACAAGTGTGCGGGGCGGCG 846
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Db 820 CAGTACTGCGACGTGTGCAACAAGAGCGCTGCGGAAACAAGTGTGCGGGGCGGCG 879
OY 847 AGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 900
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Db 880 AACGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 939
OY 901 GCGCGCGCGG 910
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Db 940 TCGCGCGGCG 949

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RESULT 3
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LOCUS      BM543472
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5' mRNA sequence.
ACCESSION BM543472
VERSION    BM543472.1 GI:18773895
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 962)
AUTHORS   NIH-MGC http://mgc.nhl.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgraphs-remail.nih.gov
            Tissue Procurement: Invitrogen
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
            Clone distribution: MGC clone distribution information can be

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found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LHAM12719 row: d column: 11
 High quality sequence start: 18
 High quality sequence stop: 692.
 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:5726554"
 /clone_1ib="NIH_MGC_124"
 /tissue_type="hippocampus"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMV-Sport6; Site_1: EcoRV (destroyed); Site_2: NotI; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."

BASE COUNT 185 a 363 c 272 g 141 t 1 others
 ORIGIN

Query Match 45.4%; Score 816.8; DB 13; Length 962;
 Best Local Similarity 99.0%; Pred. No. 2.7e-90;
 Matches 832; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

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OY 7 CCGAGCGAGCGCGGAGCCCGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 66
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Db 77 CCGAGCGAGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 136
OY 67 GCTCACCCCGGCGCGACCCCGAGGACCCCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 126
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Db 137 GCTCACCCCGGCGCGACCCCGAGGACCCCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 196
OY 127 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 186
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Db 197 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 256
OY 187 CCGAGCGAGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 246
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Db 257 CCGAGCGAGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 316
OY 247 TCGTCCAGGTGGGCAAGACGGCCATGTCGCGCTTCTCACCAGCGCGCTTCAGAGC 306
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Db 317 TCGTCCAGGTGGGCAAGACGGCCATGTCGCGCTTCTCACCAGCGCGCTTCAGAGC 376
OY 307 GCCTACAGCCTTACCATGAGACTTCCACCGCAGTCTCTCATCCGGGGGAGGTC 366
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OY 367 TACAGCTGACATCTCTGACACGTCCGGCAACACCCGTTCCCGCATCGCGGCTC 426
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OY 487 GAGGAGGTGACAGCGCTCAGCAGACAGATCTCGACACCAAGTCTGCTCAGAACAA 546
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Db 557 GAGGAGGTGACAGCGCTCAGCAGACAGATCTCGACACCAAGTCTGCTCAGAACAA 616
OY 547 ACCAAGGAGAACGTGAGAGTCCCTGCTCCTGTCATCTGCGCAACAAGGGTGAACGCTTC 606
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Db 617 ACCAAGGAGAACGTGAGAGTCCCTGCTCCTGTCATCTGCGCAACAAGGGTGAACGCTTC 676
OY 607 TACCGGAGGTGACACGAGATGAGAGATGAGAGTGTGGGCGACACCGCGCTGC 666
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Db 677 TACCGGAGGTGACACGAGATGAGAGATGAGAGTGTGGGCGACACCGCGCTGC 736
OY 667 GCCTACTCGAGATCTCGGCGCCAGAGAACAGCAGCTGAGACAGATGTCGCGGCTC 726

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Db 737 GCTACTTGGAGATCTTCGGCCAGAGACAGAGCTTGGACAGATGTTTCGGCGCTC 796
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 Db 797 TTGGCCATGGCCAGAGCTGGCCAGAGATGAGCCAGACCTGACCGAAGGTCTCGATG 856
 QY 787 CAGTACTGCGACGCTGCTGCACAAAGAGGCGCTGC -GGAACAGAGAGCTCTCGGCGCG 845
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 LOCUS AL533318 LYL_FL015_Brn1 Homo sapiens cDNA clone CSODN0037019 5

DEFINITION prime, mRNA sequence.
 ACCESSION AL533318
 VERSION AL533318.1 GI:12796811

KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 965)
 AUTHORS Li, W. B., Gruber, C., Jesse, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr.

FEATURES
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 /db_xref="taxon:9606"
 /clone="CSODN0037019"
 /clone_1lb="LYL_FL015_Brn1"
 /sex="male"
 /tissue_type="Adult brain"
 /note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies.
 Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifestech.com URL: http://fulllength.invitrogen.com"

BASE COUNT 189 a 352 c 273 g 144 t 7 others
 ORIGIN

Query Match 44.4%; Score 799.2; DB 9; Length 965;
 Best Local Similarity 96.1%; Pred. No. 3.7e-88;
 Matches 855; Conservative 7; Mismatches 20; Indels 8; Gaps 4;

QY 18 CGGACCCCAAGCCGAGCCGAGCCGAGAGAGCCCTCAGCGCTCAACCCGCG 77
 Db 55 CGGACCCCAAGCCGAGCCGAGCCGAGAGAGCCCTCAGCGCTCAACCCGCG 114
 QY 78 GTGCCACCCAGAGCCCTCAGCGCTCTGCGCTCTCTGCGCGCGCGCGCTC 137
 Db 115 GTGCCACCCAGAGCCCTCAGCGCTCTGCGCTCTCTGCGCGCGCGCGCTC 174
 QY 138 GCGGCCCCCTTCGCAATGAAGTGGCGGATGATCAAGAGATGTCGCGAGGACTC 197
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 Db 235 GGAGCTGAGTATCCGGCCAGAGACTGCTATGCTATGCTATGCTGCTGCTCAAGT 294

QY 258 GGGCAAGAGCGGCATCGTGTGCGCTTCCTCAGCCGCGCTTCAGAGAGCGCTACAGCC 317
 Db 295 GGGCAAGAGCGGCATCGTGTGCGCTTCCTCAGCCGCGCTTCAGAGAGCGCTACAGCC 354
 QY 318 TACCATGAGAGACTTCCACCGCAAGTTCTACTCATCCGCGGCGAGGTCTACAGCTCGA 377
 Db 355 TACCATGAGAGACTTCCACCGCAAGTTCTACTCATCCGCGGCGAGGTCTACAGCTCGA 414
 QY 378 CATCTGCAACAGTTCGGGCAACACCCGCTTCGCCGCAATGCGGCGGCGCTTCATCTCAC 437
 Db 415 CATCTGCAACAGTTCGGGCAACACCCGCTTCGCCGCAATGCGGCGGCGCTTCATCTCAC 473
 QY 438 AGGAGACGTTTTCATCTGTTTCAGTGTGAGACACCGGAGCTCTTCAGAGAGTGA 497
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 QY 498 GCGGCTCAGGCAAGATTCCTGACACCAAGTCTTCCTCAAGAACAAACAGAGGAA 557
 Db 534 GCGGCTCAGGCAAGATTCCTGACACCAAGTCTTCCTCAAGAACAAACAGAGGAA 593
 QY 558 CGTGGACGTCCTGCTGATCTGCGGCAACAGAGGTGACCGGACTTCACCGGAGGT 617
 Db 594 CGTGGACGTCCTGCTGATCTGCGGCAACAGAGGTGACCGGACTTCACCGGAGGT 653
 QY 618 GGACCAAGCGGAGATCGAGACAGCTGTGGGCGAGACACCCGAGCGCTCGCTACTTGA 677
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 QY 678 GATCTGCGCAAGAAAGAACAGAGAGCTGAGACAGATGTTCCGCGGCTCTTCGACATGGC 737
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 QY 738 CAAGCTGCCACAGAGATGAGAGCCAGACCTGACCGCAAGGCTCTGCTGAGTACTGCGA 797
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 Db 833 CGTGTGCAACAAAGAGCGCTCGGCAACAA-ARCTGCTGCGGCGGCGGCGGCGG 886
 QY 858 CGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 907
 Db 887 CGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 936

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 DEFINITION 5' mRNA sequence.
 ACCESSION BM920514
 VERSION BM920514.1 GI:19370893

KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 1103)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L14M12761 row: j column: 12
 High quality sequence stop: 676.
 Location/Qualifiers

FEATURES

Oy	67	GCTACCCCGGTGGCACCCCAGCACCCTGAGCCGCTCTGCGCTTCTCTGCGGCCG	126
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Oy	127	CGCCCGCCCTCGCGGGCCCTCTGCCAATGAATACTGGCGCGGATGATCAGAAGATGTGC	186
Db	173	CGCCCCCTCGCGGGCCCTCTGCCAATGAATACTGGCGCGGATGATCAGAAGATGTGC	232
Oy	187	CCGACGACTCGAGACTGATATCCCGGCCAAAGAACCTCTATCGATGATGATCATCTCGGC	246
Db	233	CCGACGACTCGAGACTGATATCCCGGCCAAAGAACCTCTATCGATGATGATCATCTCGGC	292
Oy	247	TGCTCAAGGTGGGGAAGACGGCCATCTGTTCGCGCTTCTCACCGGGCGGCTTGAGAGAC	306
Db	293	TGCTCAAGGTGGGGAAGACGGCCATCTGTTCGCGCTTCTCACCGGGCGGCTTGAGAGAC	352
Oy	307	GCTTACACGCGCTACCATGAGAGATTCCACCGCAAGTTCTACTCCATCCGCGGAGGTC	366
Db	353	GCTTACACGCGCTACCATGAGAGATTCCACCGCAAGTTCTACTCCATCCGCGGAGGTC	412
Oy	367	TACCAAGTCGATCCTGTGACACATCGTCGGGCAACACCGCGTTCGCCGATCGGGCGCTC	426
Db	413	TACCAAGTCGATCCTGTGACACATCGTCGGGCAACACCGCGTTCGCCGATCGGGCGCTC	472
Oy	427	TCCATCTCTACAGAGAGAGCTTTTCACTCCGTGTGTCACTCTGAGACMACCGGACTCTTC	486
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Oy	487	GAGGAGGTGACAGCGGCTCAGCGACGATCTCTCGACACCAAAGTCTTGCTTCANAGACA	546
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Oy	547	ACCAAGGAGAACGTGGAGAGTGGCCCTGTGTCATCTTCGGGCAACAAGGGAGACCGGACTTC	606
Db	593	ACCAAGGAGAACGTGGAGAGTGGCCCTGTGTCATCTTCGGGCAACAAGGGAGACCGGACTTC	652
Oy	607	TACCGGAGGTGACACAGCGGAGATCGAGCANCTGTGTGGGCGAGCACCACAGCGCTGC	666
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Oy	667	GCCTACTTCGAGATCTCGGGCCAAGAAACAGACAG--CCTGGACCGAATGTTCCGGGGCT	725
Db	713	GCCTACTTCGAGATCTCGGGCCAAGAAACAGACAGCCTTGGACCGAATGTTCCGGGGCT	772
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Oy	843	CGGCAAGCGGCGGGCGGGCGGACCCGGGGAC	876
Db	893	GGGCGGTAACCGTTGGGGGGCGCGGAGGAC	926

[illegible]

JOURNAL
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Invitrogen
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
 Plate: LLM12719 Row: m Column: 05
 High quality sequence stop: 637.
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 /tissue_type="hippocampus"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: EcoRV (destroyed); Site_2: NotI; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."
 BASE COUNT 196 a 378 c 281 g 168 t
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 Query Match 40.7%; Score 733; DB 13; Length 1023;
 Best Local Similarity 98.3%; Pred. No. 3.7e-80;
 Matches 762; Conservative 0; Mismatches 10; Indels 3; Gaps 2;
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Qy	600	CGACTTCTACCCGAGAGTGGACACGCGGAGATGCAGACAGCTGTGGGCAAGACCCCA	659
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ACCESSION	B1596688		
VERSION	B1596688.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Euthera; Primates; Catarrhini; Homiini; Homo.		
TITLE	1 (bases 1 to 814)		
JOURNAL	NIH-MGC http://imgc.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-remail.nih.gov		
	Tissue Procurement: Mikhail Palkovits, M.D., Ph.D.		
	cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shireki		
	Toshiyuki and Piero Carninci (RIKEN)		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)		
	DNA Sequencing by: Incyte Genomes, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNLN at:		
	http://image.lnl.gov		

[illegible]

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 QY 663 CTGCGCTACTTTCAGATCTGCGGCAAGAGAACAGAGCTGTGTGGGACGACGACGCTTCCGCG 722
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 DEFINITION AGENCOURT_8305191 Lupski_sympathetic_trunk Homo sapiens cDNA clone
 IMAGE:6193170 5', mRNA sequence.
 ACCESSION B0719566
 VERSION B0719566.1 GI:21858463
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: c9abds-remail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLNL3596 row: f column: 19
 High quality sequence stop: 514.

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 Source location/Qualifiers
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 Directionally cloned using the following adaptors:
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 5'-GACTAGTCTAGATCGGACGCGCGCTT(15)-3'. Size selected >
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 library, non-amplified. Library constructed by Life
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
 College of Medicine); available through Life
 Technologies."

BASE COUNT 185 a 339 c 275 g 159 t
 ORIGIN

Query Match 36.1%; Score 650.8; DB 14; Length 958;
 Best Local Similarity 85.1%; Pred. No. 3,4e-70;
 Matches 781; Conservative 0; Mismatches 117; Indels 20; Gaps 4;

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 Job time: 2391.42 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: December 30, 2002, 17:30:01 / Search time 3130 Seconds

(without alignments)
3086.943 Million cell updates/sec

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Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

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15: em_da.*
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23: em_pat.*
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28: em_un.*

Fig. 3 frame 1

29: em_vi.*
30: em_hgc_hum.*
31: em_hgc_hiv.*
32: em_hgc_other.*
33: em_hgc_mus.*
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38: em_sy.*
39: em_hgc_hum.*
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41: em_hgc_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1721	99.4	1758	BC018041	BC018041 Homo sapi
2	1714	99.0	1740	AF069506	AF069506 Homo sapi
3	1708	98.7	1746	AF177335	AF177335 Homo sapi
4	1659	95.8	4990	AF222979	AF222979 Homo sapi
5	1659	95.8	183334	AC020558	AC020558 Homo sapi
6	1656	95.7	5141	AF262018	AF262018 Homo sapi
7	1627	94.0	58882	AC073621	AC073621 Homo sapi
8	1615	93.3	183598	AC090608	AC090608 Homo sapi
9	1537	88.8	979	AF172846	AF172846 Homo sapi
10	1467	84.7	1623	AF009246	AF009246 Mus muscu
11	1453.5	83.0	1612	BC034166	BC034166 Mus muscu
12	1449	83.7	1187	AF498923	AF498923 Homo sapi
13	1449	83.7	1187	AF153192	AF153192 Homo sapi
14	1435.5	82.9	1616	AF239157	AF239157 Rattus no
15	1434	82.8	247899	AL603710	AL603710 Rattus no
16	1434	82.8	247899	AC025909	AC025909 Mus muscu
17	985	53.7	2973	AC122995	AC122995 Rattus no
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19	898.5	51.9	3469	AF134409	AF134409 Homo sapi
20	898	51.9	2832	AX393244	AX393244 Sequence
21	867	50.1	3020	AF279143	AF279143 Homo sapi
22	867	50.1	3020	AX393362	AX393362 Sequence
23	790	45.6	2699	HS689D19	HS689D19 Homo sapi
24	526	30.4	114771	AC076974	AC076974 Homo sapi
25	519.5	30.0	211071	AC076974	AC076974 Homo sapi
26	364.5	20.8	181528	AB062937	AB062937 Macaca fa
27	359.5	20.8	207684	AC010562	AC010562 Drosophi
28	359.5	20.8	207684	AC010562	AC010562 Drosophi
29	359.5	20.8	207684	AC010562	AC010562 Drosophi
30	359.5	20.8	207684	AC010562	AC010562 Drosophi
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32	358	20.7	66031	AC118046	AC118046 Mus muscu
33	354.5	20.5	4167	AX477382	AX477382 Sequence
34	347.5	20.1	177540	AC006538	AC006538 Homo sapi
35	340	19.6	2827	AK096600	AK096600 Homo sapi
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37	336.5	19.4	1410	BC013106	BC013106 Homo sapi
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39	334.5	19.3	1875	AB076888	AB076888 Homo sapi
40	334	19.3	2505	AB076889	AB076889 Homo sapi
41	334	19.3	143299	AL553619	AL553619 Human DNA
42	334	19.3	143299	AC021583	AC021583 Homo sapi
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RESULT 1

ALIGNMENTS

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126	GCTCACCCGCGGCGCCACCCAGCAGCCCTCAGCGCTCTCGCCCTTCTCTCGGCCCGC 185								
43	ArgProProSerArgProLeuCysProMetLysLeuAlaAlaMetLysLysMetCys 62								
186	CGCCGCGCTCGCGCCCTCTGCCCAATGAACCTGGCGCGATGATCAAGAGATGTC 245								
63	ProSerAspSerGlnLeuSerLysLeuAlaLysAsnCysTyrArgMetValLysLeuGly 82								
246	CCGAGCAGCTCGAGCTGAGTATCCCGGCCAGAACTGCTATCGCATGTCTCTCGGC 305								
83	SerSerLysValGlyLysThrAlaLysValSerArgPheLeuThrClyArgPheGluAsp 102								
306	TCGTCCAAAGTGGCAGAGCGGCATCGTCTCGCGCTTCTCACCGCGCGCTTCGAGGAC 365								
103	AlaTyrThrProThrLysGluAspPheHisArgLysPheTyrSerLysArgGlyGluVal 122								
366	GCTTACACGCTTACCATCGAGGACTTCACCGCAGAGTTCTACTCCATCCGCGCGAGGTC 425								
123	TyrGlnLeuAspLysLeuAspThrSerGlyAsnHisProPheProAlaMetArgArgLeu 142								
426	TACAGCTCGACATCTTCGACACCTCCGCGAACCCACCGCTTCCCGCGCATGCGCGCGCTC 485								
143	SerLysLeuThrGlyAspValPheLysLeuValPheSerLysLeuAspAsnArgAspSerPhe 162								
486	TCCATCTCTCACAGGAGAGCGTTTTCATCTCTGTGTTCAGTCTGGCAACACCGCGACTCTTC 545								
163	GluGluValGlnArgLeuArgGlnLysLeuAspThrLysSerCysLysLysAsnLys 182								
546	GAGAGGTGTCAGGGCTCAGGCAGCAGATCTTCGACACCAAGTCTTCGCTCAAGACAAA 605								
183	ThrLysGluAsnValAspValProLeuValLysCysGlyAsnLysGlyAspAspPhe 202								
606	ACCAAGAGAGAGCTGACGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 665								
203	TyrArgGluValAspGlnArgGluLysGluGlnLeuValGlyAspAspProGlnArgCys 222								
666	TACCGCGAGTGTGACCGCGCGAGATCGAGCAGTCTGCTGGCGCGACGCCCGCGCTGC 721								
223	AlaTyrPheGluLysSerAlaLysLysAsnSerSerLeuAspGlnMetPheArgAlaLeu 242								
726	GCCTACTTTCAGATCTCGCGCAAGAGAGACAGCAGCCTCGACCATGTTCTCGCGCGCTC 781								
243	PheAlaMetAlaLysLeuProSerGluMetSerProAspLysHisArgLysValSerVal 262								
786	TTCGCCATGGCCAGCTGCTGCGCGAGATCGAGCAGCAGCTGACCGCGAGCTCTCGGTG 841								
263	GlnTyrCysAspValLeuHisLysLysAlaLeuArgAsnLysLysLeuArgAlaGly 282								
846	CAGTACTCGCAGCTGCTGCAAGAGAGCGCTCGCGAAACAGAGAGCTGCTGCGCGCGCGC 901								
283	SerGlyGlyGlyGlyGlyAspProGlyAspAlaPheGlyLysValaProPheAlaArg 302								
906	ACG 961								
303	ArgProSerValHisSerAspLeuMetTyrLysGluLysAlaSerAlaGlySerGln 322								
966	CGGCCCGCGCTACACAGCGAGCTCATGTATATCCGCGAGAGGCCAGCGCGCGCGCGCAG 1021								
323	AlaLysAspLysGluArgCysValLysSer 332								
1026	GCCAGGACAGAGCGCGCTGCGTCTATCAGC 1055								
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LOCUS									
DEFINITION									
AF069506									
VERSION									
KEYWORDS									
SOURCE									
US-09-709-103-3F1 (1-332) x BC018041 (1-1758)									
QY	3	ProSerGlyAlaGlyAlaProSerProSerArgAlaGlnProGluGlnSerProProAla 22							

Best Local Similarity: 82.29%
Query Match: 95.84%
DB: 9
Mismatches: 0
Indels: 71
Gaps: 1

US-09-709-103-3f1 (1-332) x AF222979 (1-4990)

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QY      23 AlaHisProAlaCysHisProSerAspProGlnProLeuSerAlaLeuLeuSerAlaPro 42
DB      GCTCACCGCGGCTGCCACCCAGGAGCCCTCAGCGAGCTCTCTGCGCTTCTCTGCGCGCG
QY      43 ArgProProSerArgProLeuCysPrometLysLeuAlaAlaMetLlaLysLysMetCys 62
DB      CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
QY      63 ProSerAspSerGlnLeuSerLleProAlaLysAsnGlySerArgMetValLleLeuGly 82
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QY      83 SerSerLysValGlyLysThrAlaLleValSerArgPheLeuThrGlyArgPheGlnAsp 102
DB      TCGTCCAGGTGGGCAAGCGCGCATCGTCTGCGCTTCTCTACCGCGCGCTTCTGAGAGC
QY      103 AlaTyrThrProThrLleGlnAspPheHisArgLysPheTyrSerLleArgGlyGluVal 122
DB      GCGTACACCGCTTACATCGAGACTTCCAGCGCAAGTTCTACTCATCTCGCGCGAGGTC
QY      123 TyrGlnLeuAspLleLeuAspThrSerGlyAsnHisProPheProAlaMetArgLysLeu 142
DB      TACCGAGCTCGACATCTCGACACGTCGCGCAACACCGGTTCCCGCGCATGCGCGCTTC
QY      143 SerLleLeuThr----- 146
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QY      146 ----- 146
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QY      147 ----- 146
DB      GCCACCTCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
QY      152 uValPheSerLeuAspAsnArgAspSerPheGlnGluValGlnArgLeuArgGlnGln 172
DB      GGTGTTCAAGTCTGAGCAACCGGCACTCTTCAAGAGAGGTGCGAGCGGCTCAAGCGAG
QY      172 eLeuAspThrLysSerCysLeuLysAsnLysThrLysGlnAsnValAspValProLeuVal 192
DB      CCTCGACACCAAGTCTTGGCTCAAGAACAAACCAAGAGAAACGTGGACGTGCCCTGGT
QY      192 LlleCysGlyAsnLysGlyAspArgAspPheTyrArgLysValAspGlnArgGlnLleG 212
DB      CATCTCTCGGCAACAAAGGTGAGCGCGGACTTCAACCGGAGGTGAGCGAGCGAGATCG
QY      212 uGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGlnLleSerAlaLysLysAs 232
DB      GCAGCTGTGTGGGCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
QY      232 nSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGln 252
DB      CAGCGAGCTCGGACGAGATGTTCCGCGCGCTCTTGCATGCGCAAGTGCAGCGAGAT
QY      252 tSerProAspLeuHisArgLysValSerValGlnTyrCysAspValLeuHisLysLysAl 272
DB      GAGCCAGAGCTCGACCGCGCAAGTCTCGGTGCGAGTACTGCGAGGTGCTGACAGAAAGC
  
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QY      272 aLeuArgAsnLysLysLeuLeuArgAlaGlySerGlyGlyGlyGlyAspProGlyAs 292
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QY      292 pAlaPheGlyLleValAlaProPheAlaArgArgProSerValHisSerAspLeuMet 312
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QY      312 rLleArgLysLysAlaSerAlaGlySerGlnAlaLysAspLysGlnArgCysValLle 332
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DEFINITION AC020558
AC020558.4 GI:13242397
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 183334)
Sultana, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
99063792
MEDLINE
PUBMED
9847074
REFERENCE
2 (bases 1 to 183334)
Mulvaney, E., Maupin, R., Laplant, Y., and Bielski, L.
The sequence of Homo sapiens BAC clone RP11-524F11
Unpublished (2001)
3 (bases 1 to 183334)
Waterston, R.H.
Direct Submission
Submitted (03-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 183334)
Waterston, R.H.
Direct Submission
Submitted (07-MAR-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 183334)
Waterston, R.
Direct Submission
Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Mar 7, 2001 this sequence version replaced gi:7631041.
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Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapens@wustl.wustl.edu
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Summary Statistics
Center project name: H_NH0524F11
  
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >=

Tue Dec 31 15:27:53 2002

30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPI1-11 human BAC library was made from the blood of one male donor, as described by Osogawa, K., Woon, P.Y., Zhao, B., Frengen, E., Taten, M., Catane, J.J., and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is AC073621. Actual start of this clone is at base position 1 of RPI1-524F11; actual end is at base position 183334 of RPI1-524F11.

The sequence from position 1987 to 2253 was derived from PCR

product of RPI1-524F11 BAC DNA.

FEATURES

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00-09-103-3H1 (1-332) X AC020558 (1-183334)

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Db	1267	GAGCCACAGACTGCACCGCAAGGCTCTGGATGCAGTnCTGACGACGGCTGCACAAGAAGGC	1208
Qy	272	aLeuArAspLysLySeLySeuLeuArGyLaGlySeGlyLyGlyLyGlyLyAspProGlyAs	292
Db	1207	GCTCGGAACAAAGAGCTGTGTGGGGCTGGACGCGCGCGCGCGCGCGCGCGCGCGA	1148
Qy	292	pAlaPheGlyYIleValAlaProPheHlaArGArgProSerValHhIsSerAspLeuMetTy	312
Db	1147	CGCCTTGTGCATGTGGACACCTTCGCGCGCGCGCGCCAGCCTAACAAGCACTCATAGTA	1088
Qy	312	rIleArGlyLysAlaSerAlaGlySeGlyHhAlaLysAspLyGlyuArgCyValIleSe	332
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DEFINITION	Homo sapiens dexamethasone-induced				
ACCESSION	gene complete cds.				
VERSION	AF262018				
KEYWORDS	AF262018.1	GI:8119456			
SOURCE					
ORGANISM	Homo sapiens.				
	Homo sapiens				

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 5141)

AUTHORS Kempainen, R. J. and Behrend, E. N.
TITLE Human Dextranase gene
JOURNAL *Proc. Natl. Acad. Sci. USA* 81: 1514-1517, 1984

2 (bases 1 to 5141)
unpublished
REFERENCE
Kempainen, R. J., and Behrend, F. N
AUTHORS

Submitted (30-APR-2000) Anatomy & Physiology, Auburn University, College of Veterinary Medicine

FEATURES	Source
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BASE COUNT	1090 a	1579 c	1522 g	950 t
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Alignment Scores:
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 Core: 5141
 Length:

Percent Similarity: 82.29% Conservative: 1
 Best Local Similarity: 82.04% Mismatches: 0
 Query Match: 95.67% Indels: 71
 DB: Gaps: 1

US-09-709-103-3F1 (1-332) x AF262018 (1-5141)

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Db	2461	GCTCACCCTGGTCCACCCAGCGACCTTCAGCCGCTCTCTGCCCTTCTCTCGGCCCG	2520
QY	43	ArgProProSerArgProLeuCysProMetLysLeuAlaMetLysLysMetCys	62
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* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* be preserved.
 * 1 178215: contig of 178215 bp in length
 * 178216 178315: gap of 100 bp
 * 178217 178508: contig of 5283 bp in length.

FEATURES source

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BASE COUNT
ORIGIN

cores: 183598

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1-183598

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[illegible]

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Db 181480 GCGCCGCGCTCGGGCCCCCTCTGCCCAATGAACACTGGCGCGCATGATCAGAAAGAAGTGTG 181490
62 sProSerAspSerGluLeuSerIleProAlaLysAsnCysTyrArgMetValIleLeuGl 82

Db 181540 CCCGAGCGACTCGGAGCTGAGTATCCCGGCCAAGAAGCTGCTATCGCATGGTTCATCCTCGG 181599

Db 181600 CTCGTCCAAAGTGGGCAAGCGGCCATCGTGTGGGCTTCCTACCGSCGCTCGAGGA 181659

Dy
Db

pALATYmRfCmTmGgCTCCCGGGAGGT 181719

GcCTACGCCTACCATCGAGACTTCACCGCAAGTTCTACTCCATCCGCCGCGAGGT 181719

[illegible]

QY 142 uSerIleIeuThr-----
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 Dh 181780 CTCACATCTTCACAGGTGACCGGGGCCGGGCGAGGAGGGCGGGGAACCC 18183

QY 146 ----- 146

Qy 146 ----- 146

DB 181900 GCCTAGACGACC...
QY 147 -----GlyAspValpheIleL 152
|||||

...this is a 'working draft' sequence. It currently

SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS

Homo sapiens.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 183598)
 Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 Homo sapiens chromosome 17, clone RP11-524F11
 Unpublished
 2 (bases 1 to 183598)
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,
 Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B., Brown, A.,
 Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S.,
 Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S.,
 Dodge, S., Fero, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J.,
 Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-pierre, N.,
 Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
 Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T.,
 Lehoczyk, J., Levine, R., Liu, G., Maclean, C., Macdonald, P.,
 Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K.,
 Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Mihova, T., Menga, V.,
 O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,
 Prunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R.,
 Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M.,
 Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S., Severy, P.,
 Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
 Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
 Travers, M., Travis, N., Triglilio, J., Vassiliev, H., Viel, R., Vo, A.,
 Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J.,
 Zimmer, A. and Zody, M.

TITLE Direct Submission
JOURNAL Submitted (03-MAR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
RESEARCH Research, 320 Charles Street, Cambridge, MA 02141, USA
2 (pages 1 to 183598)

REFERENCE AUTHORS	TITLE JOURNAL	COMMENT
3 (bases 1 to 183598)		
Birken, B., Linton, L., Nussbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B., Brown, A., Camarata, J., Campobiano, A., Chang, J., Chazotte, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Fato, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, M., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kellis, C., Lacroque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Navlor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodorov, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.	Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA	On Mar 22, 2002 this sequence version replaced gi:16445176. All repeats were identified using RepeatMasker: v1.0.6 (1996-1997)

sent, <http://ftp.genome.washington.edu/RM/RepeatMasker.html>
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www.seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L11985
 Center clone name: 524 F 11

-----, this is a 'working draft' sequence. It currently

US-09-709-103-3F1 (1-332) x AF009246

QY	9	ProSerProSerArgAlaGlnProGlu-GlnSerProProAlaAlaHisProAlaCyHi	28
Db	27	CCCAGACCACTCGCGAGATCCGAGCCAGCTCTTCGCTACCTCCGG-----	75
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Db	76	----AGTTCTCTGCAGCCCTCTCTACTCTCTCTCGGCCACGCATCCGCCCTCGGGCC	131
QY	48	oleuCySPrometlyleuAlaAlaMetIlelylsysMetCySPrometAspSerGluLe	68
Db	132	CCTCTACCCAATGAATCGCCCGCGATGATCAAGAAGATGTGCCAAGCGACTCTGAAC	191
QY	68	uSerIleProAlaLysAsnCySPrometValIleuLeuCySPrometSerlyValGlyLy	88
Db	192	GAGTATCCCGGCCAAGAATCGTACAGGATGGTGTATCTCGGCTCATCCAAAGTGGGCA	251
QY	88	sThrAlaIleValSerArgPheLeuThrGlyArgPheGluAspAlaTyThrProThrI	108
Db	252	GACGGCCATGTGTGTGCGCTCTCCACGGGCCGTTTCGAGGATGCTTACACCCCTACCAT	311
QY	108	eGluAspPheHisArgLysPheTySerIleArgGlyGluValTyGlnLeuAspIleLe	128
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QY	128	uAspThrSerGlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAs	148
Db	372	GGACATATCCGGCAATCATTCGTTTCCGCCATCGCGGCCCTCTCTATCTCTCACAGAGA	431
QY	148	pValPheIleLeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLe	168
Db	432	CGTTTTCTCTGGTGTTCAGCTTAGACAACCGCGACTCATTCGAAGAGGTGCAAGGCT	491
QY	168	uArgGlnGlnIleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsnValas	188
Db	492	CAACACAGATCTAGACACCAAGTCTCTCTCAAGAACAAACCAAGAGAATGTGGA	551
QY	188	pValProLeuValIleCySGlyAsnLysGlyAspArgAspPheTyArgGluValAspGl	201
Db	552	CGTCGCGCTGTGTCATTTGCGGTAAACAAAGGGGACCGGACTTCTACCGGGAAGTAGACA	611
QY	208	nArgGluIleGluGlnLeuValGlyAspAspProGlnArgCysAlaTyThrPheGluIleSe	221
Db	612	GGCGGAGATTGACGAGCTGTGGGTGACGACCTCAGCGTTGTGCTTCTCGAGATCTC	671
QY	228	rAlaLysLysAsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLe	241
Db	672	AGCCAAGAAGAGCAGCAGCTTGACCAAGATGTTCCGTGCGCTCTTTGCCATGCCAAGCT	731
QY	248	uProSerGluMetSerProAspLeuHisArgLysValSerValGlnTyThrCysAspValle	261
Db	732	GCTTAGCGAGATGAGCCCCGACTTGACCGCAAGGTATCTGTGCAGTACTGCGACGCTACT	791
QY	268	uHisLysLysAlaLeuArgAsnLysLysLeuLeuArgAlaGlySerGlyGlyGlyGlyGl	281
Db	792	GCACAAGAAGGCTCTGAGGAACCAAGAGCTTCTGCTGCGGGCAGC---GGAGGCGGGGG	841
QY	288	yAspProGlyAspAlaPheGlyIleValAlaProPheAlaArgArgProSerValHisSe	301
Db	849	CGACCGCGCGATGCTTTTGGCATCTTGGCGCCCTTTGTCTCGACAGCCACGCGTGCAAC	901
QY	308	rAspLeuMetTyThrIleArgGluLysAlaSerAlaGlySerGlnAlaLysAspLysGluAr	321
Db	909	CGACCTCATGTATCTGCTGAAAAACCAAGTGTGCGCAGCCAGGCTAAGGACAAGGAGCG	961
QY	328	gCysValIleSer	332
Db	969	CTGTGTCACTCAGT	981

RESULT 11
BC034166
LOCUS

1612 bp
mRNA
linear
ROD 07-A

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	/db_xref="taxon:10090"						
	/cell_line="corticotrope tumor cell line AtT-20"						
	1. .1623						
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CDS	142. .984						
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	Alignment Scores:						
	Pred. No.:	3	87e-86				1623
	Score:	1467.00					293
	Percent Similarity:	92.31%					7
	Best Local Similarity:	90.15%					18
	Query Match:	84.75%					7
		10					2

DEFINITION

Mus musculus, RAS, dexamethasone-induced 1, clone MGC:36188
IMAGE:4989312, mRNA, complete cds.

ACCESSION

BC034166
BC034166.1 GI:21706874

VERSION

MGC.

KEYWORDS

house mouse.

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

REFERENCE

1 (bases 1 to 1612)

AUTHORS

Strausberg, R.

TITLE

Direct Submission

JOURNAL

Submitted (02-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mdickpax1@stanford.edu
Dickson, M., Schmitt, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

COMMENT

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAK plate: 58 Row: 5 Column: 5
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 6677672.

FEATURES

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1..1612

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/map="FVB/N"

/clone="MGC:36188 IMAGE:4989312"

/issue_type="Colon normal, 5 month old male mouse."

/clone_lib="NCI CGAP_C024"

/lab_host="DH10B"

/note="Vector: pCMV-SPORT6"

108..950

/codon_start=1

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EQLVDDPQRCAYFEISAKNSLDMORRALFPAKKPSESPULHKKVAVQCDVLI
KKALRNKKILRAGSGGGGHDPAFOIILPAPRRSVSHSDLMYIREKTSVGSQAKDER
CVTS"

BASE COUNT 417 a 424 c 420 g 351 t

ORIGIN

Alignment Scores:

Pred. No.:

Score: 2,86e-85

Percent Similarity: 1453.50

Best Local Similarity: 91.67%

Query Match: 89.51%

DB: 83.97%

10 Gaps: 3

US-09-709-103-3f1 (1-332) x BC034166 (1-1612)

QY 11 ProSerArgAlaGlnProGluInserProProAlaAlaHisProAlaCySHsProSer 30

Db 3 CCAGCTCGCGCAGTCCCGAAGCAAGCTCTTCCTGCTACT----- 41

QY 31 AspProGlnProLeuSerAla-----LeuLeuSerAlaProArgProProSerArgPro 48

Db 42 ---CCGAGTTCTTGACGCTTCTTACCTTCTTGCGGCGACGATCCGCCCCCTGGGCCC 98

QY 49 LeuCyProMetCysLeuAlaAlaMetIleLysIlyMetCysProSerAspSerGluLeu 68

Db 99 CTCACCAATGAAGTGGCCCGGATGATCAAGAGATGTGCCCAAGGCTCTGAATG 158

QY 69 SerIleProAlaLysAsnCySTyrArgMetValIleLeuGlySerSerIleValGlyLys 88

Db 159 AGTATCCCGCCCAAGACCTGACGATGTGATCTCTCGCTCATCAAGTGGGCAAG 218

QY 89 ThrAlaIleValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProthrlle 108

Db 219 ACGGCATTTGTCTCGCTTCTTCTTCAAGGCGGTTTCCAGGATCTTACACCCCTACATC 278

QY 109 GluAspPheHisArgLysPheTyrSerIleArgGlyGluValTyrGlnLeuAspIleLeu 128

Db 279 GAGGACTTCCACCAAGTTTACTCGATCCGGGGAAGTCTACCAAGTTGACATACG 338

QY 129 AspThrSerGlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAsp 148

Db 339 GACCATCCGCGCATCATTCGTTTCCCGCATGCGGCTCTCTATCCTCACAGAGAC 398

QY 149 ValPheIleLeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeu 168

Db 399 GTTTCATTTCTGCTGCTTCACTTACGACCAACCGGACTCTTCAAGAGATGCCAAGGCTC 458

QY 169 ArgGlnIleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsnValAsp 188

Db 459 AAACAGAGATCTTCAACCAAGTCTGTCTCAAGAACCAAGAGATGTGGAC 518

QY 189 ValProLeuValIleCysGlyAsnLysGlyAspArgAspPheTyrArgGluValAspGln 208

Db 519 GTCCGCTGCTGCTTGGCGTAAACAAAGGACCGGACTTCTACCGGAGATGACAGCAG 578

QY 209 ArgGlnIleGluGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGluIleSer 228

Db 579 CCGGATTTGAGCAGCTGTGGGTGACACCTCAGCCTTGTGCTACTTCGAGATCTCA 638

QY 229 AluLysLysAsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeu 248

Db 639 GCCAAGAAAGACAGCAGCTTGGACCAAGATGCTTCTGCTGCTTGTGCATGGCCAGCTG 698

QY 249 ProSerGluMetSerProAspLeuHisArgLysValSerValGlnTyrCysAspValLeu 268

Db 699 CTTAGCAATGATGAGCCCGACTTGCACCGCAAGGTATCTGTGAGTACTGCAACGACTG 758

QY 269 HisLysLysAlaLeuArgAsnLysLysLeuLeuArgAlaGlySerGlyGlyGlyGly 288

Db 759 CACAAGAAAGCTCTGAGGAACAAGAACTTCTGCTGCGGCGCGC---GGAAGCGGCGGC 815

QY 289 AspProGlyAspAlaPheGlyIleValAlaProPheAlaArgArgProSerValHisSer 308

Db 816 GACCAAGGCGAGTCTTGGCATCTTGGCGCTTGTCTGCGAGCCAGCTGACAGCC 875

QY 309 AspLeuMetTyrIleArgGlyLysAlaSerAlaGlySerGlnAlaLysAspLysGluArg 328

Db 876 GACCTCATGTACATTCGTGAAGAAACCAAGTGTGGCGCAGCGCTTAAGACAGAGAGCGC 935

QY 329 CysValIleSer 332

Db 936 TGTGTATCATGAGT 947

RESULT 12

AF498923

LOCUS

DEFINITION

AF498923

ACCESION

AF498923

VERSION

AF498923.1 GI:20379021

KEYWORDS

Homo sapiens.

846 bp mRNA linear PRI 01-MAY-2002

complete cds.

complete cds.

complete cds.

complete cds.

complete cds.

complete cds.

complete cds.

complete cds.

complete cds.

complete cds.

complete cds.

complete cds.

complete cds.

complete cds.

complete cds.

complete cds.

complete cds.

complete cds.

1187

Tue Dec 31 15:27:53 2002

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WORMPEP; information on the WORMPEP database can be found at http://www.sanger.ac.uk/projects/C_elegans/wormpep RP23-247B13 is from the RPI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>.
VECTOR: pBACE3.6.

FEATURES

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/clone="RP23-247B13"
/clone_lib="RPI-23"
46162 a 43228 c 43736 g 45998 t

BASE COUNT 46162 a 43228 c 43736 g 45998 t
ORIGIN

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Pred. No.: 1434.00 Matches: 295
Score: 79.12% Conservative: 5
Percent Similarity: 76.82% Mismatches: 27
Best Local Similarity: 82.84% Indels: 57
Query Match: 10 Gaps: 3
DB:

US-09-709-103-3F1 (1-332) x AL603710 (1-179124)

QY 5 GlyAlaGlyAlaProSerProSerArgAlaGlnProGluGlnSerProProAlaAlaHis 24
DB 122579 GGGCGCGAAGCTGTGCTGTCTGTACCAAGAGCCAGCCAGCTCGCGCAGTC 122520
QY 25 Pro-----AlaCysHisPro-SerAspProGlnProLeuSerAlaLeuSe 40
DB 122519 CCGAAGCCAGCTCTCCGTCACTCCGGAGTTCTCTGCAGCCCTCTCTTACCTCTCTC 122460
QY 40 rAlaProArgProProSerArgProLeuCysProMetLysLeuAlaAlaMetileLysly 60
DB 122459 GGCACGCGATCGCCCTCGGGGCCCCCTCTACCCCAATGAACCTGGCCGCGATGATCAAGAA 122400
QY 60 sMetCysProSerAspSerGluLeuSerileProAlaLysAsnCysTyrArgMetValil 80
DB 122399 GATGTGCCACAGGACTCTGAACAGTATCCCGCCCAAGAACTGCTACAGGATGTCAT 122340
QY 80 eLeuGlySerSerLysValGlyLysThrAlaileValSerArgPheLeuThrGlyArgPh 100
DB 122339 CCTCGGCTCATCAAGTGGGCGAGAGCCGCTTGTGTGCGCTTCTCAGCGCGCTTT 122280
QY 100 eGluAspAlaTyrThrProThrIleGluAspPheHiaArgLysPheTyrSerileArgG1 120
DB 122279 CGAGGATGCTTACACCCCTTACCATCGAGGACTTCCACCGAAGTTTACTCGATCCGCG 122220
QY 120 yGluValTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisProPheProAlaMetAr 140
DB 122219 CGAAGTCTACAGTGGACATCTGACACATCCGCAATCATCGGTTTCCCGCGCATGCG 122160
QY 140 gArgLeuSerileLeuThr----- 146
DB 122159 CGGCTCTCTATCTCTACAGGTGAGTGGGGAGTCGACCGGGATAGGGGACCGGAGTCTT 122100
QY 146 ----- 146
DB 122099 GAGGGAGTGGATGGGCTGGTGTGTGTGGGCTTGGCCCTTACCTGGGGTCTC 122040
QY 147 -----GlyAspVa 149

QY 109 GluAspPheHisArgLysPheTyrSerileArgGlyGluValTyrGlnLeuAspIleLeu 128
DB 289 GAGACATTCACCAAGATTTTACTCGATCCGCGGAGTCTACCAAGTTGGACATCTG 348
QY 129 AspThrSerGlyAsnHisProPheProAlaMetArgArgLeuSerileLeuThrGlyAsp 148
DB 349 GACACATCTCGCAATCATCGTTTCCCGCATCGCGGCTCTCTATCTCTCACAGGAGAC 408
QY 149 ValPheileLeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeu 168
DB 409 GTTTTCATCTCGTGTTCAGCTAGACAACCGGACTCTCTCGAGAGGTGCAAGGCTC 468
QY 169 ArgGlnGlnIleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsnValasp 188
DB 469 MAACAGCAGATCTCTAGACACCAAGTCTCTCTCAAGAACAAACCAAGAGAATGTGAC 528
QY 189 ValProLeuValIleCysGlyAsnLysGlyAspArgAspPheTyrArgGluValaspGln 208
DB 529 GTTCGCTGTTCATTTGCGTTAACAAGGGGAGCGGACTTCTACCCGCAAGTGGAGCAG 588
QY 209 ArgGluIleGluGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGluLeuSer 228
DB 589 CGGAGATTGAGCAGCTGTGGGCGATGACCTCAGCGTTGTGCTTACCTTCGAGATCTCG 648
QY 229 AlaLysLysAsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeu 248
DB 649 GCCAAGAGATAGCAGCTGACGACAGATGTTCCGTGCGCTTTTGGCATGGCCAGCTG 708
QY 249 ProSerGluMetSerProAspLeuHisArgLysValSerValGlnTyrCysAspValLeu 268
DB 709 CCTAGCGAGATGAGCTTGTGGCATCTTGGGCGCTTGTGTGCGAGTACTGTGACGTGCTG 768
QY 269 HisLysLysAlaLeuArgAsnLysLysLeuLeuArgAlaGlySerGlyGlyGlyGly 288
DB 769 CACAAAAGGCTCTGAGGAACAAGAGCTTCTGCGTGGCGGAGC- --GGAGTGGGGGC 825
QY 289 AspProGlyAspAlaPheGlyIleValAlaProPheAlaArgArgProSerValHisSer 308
DB 826 GACCACGAGATGCTTGTGGCATCTTGGGCGCTTGTGTGCGAGACCTAGCGTGCATAGC 885
QY 309 AspLeuMetTyrIleArgGluLysAlaSerAlaGlySerGlnAlaLysAspLysGluArg 328
DB 886 GACCTCATGTACATTCTGTGAGAAACAGTGTGACAGCGCCAGCTTAGGACAGAGGAGCGC 945
QY 329 CysValIleSer 332
DB 946 TGTGTCTATCAGT 957

RESULT 15
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LOCUS Mouse DNA sequence from clone RP23-247B13 on chromosome 11,
DEFINITION complete sequence.
ACCESSION AL603710
VERSION AL603710.8 GI:20069514
KEYWORDS HTG.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 Almeida, J.
REFERENCE
AUTHORS Direct Submission
TITLE Wellcome Trust Sanger Institute, Hinxton,
JOURNAL Submitted (04-APR-2002) Cambridge, UK. E-mail enquiries:
Cambridge, UK. E-mail enquiries: clonerequest@sanger.ac.uk
humquery@sanger.ac.uk
On Apr 7, 2002 this sequence version replaced gi:18070899.
During differences are found these are annotated as variations
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

Db 122039 TGCACTCTGTGCTGCGACGCTGCTCCTCCTTCCACTGCTTCCCTTATAGAGACGT 121980
QY 149 lPhe1leLeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuAr 169
Db 121979 TTTCACTTCTGCTGCTTTCAGCTTGAACACCGGACCTCATTCGAGAGAGGTGCAAGGCTCA 121920
QY 169 gGlnGln1leLeuAspThrLySerCysLeuLysAsnLysThrLyGluValAspVal 189
Db 121919 ACAGCGATCTTGAACACCAAGTCTGTCTCAAGAACAAAACAAAGAGATGTGACGT 121860
QY 189 lProLeuVal1leCysGlyAsnLysGlyAspArgAspPheTyrArgGluValAspGlnAr 209
Db 121859 GCGGCTGCTCATTTCCGCTTAACAAAGGGGACCGGACCTTCTACCGGGAGTAGAGCAGCG 121800
QY 209 gGlu1leGluGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGlu1leSerAl 229
Db 121799 GGAGATTGAGCAGCTGTGGGTGACGACCTTCAGCGTTGTGCTTCTCGAGATCTCAGC 121740
QY 229 aLy1ysAsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuPr 249
Db 121739 CAAGAAAGAACAGCAAGCTTGGACAGATGTTCCGTGGCTCTTGGCCATGCGCAAGCTGCC 121680
QY 249 oSerGluMetSerProAspLeuHisArgLysValSerValGlnTyrCysAspValLeuHi 269
Db 121679 TAGCGAGATGAGCCCGACTTGCACCGCAAGGTATCTGTGACGTACTGCGAGTACTGCA 121620
QY 269 sLy1ysAlaLeuArgAsnLysLysLeuLeuArgAlaGlySerGlyGlyGlyGlyAs 289
Db 121619 CAAGAAAGCTCTTGAGAACAAAGCTTCTGCGGTGCGGCGCAGC---GGAGCGGGGGCGCA 121563
QY 289 pProGlyAspAlaPheGly1leValAlaProPheAlaArgArgProSerValHisSerAs 309
Db 121562 CCACGGGATGCTTTGGATCTTGCGCGCCCTTTGCTGCGAGACCAAGCTGCAACAGCA 121503
QY 309 PleuMetTyr1leArgGluLysAlaSerAlaGlySerGlnAlaLysAspLysGluArgCy 329
Db 121502 CTTCACTTACATTCGTAAGAAAAACAGTGTGCGCAGCCAGGCTAAGAGCAAGAGCGCTG 121443
QY 329 sVal1leSer 332
Db 121442 TGTCACTCAGT 121433

Search completed: December 30, 2002, 19:08:33
Job time : 3287 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus.p2n model

Run on: December 30, 2002, 16:29:50 ; Search time 87 Seconds

(without alignments)
1316.766 Million cell updates/sec

Title: US-09-709-103-1f4

Sequence: 1 LADDAALLVIGLAAGAGLLA.....RDTQVARAHLDHRCQFH 282

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 363474 segs, 203117208 residues

Total number of hits satisfying chosen parameters: 726948

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-TRANS=humano.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=SU/LIVANI14@cgn_1_1_36 @runat_30122002_144047_21556
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Database :

Published Applications NA:
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	397	28.1	405	10	US-09-960-352-10273
C 3	371.5	26.3	11221	10	US-09-778-963A-3
C 4	219	15.5	368	10	US-09-864-761-21643

C 5	164.5	11.7	452	10	US-09-960-352-4253	Sequence 4253, Ap
C 6	160.5	11.4	454	10	US-09-960-352-5830	Sequence 5830, Ap
C 7	159.5	11.3	2322	10	US-09-476-242-20	Sequence 20, Appl
C 8	155	11.0	2322	10	US-09-476-242-18	Sequence 18, Appl
C 9	155	11.0	2324	10	US-09-476-242-7	Sequence 7, Appl
C 10	154	10.9	1224	10	US-09-972-529-1	Sequence 1, Appl
C 11	154	10.9	2392	10	US-09-788-654A-1	Sequence 1, Appl
C 12	153	10.8	2322	10	US-09-476-242-19	Sequence 19, Appl
C 13	146.5	10.4	2010	12	US-10-032-717-9	Sequence 9, Appl
C 14	146.5	10.4	4074	10	US-09-815-242-7899	Sequence 7899, Ap
C 15	143	10.1	612	10	US-09-476-242-12	Sequence 12, Appl
C 16	143	10.1	2541	10	US-08-841-635A-32	Sequence 32, Appl
C 17	142	10.1	1894	7	US-09-934-060A-5	Sequence 5, Appl
C 18	139	9.9	1668	9	US-09-476-242-26	Sequence 26, Appl
C 19	139	9.9	2352	10	US-09-476-242-9	Sequence 9, Appl
C 20	139	9.9	2541	10	US-09-476-242-10	Sequence 10, Appl
C 21	139	9.9	2541	10	US-09-476-242-11	Sequence 11, Appl
C 22	139	9.9	2541	10	US-09-934-060A-3	Sequence 3, Appl
C 23	137.5	9.7	2159	9	US-09-860-846-9	Sequence 9, Appl
C 24	137	9.7	1458	10	US-09-815-242-7835	Sequence 7835, Ap
C 25	137	9.7	1629	10	US-09-815-242-4085	Sequence 21, Appl
C 26	137	9.7	1707	10	US-09-476-242-13	Sequence 13, Appl
C 27	137	9.7	2310	10	US-09-861-289-3	Sequence 3, Appl
C 28	137	9.7	2535	10	US-10-025-380-1058	Sequence 1058, Ap
C 29	137	9.7	13613	9	US-09-922-217-1058	Sequence 1058, Ap
C 30	137	9.7	13613	9	US-09-833-263-1058	Sequence 1058, Ap
C 31	137	9.7	13613	9	US-10-104-484-1	Sequence 1, Appl
C 32	136.5	9.7	15720	10	US-09-476-242-25	Sequence 25, Appl
C 33	136.5	9.7	15720	10	US-10-124-800-17	Sequence 17, Appl
C 34	136.5	9.7	15720	10	US-09-861-289-3	Sequence 3, Appl
C 35	136	9.6	570	12	US-09-476-242-22	Sequence 22, Appl
C 36	136	9.6	2258	10	US-09-476-242-24	Sequence 24, Appl
C 37	136	9.6	2133	9	US-10-124-800-1	Sequence 1, Appl
C 38	135.5	9.6	8730	9	US-09-476-242-22	Sequence 22, Appl
C 39	135.5	9.6	2298	10	US-09-476-242-15	Sequence 15, Appl
C 40	135	9.6	2298	10	US-09-476-242-14	Sequence 14, Appl
C 41	135	9.6	2298	10	US-09-476-242-14	Sequence 14, Appl
C 42	135	9.6	2298	10	US-09-476-242-14	Sequence 14, Appl
C 43	135	9.6	2523	10	US-10-124-800-5	Sequence 5, Appl
C 44	135	9.6	2523	10	US-10-124-800-5	Sequence 5, Appl
C 45	135	9.6	4509	9	US-10-124-800-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-778-963A-1/c
; Sequence 1, Application US/09778963A
; Patent No. US20020115172A1
; GENERAL INFORMATION:
; APPLICANT: NEELAM, Beena et al
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
; FILE REFERENCE: CLO01112
; CURRENT APPLICATION NUMBER: US/09/778, 963A
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-778-963A-1

Alignment Scores:

Pred. No.:	3.05e-44	Length:	3082
Score:	575.50	Matches:	145
Percent Similarity:	61.23%	Conservative:	24
Best Local Similarity:	52.54%	Mismatches:	94
Query Match:	40.79%	Indels:	13
DB:	10	Gaps:	5

Tue Dec 31 15:27:52 2002

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US-09-709-103-1F4 (1-282) x US-09-778-963A-1 (1-3082)
QY 4 AspAlaAlaLeuValLeu---GlyLeuAlaAlaGlyAlaGlyLeuLeuAlaAspVal 22
Db 1005 GATGTCACCTTGGCTTCCCTCACGGCGCTGGCTTCCGGAAGACCTTGGCCCTTGATGTA 946
QY 23 HisGluValAlaValTyrAlaGlyProAlaArgGluGlyCysHisAspAlaLysGlyVal 42
Db 945 CTTGAGGTCACTGTGACCTTGGCGCGCGCGGCGGCGGCGGAGACCATGCGATAGGCGTC 886
QY 43 AlaArgValAlaAlaAlaAlaAlaAlaGlyProGlnGlnLeuLeuValProGlnArg 62
Db 895 ---CATCTCTTCCGCGCGCATGACAGAGGCGCTGGG----- 850
QY 63 LeuLeuValGlnHisValAlaValLeuHisArgAspLeuAlaValGlnValTyrAlaHis 82
Db 849 -----GTGGAAGGCGTCACTGACGAGGATCTTGGCATGCGAGCGGCGGCTCAT 796
QY 83 LeuAlaGlyGlnLeuGlyHisGlyGluGluArgAlaGluHisLeuValGlnAlaAlaVal 102
Db 795 CTCGTGTGGCAGCTTGGCATGCTGAAGACGACGTAGAACATCTCGTCCACGTTGGTGT 736
QY 103 LeuLeuGlyArgAspLeuValGlyAlaAlaLeuGlyValValAlaHisGlnLeuLeu 122
Db 735 CTTCTTGGCGGACACCTCGAAGTAGCGGAGTTCTC---GTGCGCGGACACGACGCTC 679
QY 123 AspLeuAlaLeuValHisLeuAlaValGluValAla---ValThrLeuValAlaAlaAsp 141
Db 678 GGCCTCGGTGGGACCTGGCGGACGACGTGCGCGGTGCTTCTTGTGGCCACAGAT 619
QY 142 AspGlnGlyHisValHisValLeuLeuGlyPheValLeuGluAlaArgLeuGlyValGlu 161
Db 618 GACCATGGSCAGCTCCGCGCGCTCTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 559
QY 162 AspLeuLeuProGlnProLeuHisLeuLeuGlyValAlaValAlaValGlnThrGluHis 181
Db 558 GATCTGCTTCTGAAGCGCTTGACCTCATCGAAGGACCTCCCGGTATCCAGCTGGAACAC 499
QY 182 GlnAspGluAsnValSerCysGluAspGlyGluAlaProHisGlyGlyGluArgValVal 201
Db 498 CAGGATGAAGACATCCCTGTGAGGATGACACGCTGCGCATGTCGGGGAAGGGTGT 439
QY 202 AlaGlyArgValGluAspValGluLeuValAspLeuAlaAlaAspGlyValGluLeuAla 221
Db 438 GCCAGAGGTATCCAGATTCGAGTGTGTATCATGTCGCGCGGATGTTGTATACCTTACG 379
QY 222 ValGluValLeuAspGlyArgValGlyValLeuGluAlaAlaGlyGluGluAlaArg 241
Db 378 GTGGAAGTCTCTCATGTTGGTGTGTACTGTGTCCTCAAGCGGCCCATGAGGAGCGAGA 319
QY 242 HisAspGlyArgLeuAlaHisLeuGlyArgAlaGluAspHisAlaLeuAlaValLeu 261
Db 318 CACGATGGAGCTCTTGCCACCCGAGAGGACCCAGCACCCAGCATGCGGTATGAGTTT 259
QY 262 GlyArgAspThrGlnLeuArgValAlaAlaArgAlaHisLeuLeuAspHis 277
Db 258 GCGCGGCGACATGAGCTGCGATTCCTCGCTGGGACAAAGTCTTCATCAT 211

RESULT 2
US-09-960-352-10273/c
; Sequence 10273, Application US/09960352
; Patent No. US2002013139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Bvatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112

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; SEQ ID NO 10273
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3), (23), (31)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 44-LIB3058-050-Q1-K1-C8
US-09-960-352-10273

Alignment Scores:
Pred. No.: 7, 61e-29 Length: 405
Score: 397.00 Matches: 82
Percent Similarity: 81.98% Conservativeness: 9
Best Local Similarity: 73.87% Mismatches: 20
Query Match: 28.14% Indels: 0
DB: 10 Gaps: 0

US-09-709-103-1F4 (1-282) x US-09-960-352-10273 (1-405)
QY 172 GluGlyValAlaValValGlnThrGluHisGlnAspGluAsnValSerCysGluAspGly 191
Db 404 GAAGGAGTCCGCGTGTACTGTCTGAACCTTAGGATGAACACGCTCTCCGGTAAGGATGCA 345
QY 192 GluAlaProHisGlyGlyGluArgValValAlaGlyArgValGluAspValGluLeuVal 211
Db 344 GAGGCGTCGATGCGCGGGAATGCGCGGTGCGGTACGTGTCGAGGATGTCAGCTGGTA 285
QY 212 AspLeuAlaAlaAspGlyValGluLeuAlaValGluLeuAlaValLeuAspGlyArgArgValGly 231
Db 284 CCTCTCGCTCGAATCAGTAGAATCTTGGGTGGAAGTCTTCGATGTTGGCGGTGTAGGC 225
QY 232 ValLeuGluAlaAlaGlyGluGluAlaArgHisAspGlyArgLeuAlaHisLeuGlyArg 251
Db 224 GTCTCTGTAGCGCGCTCAGGAAGCGGACACGATGCGCGCTTTCGCCACCTTGACCA 165
QY 252 AlaGluAspHisAlaLeuAlaValLeuGlyArgAspThrGlnLeuArgValAlaArg 271
Db 164 GCCGAGGACCACTCGGTGTAGGATGTTCTTGGCGGATCCCTCACATCCGAGTCCGTCGG 105
QY 272 AlaHisLeuLeuAspHisArgGlyGlnPheHis 282
Db 104 GCACATTTCTTCATCATCGGCACAGTTTCAT 72

RESULT 3
US-09-778-963A-3/c
; Sequence 3, Application US/09778963A
; Patent No. US20020115172A1
; GENERAL INFORMATION:
; APPLICANT: NEELAM, Beena et al
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001112
; CURRENT APPLICATION NUMBER: US/09/778,963A
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 11221
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-778-963A-3

Alignment Scores:
Pred. No.: 8, 7e-25 Length: 11221
Score: 371.50 Matches: 97
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Best Local Similarity: 51.32% Mismatches: 62
Query Match: 26.33% Indels: 13
DB: 10 Gaps: 5

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us-09-709-103-1f4.p2n.rnpb

Tue Dec 31 15:27:52 2002

APPLICANT: Tao, Nengbing
 APPLICANT: Byatt, John C.
 APPLICANT: Mathialagan, Nagappan
 TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
 TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
 FILE REFERENCE: 16511.006/37-21(10298)C
 CURRENT APPLICATION NUMBER: US/09/960,352
 CURRENT FILING DATE: 2001-09-24
 NUMBER OF SEQ ID NOS: 15112
 SEQ ID NO 5830
 LENGTH: 454
 TYPE: DNA
 ORGANISM: Bos taurus
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (181),(244),(385)
 OTHER INFORMATION: unsure at all n locations
 OTHER INFORMATION: Clone ID: 25-LIB3058-057-Q1-K1-G1
 US-09-960-352-5830

Alignment Scores:
 Pred. No.: 5,298-07 Length: 454
 Score: 160.50 Matches: 46
 Percent Similarity: 46.21% Conservative: 15
 Best Local Similarity: 34.85% Mismatches: 64
 Query Match: 11.37% Indels: 7
 Gaps: 2

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 QY 126 LeuValHisLeuAlaValGluValAlaValThrLeuValAlaAlaAspGlnGlyHis 145
 Db 445 CTCACCTACCTCCCGAGGCTCTC---ATCGCACTTGTTCCTCCACCGATGACGGGCA 389
 QY 146 ValHisValLeuLeuGlyPheValLeuGlyValGluAlaAargLeuGlyValGluAspLeuPro 165
 Db 388 CTNTGCGGGTGTACCTTTGAGTTG-----ACGGATCAGCTCAAA 347
 QY 166 GluProLeuHisLeuLeuGlyValAlaValAlaValGlnThrGluHisGlnAspGluAsn 185
 Db 346 GAGCGGCTTCAGCTCTCCAGGGTTGCTCTCTGCTAGTAGATAAAACACGATGAAGGC 287
 QY 186 ValSerCysGluAspGlyGluAlaProHisGlyGlyGluArgValValAlaGlyA-gVal 205
 Db 286 GTGACCTGGCAATGCAAGCGCTGCAGCGCCCGGTAGCGCGCCACCGGTGGTGC 227
 QY 206 GluAspValGluLeuValAspLeuAlaAspGlyValGluLeuAlaValGluValLeu 225
 Db 226 GGTGATGTGACGCGCACCGCTTTGCTGCTGAGCTAGCGCTGCGGTAGGTATCTTC 167
 QY 226 AspGlyArgArgValGlyValLeuGluAlaAlaGlyGluAlaAargHisAspGlyArg 245
 Db 166 GATGCTGGCAGGTAGCTCTACGGAAGTTGCGCGCACCGACCTTTCACACGAGCGCT 107
 QY 246 LeuAlaHisLeuGlyArgAlaGluAspAspHisAla 257
 Db 106 CTTGCG 71

RESULT 7

US-09-476-242-20/c
 ; Sequence 20, Application US/09476242
 ; Patent No. US20020146683A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BARNETT, Susan
 ; APPLICANT: MARTIN, Eric
 ; APPLICANT: HARTOG, Karin
 ; TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES
 ; FILE REFERENCE: 1605.002
 ; CURRENT APPLICATION NUMBER: US/09/476,242
 ; CURRENT FILING DATE: 1999-12-30
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 20

US-09-960-352-4253/c
 ; Sequence 4253, Application US/09960352
 ; Patent No. US20020137139A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Warren, Wesley C.
 ; APPLICANT: Tao, Nengbing
 ; APPLICANT: Byatt, John C.
 ; APPLICANT: Mathialagan, Nagappan
 TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
 TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
 FILE REFERENCE: 16511.006/37-21(10298)C
 CURRENT APPLICATION NUMBER: US/09/960,352
 CURRENT FILING DATE: 2001-09-24
 NUMBER OF SEQ ID NOS: 15112
 SEQ ID NO 4253
 LENGTH: 452
 TYPE: DNA
 ORGANISM: Bos taurus
 OTHER INFORMATION: Clone ID: 18-LIB34-086-Q1-E1-E5
 US-09-960-352-4253

Alignment Scores:
 Pred. No.: 2,258-07 Length: 452
 Score: 164.50 Matches: 56
 Percent Similarity: 46.58% Conservative: 19
 Best Local Similarity: 34.78% Mismatches: 73
 Query Match: 11.66% Indels: 13
 Gaps: 5

US-09-709-103-1f4 (1-282) x US-09-960-352-4253 (1-452)
 QY 97 LeuValGlnAlaAlaValLeuLeuGlyArgAspLeuGluValGlyAlaAlaAlaLeuGly 115
 Db 447 CTCCTGGACGTGTATTCATCTTGGCGAGGCTCCCAAGAGCGCAATTCATCTCGCA 388
 QY 116 ValValAlaHisGlnLeuLeuAspLeuAlaValHisValLeuAlaValGluValAlaVal 135
 Db 387 CGCATAGGCGACCTCTCTT-----CTCACTCACCTCCGACGCGCTCTC---ATC 340
 QY 136 ThrLeuValAlaAlaAspAspGlnGlyHisValHisValLeuLeuGlyPheValLeuGlu 155
 Db 339 GCACCTTGTTCGCCACCGATGACGGGCACTTTTGGGGTGTGTACCTTTGAGTTG--- 283
 QY 156 AlaArgLeuGlyValGluAspLeuProGluProLeuHisLeuLeuGlyValAlaAla 175
 Db 282 -----ACGGATCAGCTCATAGCGGCTTCAGCTCTCCAGGGTTGCTT 238
 QY 176 ValValGlnThrGluHisGlnAspGluAsnValSerCysGluAspGlyGluAlaProHis 195
 Db 237 CCTGGTATAGATAAACACGAGTAAAGCGGTGACCCCTGGCATGGCAAGCGCTCGAG 178
 QY 196 GlyGlyGluArgValValAlaGlyArgValGluAspValGluLeuValAspLeuAlaAla 215
 Db 177 GCCCGGTAGCG 118
 QY 216 AspGlyValGluLeuAlaValGluLeuAspGlyArgArgValGlyValLeuGluAla 235
 Db 117 GCAGCTAGCGCTTGGCGGTAGGTATCTTCGATGGTGGCGAGGTAGCGCTCAGGAAGTT 58
 QY 236 AlaGlyGluGluAlaAargHisAspGlyArgLeuAlaHisLeuGlyArgAlaGluAspAsp 255
 Db 57 GCCCGCGCACCCACCTTTGCGACCGAGCGCTCTTGGCCACCGCGCGCGCGCGCGCG 4
 QY 256 His 256
 Db 3 CAC 1

RESULT 6

US-09-960-352-5830/c
 ; Sequence 5830, Application US/09960352
 ; Patent No. US20020137139A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Warren, Wesley C.

; LENGTH: 2322
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Leu122-Ser199;
 ; US-09-476-242-20

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
159.50	159.50	2322	94	15	116	81	14
Best Local Similarity:	35.62%						
Query Match:	11.30%						
DB:	10						

US-09-709-103-1f4 (1-282) x US-09-476-242-20 (1-2322)

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QY 12 LeuAlaAlaGlyValAlaGlyLeuAlaAspValHisGluValAlaValTyrAlaGlyPro 31
DB 1086 GTTGGCTGTCGACGCGGATCTGGCGCGGAGTGGGGGCGGACATGGCGCTTGGCGCCCA 1027
QY 32 AlaArgGluGlyCysHisAspAlaGly-----ValAlaArgValAla 46
DB 1026 GCGGTTGATGATCTGCTTGTATGCGGACGCGGCGGATGATGCGCTTGGCTTGTGGG 967
QY 47 AlaAlaAlaAlaAlaAlaGlyProGlnGlnLeu-----ValProGlnArgLeuLeu 64
DB 966 GCGGATGCTGTTCCAGTCTGCTGTTGACACGCTGGGCTGTTGTCGATGACAGAAATCTC 907
QY 65 ValGlnHisValAlaValLeuHisAspLeuAlaValGlnValTyrAlaHisSleuAla 84
DB 906 GCGCGCGGACGTTGACGCTGTCATCATCATCTCGG----- 871
QY 85 GlyAlnLeuGlyHisGlyGluGluAlaGlyAlaHisSleuValGlnAlaValLeuLeu 104
DB 870 -----GTCCCCCGCCCTGCTGCTT 850
QY 105 GlyArgAsp-----LeuGluValAlaGlyAlaAlaLeuGlyValAlaHisSleuLeu 121
DB 849 GACACGATGCTGTTGCTGTCGACGACGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 799
QY 122 LeuAspLeuAlaLeuValHisSleuAlaValGluValAlaValThreLeu-----ValAla 139
DB 798 CTTGACGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 739
QY 140 AlaAspArgGlnGlyHisValHis-----ValLeuLeuGly 151
DB 738 GATGATGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 679
QY 152 PheValLeuGluAla----- 157
DB 678 GTTGTGTTGGGCGGCGGATGATCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 619
QY 158 LeuGly-----ValGluAspLeuLeuProGlnProLeuHisSleuLeuGlyValAlaVal 176
DB 618 CTTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 559
QY 177 ValGlnThiGlnHisSleuAspLeuValSerCysGluAspGlyGluAlaProHisSleu 196
DB 558 GTTTCAG-----CAGCAGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 529
QY 197 GlyGluArgValAlaAlaGlyValArgValGluValHisSleuValAspLeuAlaValAsp 216
DB 528 GCGGATGCGCTG-----GTCGACCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 478
QY 217 GlyValGluValAlaValGluValLeuAspGlyValArgValGlyValLeuGluAlaVal 236
DB 477 GCGGTTGAATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 430
QY 237 GlyGluGluAlaArgHisAspGlyValGluValHisSleuGlyValArgValAspArgHis 256
DB 429 GCGGACGATGATGATGCGGATGCGGCTGCAAGCTCATCTTGGGCGAGGCTGCGGATGATCATC 370

```

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QY 257 AlaIleAlaValLeuGlyArgAspThrGlnLeuArgValAlaArgAla----- 272
DB 369 GCTGTGCTGCGGACGCTTACGACGAGGCTTACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 310
QY 273 ---HisLeuLeuAspHis 277
DB 309 GTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 292

```

RESULT 8

US-09-476-242-18/c
 ; Sequence 18, Application US/09476242
 ; Patent No. US20020146683A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BARNETT, Susan
 ; APPLICANT: HARTOG, Karin
 ; APPLICANT: MARTIN, Eric
 ; TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES
 ; FILE REFERENCE: 1605,002
 ; CURRENT APPLICATION NUMBER: US/09/476,242
 ; CURRENT FILING DATE: 1999-12-30
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 18
 ; LENGTH: 2322
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Leu122-Ser199;
 ; US-09-476-242-18

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
1.17e-05	155.00	2322	103	16	129	92	16
Percent Similarity:	35.00%						
Best Local Similarity:	30.29%						
Query Match:	10.99%						
DB:	10						

US-09-709-103-1f4 (1-282) x US-09-476-242-18 (1-2322)

```

QY 10 LeuGlyLeuAlaAlaGlyValAlaGlyLeuAlaAspValHisGluValAla----- 26
DB 1251 CTTGGCTGTTGGGCGGCGACGCGGCGGCTGATCTTACACCTGTACTGTACAG 1192
QY 27 -----ValTyrAlaGlyProAlaArgGlyCysHisAspAlaGlyVal 42
DB 1191 CTCGCTGCGGACGTTGTCGCGCATGTCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1132
QY 43 Ala-----ArgValAlaAlaAla 49
DB 1131 GCTGATCTCTTCCGCGCGCTGCGGCTGACGACGCGCGGCTGATGTTGCTGCGACGG 1072
QY 50 -----AlaAlaAlaGlyProGlnGlnLeu 57
DB 1071 GATTCGCGCGGATGAGGCGGCGGACATGCGCTGCGCGCGCGCGGCTGATGATGATGATGAT 1012
QY 58 LeuValProGlnArgLeuValGlnHisValAlaValLeuHisAspLeuAlaVal 77
DB 1011 CTTGATCGCGGCGGCGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 952
QY 78 -----GlnValTyrAlaHisSleuAlaGlyGlnLeuGlyHisSleuGlyGlu 92
DB 951 CCAAGTCTGTTGAACAGCTGGGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 892
QY 93 ArgAlaGluHis-----LeuValGlnAlaValLeuLeuGlyArgAsp----- 107
DB 891 GCTGTCATCAAGATCTGCGGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 832
QY 108 LeuGluValGlyAlaAlaLeuGlyValAlaValHisSleuLeuAspLeuAlaVal 127
DB 831 GCGGAATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 781

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Tue Dec 31 15:27:52 2002

QY 27 -----ValtyralaGlyProAlaArgGluGlyCysHisAspAlaLysGlyVal 42
 Db 1197 CTGCTGCCCGCAGTTGTCGCGCATGTCGCCCGCGCGCGGCGGAGATCTCGGTGTGT 1138
 QY 43 AlaArgValAlaAlaAlaAlaAlaAlaGlyProGlnGlnLeuLeuValProGlnArg 62
 Db 1137 GCTGATCTC-----CTTCCCGCGCTCGCGGTTCAGCAGCAG----- 1102
 QY 63 LeuLeuValGlnHisValAlaValLeuHisArgAspLeuAla-----Val 77
 Db 1101 -----GCCCGTGATGTTGCTGTGCA-----GCGGATCTGGCCCGGATGGGGGGCGGTA 1051
 QY 78 GlnValTrpAlaHisLeu-----AlaGlyGlnLeu 87
 Db 1050 CATGGCTTGGCCACCTCTCCGCCAGCGGTGTGATGATCTGCTTGTGATGCGCGAGGCGAG----- 994
 QY 88 GlyHisGly-----GluGluArgAlaGluHisLeu----- 90
 Db 993 GGTGATGTGTCCTGTTGTTGGGCGCATGTTGTTGTTCCAGGTGCTGTTGAACAG 934
 QY 91 -----GluGluArgAlaGluHisLeu----- 97
 Db 933 CTGGGTGCTGTTGCAGTAGAAGAACTCCGCCCGCAGCTTGAAGCTGTGCATCAGCATCTC 874
 QY 98 -----ValGlnAlaAlaValLeuLeuGlyArgAsp-----LeuGluValGlyAlaAla 113
 Db 873 GGGGTCCCGCGCTGCTCTGCTTGAACACAGATGCTGTTGTTGCCGAACCTGGGCTCCAG 814
 QY 114 LeuGlyValValAlaHisGlnLeuLeuLeuLeuValHisLeuAlaValGluVal 133
 Db 813 CTGTGT-----CACGATCTGCTTCCAGGTGTTGTTCCACTTCTCGCGCTGATGTT 763
 QY 134 AlaValThrLeu-----ValAlaAlaAspAspGlnGlyHisValHis----- 147
 Db 762 GCATGGGCTGCGCGGATGTCGCCGATGATGTCGCCGCTAGAGAGCGCGCGCGG 703
 QY 148 -----ValLeuLeuGlyPheValLeuGluAla----- 156
 Db 702 GCCGATGCTGCTCTGCGGTGTTGTTGGGCGGCTGCGATGTTGATCTCCACGCT 643
 QY 157 -----ArgLeuGly-----ValGluAspLeuLeuProGluProLeu 168
 Db 642 CTCCTTCAGCTGCAGCATGATGCTTGGGTTGTCGTTGAAAGTTCTCGCTCGGATCAC 583
 QY 169 HisLeuLeuGluGlyValAlaValValGlnThrGluHisGlnAspGluAsnValSerCys 188
 Db 582 CACGCCCTCTCCGCCAGGCTGCGCTCAG-----GGTGCACCTGCACGCTGCT 499
 QY 189 GluAspGlyGluAlaProHisGlyGlyGluArgValValAlaGlyArgValGluAspVal 208
 Db 552 CAGCAGCTGGGTGCTCACCACCGGCGGATGCCGTG-----GGTGCACCTGCACGCTGCT 499
 QY 209 GluLeuValAspLeuAlaAlaAspGlyValGluLeuAlaValGluValLeuAspGlyArg 228
 Db 498 CAC-----GTTGGTGCAGGGCGCTGCCGTTGAACTTTTGTGTTGCTTCAGGTGGC 442
 QY 229 ArgValGlyValLeuGluAlaAlaGlyGluAlaArgHisAspGlyArgGluAlaHis 248
 Db 441 GAAGCCGCGC-----GGGGCGCAGTAGTGGATGGGATGGGCTCGAAGCTCAC 394
 QY 249 LeuGlyArgAlaGluAspHisAlaAlaValLeuGlyArgAspThrGlnLeuArg 268
 Db 393 CTGGGGCAGGCTGGGTGATCACGCTGTTGCCACGCTTCACGAGGCTTCAGGCTCTG 334
 QY 269 ValAlaArgAla-----HisLeuLeuAspHis 277
 Db 333 GTCCCAACGCTGATGATGCTCTGCTGCTGCTCTGCTCCACCAT 292

RESULT 10
 US-09-709-103-1f4 (1-282) x US-09-476-242-7 (1-2334)
 ; Sequence 1, Application US/09972529
 ; Patent No. US20020150916A1
 ; GENERAL INFORMATION:

QY 128 HisLeuAlaValGluValAlaValThrLeu-----ValAlaAlaAspGlnGlyHis 145
 Db 780 CTTCTCGCGCTGATGTTGCAGTGGGCTGCGGATGTCGCCGATGATGTCGCCGTGGC 721
 QY 146 ValHis-----ValLeuLeuGlyPheValLeuGluAla----- 156
 Db 720 GTAGAAGCGCGCGCGCGCGATGCTTTCGCGGTGTTGTTGGGCGGCT 661
 QY 157 -----ArgLeuGly-----ValGluAsp 162
 Db 660 GAGTGTGATCTCCAGCTCTCTTCAGCTGCACGATGATGCTTTCGCGTTCGTTGA 601
 QY 163 LeuLeuProGluProLeuHisLeuLeuGlyValAlaValValGlnThrGluHisGln 182
 Db 600 GTTCTGCTGCGGATCACACGCCCTCTCCGCCAGGCTGCGCTCAG----- 553
 QY 183 AspGluAsnValSerCysGluAspGlyGluAlaProHisGlyGlyGluArgValValAla 202
 Db 552 -----CAGCAGCTGGGTGCTCACACCGGCGGATGCCGTG----- 517
 QY 203 GlyArgValGluAspValGluLeuValAspLeuAlaAlaAspGlyValGluLeuAlaVal 222
 Db 516 GGTGCTGCTGCGGATGCTCAG-----GTTGTGTCAGGGCGCGCTGCGCTTGAACCTTCTGTC 460
 QY 223 GluValLeuAspGlyArgValGlyValLeuGluAlaAlaGlyGluGluAlaArgHis 242
 Db 459 GTTGCACTTCAGATGGCGAAGCGGC-----GGGGCGCGCATGATGATGGG 412
 QY 243 AspGlyArgLeuAlaHisLeuGlyArgAlaGluAspHisAlaAlaValLeuGly 262
 Db 411 GATGGCTGAAAGCTACCTTGGGCGAGGCTGGGTGATGATCAGCTGTTGCCAGCTTCAC 352
 QY 263 ArgAspThrGlnLeuArgValAlaAlaAla-----HisLeuLeuAspHis 277
 Db 351 GCAGGGCTTCAGGCTCTGTTCCACAGGCTGATGATGCTCTGCTGATCTGCTCCACCAT 292

RESULT 9
 US-09-476-242-7/c
 ; Sequence 7, Application US/09476242
 ; Patent No. US20020146683A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BARNETT, Susan
 ; APPLICANT: HARTOG, Karin
 ; APPLICANT: MARTIN, Eric
 ; TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES
 ; FILE REFERENCE: 1605.002
 ; CURRENT APPLICATION NUMBER: US/09/476,242
 ; CURRENT FILING DATE: 1999-12-30
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 7
 ; LENGTH: 2334
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Leu122-Ser199
 US-09-476-242-7

Alignment Scores:
 Pred. No.: 1.18e-05 Length: 2334
 Score: 155.00 Matches: 107
 Percent Similarity: 34.46% Conservative: 15
 Best Local Similarity: 30.23% Mismatches: 114
 Query Match: 10.99% Indels: 118
 DB: 20 Gaps: 20

US-09-709-103-1F4 (1-282) x US-09-476-242-7 (1-2334)
 QY 10 LeuGlyLeuAlaAlaGlyAlaGlyLeuLeuAlaAspValHisGluValAla----- 26
 Db 1257 CTTGGCCCTTGGTGGGCGCGCGGCTCGATCTTCCACACCTTGTACTTGTACAG 1198

APPLICANT: Millennium Pharmaceuticals, Inc.
 APPLICANT: Meyers, Rachel
 TITLE OF INVENTION: 47316, A NOVEL HUMAN G-PROTEIN AND USES
 FILE REFERENCE: 38155-20041.00
 CURRENT APPLICATION NUMBER: US/09/972,529
 PRIOR FILING DATE: 2002-04-08
 PRIOR FILING DATE: 2000-10-05
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 1224
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (313)...(924)
 US-09-972-529-1

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
154.00	1224	84	34	100	77	14	
Best Local Similarity:	40.14%						
Query Match:	10.91%						

US-09-709-103-1f4 (1-282) x US-09-972-529-1 (1-1224)

```

QY 2 AlaAspAspAlaAlaLeuValLeuGlyLeuAlaAlaGlyLeuLeuAla--- 20
Db 1068 GCTCCCTCCGCGCTGCTGCTTCTCAGCGGAGTGCGTGCAGGCGGCTCAGCGCGG 1029
QY 21 AspValHisGlu-----ValAlaValTyrAlaGlyProAla 32
Db 1028 GACCGTCACAGTTCATTTCCCGCGCTCCCGCCAGCCCGCCAGTACGAGCGCGCC 969
QY 33 ArgGluGlyCysHisAspAlaIleValAlaArgValAlaAlaAlaAlaAla 52
Db 968 -----CTCCGCTCCGCGCGAGTCCCGGTCAGCGCGA 939
QY 53 GlyProGlnGlnLeuValProGlnArgLeuValGlnHisValAlaValLeuHis 72
Db 938 GGGGCGGCGAGG-----CGTCACATGATGCGCGAGCGG-GTTGCGCGCG---CAG 895
QY 73 ArgAspLeuAlaValGlnValTyrAlaHisLeu-----AlaGlyGlnLeuGlyHisGly 90
Db 894 CGCGCCCTGGAGCGGAGCGGCGAGCGTGCAGTCTTGCAGGCGGCGAGCGCGCTTT 835
QY 91 GluGluTyrGlnGlnHisLeuValGlnAlaValLeuLeuGlyAlaArgAspLeuGluVal 110
Db 834 GAGCAGCTCGCTTAAGAGCAGCAGATGTGCGCATTTGCTGGCGCGAGTTCACAGTA 775
QY 111 GlyAlaAlaLeuGlyValValAlaHisGlnLeuLeuAspLeuAlaLeuValHisLeuAla 130
Db 774 ---GCGGCACTTCAGAGTCTTGGCTGACAGGTGCGAGCGTTCGAGCGGAGTACGCG 718
QY 131 ValGluValAlaValThrLeuValAlaAlaAspArgGlnGlyHisVal----- 146
Db 717 TCCGCGCTGGAGTCCCGCTTGTGCGCAGATGATGAGGCGGCTGAGAGTTCCGAT 658
QY 147 HisValLeuLeuGlyPheValLeuGlnAlaArgLeuValGlnAspLeuProGlu 166
Db 657 CACCTTCGCTC-----CAGGATCTCTGCGCGAT 628
QY 167 ProLeuHisLeuLeuGlnGlyValAlaValAlaGlnThrGlnHisGlnAspGluAsnVal 186
Db 627 GGTCTTGAGCTACTAAG-----GCTGCAAGAGCAGAGATGTGTAAGCAGAGATGTA 574
QY 187 SerCysGluAspGlyGlyAlaProHisGlyGly----- 197
Db 573 GGGGTGGAACACTCCGAGTCCCTCTGACAGAGGTGTGTCGCACTCTGAGAGCGTATTGAC 514

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QY 198 ---GluArgValAlaAlaGlyArgValGluAspValGluLeuValAspLeuAlaAsp 216
Db 513 AGGGAAGCGCGATGGGTGGAAAGTCCAGAGATTCGAGAGGTCGCGACGCGCTTCAT 454
QY 217 GlyValGluLeuAlaValGluValLeuAspGlyArgArgValGlyValLeuGluAlaAla 236
Db 453 GAC-----GACAGCAGCAGGTA-----AAGCGCGCG 427
QY 237 Gly-----GluGluAlaArgHisAspGly 244
Db 426 GCGCGGTGGTGGGAGCAGCAGACTCGCTGAACCTGTTGTACAAAGTGGCGCAGATGCG 367
QY 245 ArgLeuAlaHisLeuGlyArgAlaGluAspAspHisAlaIle 258
Db 366 ACTCTTGCCCACTCGCGCGCGCCCGCCAGCAGCGGACCCGGTA 325

```

RESULT 11

US-09-788-654A-1/c

Sequence 1, Application US/09788654A

Patent No. US20020119920A1

GENERAL INFORMATION:

APPLICANT: YE, Jane et al.

TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE

FILE REFERENCE: CL001143

CURRENT APPLICATION NUMBER: US/09/788,654A

NUMBER OF SEQ ID NOS: 20

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 3192

TYPE: DNA

ORGANISM: Human

US-09-788-654A-1

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
2.12e-05	3192	84	34	100	77	14	
Percent Similarity:	154.00						
Best Local Similarity:	40.14%						
Query Match:	28.57%						

US-09-709-103-1f4 (1-282) x US-09-788-654A-1 (1-3192)

```

QY 2 AlaAspAspAlaAlaLeuValLeuGlyLeuAlaAlaGlyLeuLeuAla--- 20
Db 1103 GCTCCCTCCGCGCTGCTGCTTCTCAGCGGAGTGCGTGCAGGCGGCTCAGCGCGG 1044
QY 21 AspValHisGlu-----ValAlaValTyrAlaGlyProAla 32
Db 1043 GACCGTCACAGTTCATTTCCCGCGCTCCCGCCAGCCCGCCAGTACGAGCGCGCC 984
QY 33 ArgGluGlyCysHisAspAlaIleValAlaArgValAlaAlaAlaAlaAla 52
Db 983 -----CTCCGCTCCGCGCGAGTCCCGGTCAGCGCGA 954
QY 53 GlyProGlnGlnLeuValProGlnArgLeuValGlnHisValAlaValLeuHis 72
Db 953 GGGGCGGCGAGG-----CGTCACATGATGCGCGAGCGG-GTTGCGCGCG---CAG 910
QY 73 ArgAspLeuAlaValGlnValTyrAlaHisLeu-----AlaGlyGlnLeuGlyHisGly 90
Db 909 CGCGCCCTGGAGCGGAGCGGCGAGCGTGCAGTCTTGCAGGCGGCGAGCGCGCTTT 850
QY 91 GluGluTyrGlnGlnHisLeuValGlnAlaValLeuLeuGlyAlaArgAspLeuGluVal 110
Db 849 GAGCAGCTCGCTTAAGAGCAGCAGATGTGCGCATTTGCTGGCGCGAGTTCACAGTA 790
QY 111 GlyAlaAlaLeuGlyValValAlaHisGlnLeuLeuAspLeuAlaLeuValHisLeuAla 130

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Tue Dec 31 15:27:52 2002

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Db 789 ---GCCGCACCTTCAGGCTTGGTACCAGGTGCGACACGTTCCAGCGGGGATCACGCG 733
Qy 131 ValGluValAlaValThrLeuValAlaAlaAspAspGlnGlyHisVal----- 146
Db 732 TCCGCGTGCAGGTCCTGGCTTTGGTCCAGCATGATGATGGGCGTCTCGAGGTTCCGAT 673
Qy 147 HisValLeuLeuGlyPheValLeuGluAlaArgLeuGlyValGluAspLeuLeuProGlu 166
Db 672 CACCCCTCGTCTC-----CAGGATCTGCTGGCGGAT 643
Qy 167 ProLeuHisLeuLeuGluGlyValAlaValAlaValThrGluHisGlnAspGluAsnVal 186
Db 642 GGTCTTGACGTACTCAA-----GCTGTCAAAGCAGCAGATGCTGTAGACACGATGTA 589
Qy 187 SerCysGluAspGlyGluAlaProHisGlyGly----- 197
Db 588 GCGGTGGACACTCCGGAGTCCCTCCGACGAGGTGTGCGCCACTCTCCGTAGCGATTGAC 529
Qy 198 ---GluArgValValAlaGlyArgValGluAspValGluLeuValAlaAsp 216
Db 528 AGGGAAGCGCTGATGGTGAAGTCAAGATCTGGAGTCTGCGACGTCGGCGCTTCAT 469
Qy 217 GlyValGluLeuAlaValGluValLeuAspGlyArgArgValGlyValLeuGluAlaAla 236
Db 468 GAC-----GACAGCAGGCGGTA-----AAGCGCGCG 442
Qy 237 Gly-----GluGluAlaArgHisAspGly 244
Db 441 GCGGTGGTGGGACGACACTCGCTGAACTCGTTGTACAGAACTGGCGCAGATGGC 382
Qy 245 ArgLeuAlaHisLeuGlyArgAlaGluAspAspHisAlaAla 258
Db 381 ACTCTGCCACACCTCGCGCCCCCAGCAGCAGCGCCACCGGTA 340

RESULT 12
US-09-476-242-19/c
; Sequence 19, Application US/09476242
; Patent No. US20020146683A1
; GENERAL INFORMATION:
; APPLICANT: BARNETT, Susan
; APPLICANT: HARTOG, Karin
; APPLICANT: MARTIN, Eric
; TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES
; FILE REFERENCE: 1605.002
; CURRENT APPLICATION NUMBER: US/09/476,242
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 19
; LENGTH: 2322
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Leu122-Ser199;
; OTHER INFORMATION: Arg426-Lys432
US-09-476-242-19

Alignment Scores:
Pred. No.: 1,79e-05 Length: 2322
Score: 153.00 Matches: 101
Percent Similarity: 35.78% Conservative: 21
Best Local Similarity: 29.62% Mismatches: 126
Query Match: 10.84% Indels: 94
DB: 15 Gaps: 15

US-09-709-103-1f4 (1-282) x US-09-476-242-19 (1-2322)

Qy 10 LeuGlyLeuAlaAlaGlyAlaGlyLeuLeuAlaAspValHisGluValAla----- 26
Db 1251 CTGGCGCTTGGTGGGGCCAGCCAGCGGGCTGATCTTCCACCTTGTACTTGTACAG 1192
Qy 27 -----ValTyrAlaGlyProAlaArgGluGlyCysHisAspAlaLysGlyVal 42

```

RESULT 13
 US-10-032-717-9/c
 ; Sequence 9, Application US/10032717
 ; Patent No. US20020151709A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Andre R. Abad
 ; APPLICANT: Nicholas B. Duck

APPLICANT: Xiang Feng
 APPLICANT: Ronald D. Flannagan
 APPLICANT: Theodore W. Kahn
 APPLICANT: Lynn E. Sims
 TITLE OF INVENTION: Genes Encoding No. US20020151709A1el Proteins with
 TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
 FILE REFERENCE: 35716/237005
 CURRENT APPLICATION NUMBER: US/10/032,717
 PRIOR FILING DATE: 2001-10-23
 PRIOR APPLICATION NUMBER: 60/242,838
 NUMBER OF SEQ ID NOS: 48
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 9
 LENGTH: 2010
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)...(2010)
 OTHER INFORMATION: Maize optimized Cry1218-1
 LOCATION: (0)...(0)
 OTHER INFORMATION: mol218-1
 US-10-032-717-9

Alignment Scores:
 Pred. No.: 6e-05 Length: 2010
 Score: 146.50 Matches: 114
 Percent Similarity: 36.53% Conservative: 23
 Best Local Similarity: 30.40% Mismatches: 95
 Query Match: 10.38% Indels: 143
 Gaps: 25

US-09-709-103-1f4 (1-282) x US-10-032-717-9 (1-2010)

QY 7 LeuLeuValLeuGluLeuAlaAlaGlyAlaGlyLeuLeuAlaAspValHisGluValAla 26
 Db 1155 CTGCTGAGAGTTGA---GCCGCGGAGACACGCGGTGTAGAGAT----- 1114
 QY 27 ValTyAlaGlyProAlaArgLys-----GlyCys 36
 Db 1113 CTGCTGAGAGTTGA---GCCGCGGAGACACGCGGTGTAGAGAT----- 1114
 QY 37 HisAspAlaLysGly-----ValAlaArgValAlaAlaAla----- 48
 Db 1053 CACGCTGAGGCGCGGTATGATGCAACACGTCGCGCGCGGATCACGAGAGATCGAT 994
 QY 49 ---AlaAlaAlaAlaGlyProGlnGlnLeuLeuValProGlnArgLeuLeuValGlnHis 67
 Db 993 CAGCGCGAGCTGGGCGC-----CTGTCTGATCCACAGA 961
 QY 68 ValAlaValLeuHisArgAspLeuAlaValGlnValTrpAlaHisLeuAlaGlyGlnLeu 87
 Db 960 GCCGATGAGAGACACGTTACGCGCGGAGCGGCTGCTGATACCTCCGCGGTAGCTG 901
 QY 88 Gly----- 88
 Db 900 GGCCTTGCTCCATGAGGAGTGGCGGCTGTCTAGTTGGGAGAGAGGCCACACGTC 841
 QY 89 ---HisGlyGluGluArg-----AlaGlnHisLeuValGlnAlaAlaValLeuLeuGly 105
 Db 840 GAGCAGCGGAGGATCATCTCGCGCGGAGCTGTTGTCTCCACCCACTGCTGCGGGA 781
 QY 106 ArgAspLeuGluValGly-----AlaAlaLeuGlyValVal 117
 Db 780 GGTGCTTGAGCTTGGCAGGCGGCTCATATACACTTCACGACGTGTGCGAGTACTC 721
 QY 118 AlaHisGlnLeuLeuAspLeuAlaLeuValHisLeuAlaValGluValAlaVal----- 135
 Db 720 GCGCGTGAAGCTT-----CATCTGGCGGTGTGTAGTGTGTATGATGAT 679
 QY 136 -----ThrLeuValAlaAlaAsp----- 141

Db 678 GGTGTGACACAGCCCACTCTCCGCGAAGTGGAGGCGTCTTGAGAGAGAGCTG 619
 QY 142 -----AspGlnGlyHisVal-----HisValLeu 149
 Db 618 GAGTTGGCGGCATGCGGTACACGCTGAGAGAGGACCTCGAAGTTGTGTACCCGGA 559
 QY 150 LeuGlyPheValLeuGluAlaArgLeuGlyValGluAspLeuLeuProGluProLeuHis 169
 Db 558 GAGGCGCATGTACTG---GTTAGAGAGGAGTCCAGAT---CTCGAAGCGGTTCCGCAC 505
 QY 170 LeuLeuGluGly-----ValAlaValAlaGlnTrpGlnHisGlyAspGluAsnVal 186
 Db 504 GTGCGGAGAGCGCGCGAGCCCTTGCGGTCTCTCCCACTCTCCAGGCGCTAGGTA 445
 QY 187 Ser---CysGluAspGlyGluAlaProHisGlyGlyGluArgValAlaGlyArgVal 205
 Db 444 GAGCTGTGATTGTTGCGGAGGCTCTCCAGCTCGAGAGGCGCTTGTGCGGCGTACTC 385
 QY 206 GluAspValGluLeuValAsp----- 212
 Db 384 GCGCATCTT---CTGTTGATGAGCTCTCCACCTGTCATGAAGATTCCCACTGGGA 328
 QY 213 LeuAlaAlaAspGlyVal-----GluLeuAlaValGluValLeuAspGlyArg 228
 Db 327 CTCTCGCGCGAGGCGCGAGAGATGTCGATGAGCTGGGTGTAGAGGACACAGATGGGCC 268
 QY 229 ArgValGlyValLeuGluAlaAlaGlyGluGluAlaArgHisAsp----- 243
 Db 267 CACGAAGGACACCGCGAG---GCCGAGAGAGAGCTTGGCCACATGTGATGCGGCGCTT 211
 QY 244 ---GlyArgLeuAla-----HisLeuGlyArgAlaGluAspAspHisAlaAla 259
 Db 210 GCGGCGCTCTGCGCGGACACAGACACTCGGAGAGC-----GGG 169
 QY 260 ValLeuGlyArgAspTrpGlnLeuArgValAlaAlaArgAlaHisLeu 274
 Db 168 GTACTCGGA-----GGCGTTCGCGGAGACTCTT 139
 RESULT 14
 US-09-815-242-7899/c
 Sequence 7899, Application US/09815242
 Patent No. US20020061569A1
 GENERAL INFORMATION:
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlsen, Kari L.
 APPLICANT: Zyskind, Daniel
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John D.
 APPLICANT: Carr, Grant J.
 APPLICANT: Yamamoto, Robert T.
 APPLICANT: Xu, H. Howard
 TITLE OF INVENTION: Identification of Essential Genes in
 TITLE OF INVENTION: Prokaryotes
 FILE REFERENCE: ELITRA.011A
 CURRENT APPLICATION NUMBER: US/09/815,242
 PRIOR FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 NUMBER OF SEQ ID NOS: 14110
 SOFTWARE: FastSeq for Windows Version 4.0


```
; SEQ ID NO 7899
; LENGTH: 4074
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(4074)
US-09-815-242-7899

Alignment Scores:
Pred. No.: 0.000139 Length: 4074
Score: 146.50 Matches: 110
Percent Similarity: 33.63% Conservative: 43
Best Local Similarity: 24.18% Mismatches: 111
Query Match: 10.38% Indels: 191
DB: 10 Gaps: 24

US-09-709-103-1F4 (1-282) x US-09-815-242-7899 (1-4074)
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Db 4017 GTTGAAGACTCGGGCATGCGGGCTCCATGCGGTGATCGCGTCCACGATGTTCTGTGA 3958
QY 28 TyrAlaGlyProAla-----ArgGluGlyCysHisAspAlaLysGlyVal 42
Db 3957 CATCTTGGTCGGCGGCTTACAGTCGTCGACTTACCGCTTACCGCTTCTTCTGCGAGGTGA 3898
QY 43 AlaArgVal----- 45
Db 3897 CGCGCGCCATAGGCTTCCAGCGGCCACACCTCCATCCACGAAGCGCTGACCACCGAA 3638
QY 46 -----AlaAlaAlaAlaAlaAlaGlyPro 54
Db 3837 CTGTGCTTACCACCCAGCGGTGCTGGTAAACAGGCTGTACGAGCGGTGGAACGGGC 3778
QY 55 GlnGlnLeuLeuValProGlnArgLeuLeuValGlnHisValAlaValLeuHisArgAsp 74
Db 3777 GTGCATCTTGTGTCACACAGGTGTTTTCAGCTTGAGCATGTACATGTAGCCGACGGTGGT 3718
QY 75 LeuAlaValGlnValTrpAla-----HisLeuAla----- 84
Db 3717 CGGACGCTCGAACTGTTGCGGTACGCGCTGCGACAGAGCATCTTGGCGGCTTCCGG 3658
QY 85 -----GlyGlnLeuGlyHisGly-----GluGluArg 93
Db 3657 CAGGTCGGCCAGCTTCAGCATGGCTTGTATCTCGGTTCTTGGCGGCATCGAACACCGG 3598
QY 94 AlaGluHis----- 96
Db 3597 GGTGCCCATCGGTACGCCACCGCAGGTTCTTGGCCAGCGGAGGATCTCGTTGTGCGCC 3538
QY 97 -----LeuValGln----- 99
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QY 100 -----AlaAlaValLeu 103
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QY 104 LeuGlyArgAspLeuGluValGly----- 111
Db 3417 CTTGGCGCGGAGCCCGAGGTGGTTTCGAGGATCTGACCGAGTTCATACCGACGGTAC 3358
QY 112 -----AlaAlaLeuGlyValValAla----- 118
Db 3357 GCCCAGCGGTTTGAGGACGATGTCGACCGGGGTGCGTGGCATCTGTCGGCATGCTCTTC 3298
QY 119 -----HisGlnLeuLeuAspLeuAlaLeuValHisLeuAlaVal 131
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QY 132 GluValAlaValThrLeu-----ValAlaAlaAspGlnGlyHisValHisVal 148
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Alignment Scores:
Pred. No.: 3.08e-05 Length: 612
Score: 143.00 Matches: 66
Percent Similarity: 37.11% Conservative: 29
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; SEQ ID NO 3
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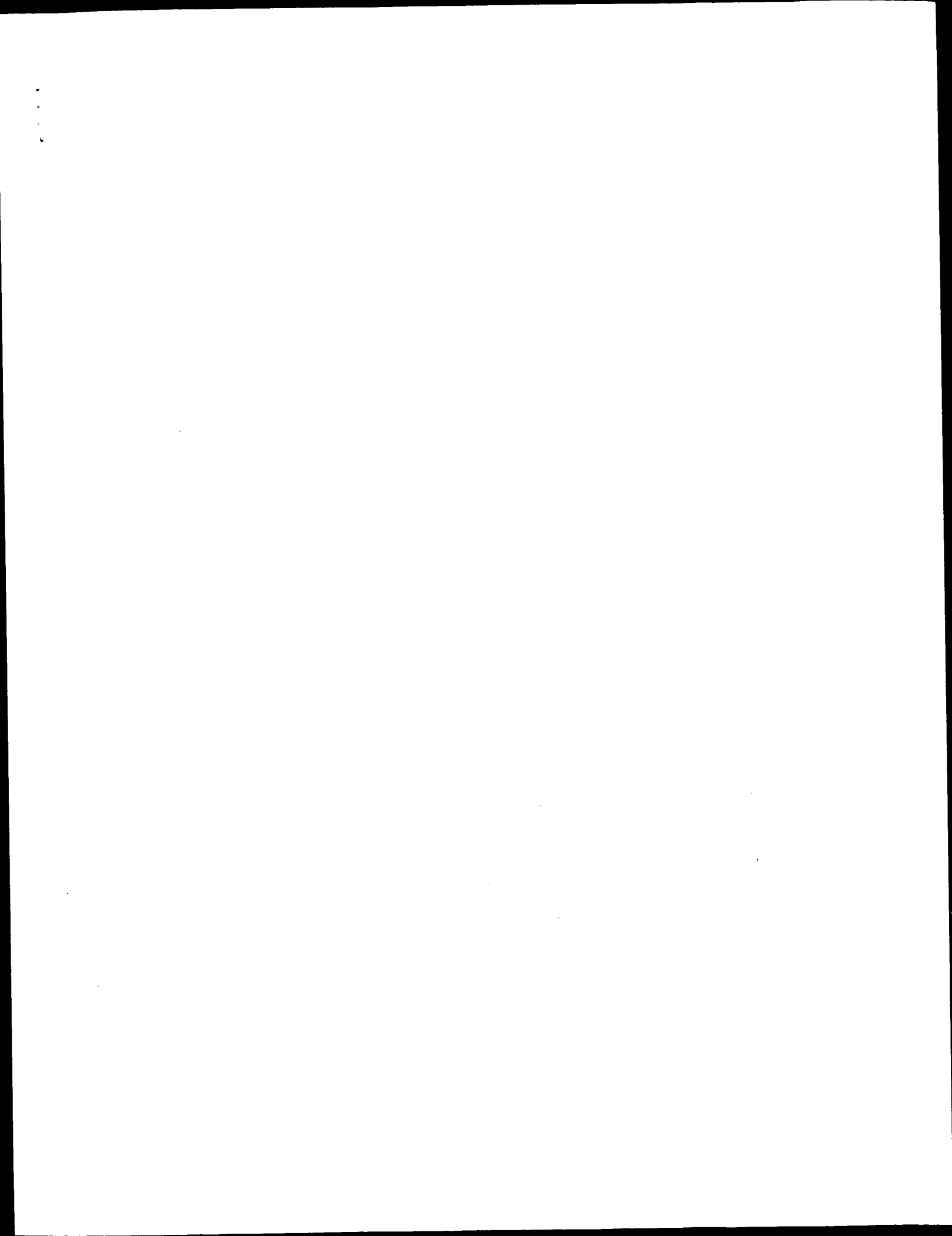
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; Sequence 3, Application US/09972529
; Patent No. US20020150916A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; TITLE OF INVENTION: 47316. A NOVEL HUMAN G-PROTEIN AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 38155-20041.00
; CURRENT APPLICATION NUMBER: US/09/972,529
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 60/237,716
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 612
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-972-529-3

RESULT 15
US-09-972-529-3/c
; Sequence 3, Application US/09972529
; Patent No. US20020150916A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; TITLE OF INVENTION: 47316. A NOVEL HUMAN G-PROTEIN AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 38155-20041.00
; CURRENT APPLICATION NUMBER: US/09/972,529
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 60/237,716
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 612
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-972-529-3
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Db 513 -----GCTGAAGACGACAGAGATGTGCCAGTTGCTTGTGACGAGCATTC 469
QY 109 GluValGlyAlaAlaLeuGlyValAlaAlaHisGlnLeuLeuAspLeuAlaLeuValHis 128
Db 468 CACGTA--GCCGACCTTCAGGCTTGTGCGTACGAGGTGCGACACGTTCCAGCGCGGAT 412
QY 129 LeuAlaValGluValAlaValThrLeuValAlaAlaAspArgGlnGlyHisVal----- 146
Db 411 CACGGGTCCGGCGCTGACAGTCCCGCTTGTGCGACGATGATGAGGCGCTCTGAGGT 352
QY 147 -----HisValLeuLeuGlyPheValLeuGlnAlaArgLeuGlyValGluAspLeu 164
Db 351 TCCGATCACCTCGCTC-----CAGGATCTGCTG 322
QY 165 ProGluProLeuHisLeuLeuGlnGlyValAlaValValGlnThrGlnHisGlnAspGlu 184
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QY 185 AsnValSerCysGluAspGlyGluAlaProHisGlyGly----- 197
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QY 198 -----GluArgValValAlaGlyArgValGluAspValGluLeuValAspLeuAla 214
Db 207 ATTGACAGGAGAGCGCTGATGGGTGGAAGTCTGAGATCTGAGAGTCTGACAGCTGGCC 148
QY 215 AlaAspGlyValGluLeuAlaValGluValLeuAspGlyArgArgValGlyValLeuGlu 234
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QY 235 AlaAlaGly-----GluGlnAlaArgHis 242
Db 120 GCGGCGGCGGCTGTGGGAGCGACACTCGCTGACTGTTGTACAGAACTGGCGCAC 61
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Search completed: December 30, 2002, 18:07:35
Job time : 99 secs



GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus.p2n model

Run on: December 30, 2002, 16:16:46 ; Search time 77 seconds

(without alignments)
1123.154 Million cell updates/sec

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Perfect score: 1411
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Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 segs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seg length: 0
Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database :

1: Issued Patents NA.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	1411	100.0	1841	4	US-09-053-374A-1 Sequence 1, Appl1
C 2	1348	95.5	3986	4	US-09-053-374A-1 Sequence 3, Appl1
C 3	963.5	68.3	1689	4	US-09-053-374A-4 Sequence 4, Appl1
C 4	911	64.6	3079	4	US-09-053-374A-6 Sequence 6, Appl1
C 5	166	11.8	3468	2	US-07-951-715A-2 Sequence 2, Appl1
C 6	166	11.8	3468	2	US-08-459-448A-2 Sequence 2, Appl1
C 7	166	11.8	3468	3	US-08-459-595A-2 Sequence 2, Appl1
C 8	166	11.8	3468	3	US-08-459-504B-2 Sequence 2, Appl1
C 9	166	11.8	3468	3	US-08-459-504B-2 Sequence 2, Appl1
C 10	166	11.8	3468	3	US-09-053-549-3 Sequence 3, Appl1
C 11	166	11.8	3468	4	US-09-547-422-2 Sequence 2, Appl1
C 12	159	11.3	3468	1	US-07-951-715A-4 Sequence 4, Appl1

C 13	159	11.3	3468	2	US-08-459-448A-4 Sequence 4, Appl1
C 14	159	11.3	3468	3	US-08-459-595A-4 Sequence 4, Appl1
C 15	159	11.3	3468	3	US-08-459-504B-4 Sequence 4, Appl1
C 16	159	11.3	3468	3	US-08-459-444-4 Sequence 4, Appl1
C 17	159	11.3	3468	3	US-09-053-549-5 Sequence 5, Appl1
C 18	159	11.3	3468	4	US-09-547-422-4 Sequence 4, Appl1
C 19	153.5	10.9	1227	3	US-09-074-912-3 Sequence 3, Appl1
C 20	153.5	10.9	1227	4	US-08-290-136-3 Sequence 3, Appl1
C 21	153.5	10.9	3157	2	US-08-939-002A-1 Sequence 1, Appl1
C 22	153.5	10.9	3624	2	US-07-951-715A-6 Sequence 6, Appl1
C 23	153.5	10.9	3624	3	US-08-459-448A-6 Sequence 6, Appl1
C 24	153.5	10.9	3624	3	US-08-459-595A-6 Sequence 6, Appl1
C 25	153.5	10.9	3624	3	US-08-459-504B-6 Sequence 6, Appl1
C 26	153.5	10.9	3624	3	US-08-459-444-6 Sequence 6, Appl1
C 27	153.5	10.9	3624	4	US-09-547-422-6 Sequence 6, Appl1
C 28	153.5	10.9	3546	1	US-07-951-715A-12 Sequence 12, Appl1
C 29	152	10.8	3546	2	US-08-459-448A-12 Sequence 12, Appl1
C 30	152	10.8	3546	2	US-08-459-595A-12 Sequence 12, Appl1
C 31	152	10.8	3546	3	US-08-459-504B-12 Sequence 12, Appl1
C 32	152	10.8	3546	3	US-08-459-444-12 Sequence 12, Appl1
C 33	152	10.8	3546	3	US-08-459-444-12 Sequence 12, Appl1
C 34	152	10.8	3546	4	US-09-547-422-12 Sequence 12, Appl1
C 35	151	10.7	1848	1	US-08-635-137-1 Sequence 1, Appl1
C 36	151	10.7	1848	4	US-09-136-981-1 Sequence 1, Appl1
C 37	150	10.6	3546	1	US-07-951-715A-14 Sequence 14, Appl1
C 38	150	10.6	3546	2	US-08-459-448A-14 Sequence 14, Appl1
C 39	150	10.6	3546	3	US-08-459-595A-14 Sequence 14, Appl1
C 40	150	10.6	3546	3	US-08-459-504B-14 Sequence 14, Appl1
C 41	150	10.6	3546	3	US-08-459-444-14 Sequence 14, Appl1
C 42	150	10.6	3546	3	US-09-547-422-14 Sequence 14, Appl1
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C 44	144.5	10.2	1947	2	US-08-459-448A-3 Sequence 3, Appl1
C 45	144.5	10.2	1947	3	US-08-459-595A-3 Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-09-053-374A-1/c
; Sequence 1, Application US/09053374A
; Patent No. 6462177
; GENERAL INFORMATION:
; APPLICANT: YEN, KWANG-MU
; TITLE OF INVENTION: MAMMALIAN BLOOD LOSS-INDUCED GENE, KD312
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: AMGEN INC.
; STREET: ONE AMGEN CENTER DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: US
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/053,374A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1841 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULAR TYPE: cDNA
; FEATURE:

NAME/KEY: CDS
LOCATION: 255..1097
US-09-053-374A-1

Alignment Scores:

Alignment Scores:	4.47e-126	Length:	184
Score. No.:	1411.00	Matches:	282
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

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QY	21	AspValHisGluValAlaValTrAlaAGlyProAlaArgGluGlyCyHisAspAlaLys	40
DB	1040	GATGTACTAGCTCGCTGTGTACGTGGCGCGCGCGAGGGTGCACCAGTCCAAA	981
QY	41	GlyValAlaArgValAlaAlaAlaAlaAlaAGlyProGlnGlnLeuLeuValPro	60
DB	980	GGCGTCGCCCGGTTCGCCCGCGCGCGCTCGCCCCCGCAGCAGCTTCTTGTCGG	921
QY	61	GlnArgLeuLeuValGlnHisValAlaValLeuHisArgAspLeuAlaValGlnValTrp	80
DB	920	CAGCGCTTCTTGTGCAGCACGTTCGCAGTACTGCACCGAGACCTTCGCGTGCAGGTCTGG	861
QY	81	AlaHisLeuAlaGlnLeuGlyHisGlyGluGluArgAlaGluHisLeuValGlnAla	100
DB	860	GCTCATCTCGTGGCGAGCTTGCCCATCGCAAGACGCGCGGAACATCTGTGCCAGGCT	801
QY	101	AlaValLeuLeuGlyArgAspLeuGluValGlyAlaAlaLeuGlyValValAlaHisGln	120
DB	800	GCTGTCTTCTTGGCCGAGATCTCGAAGTAGCGCAGCGCTGGGGGTCTGCCACCACG	741
QY	121	LeuLeuAspLeuAlaLeuValHisLeuAlaValGluValAlaValThrLeuValAlaAla	140
DB	740	CTGTCTCATCTCGCGCTGGTCCACTCTCGGTAGAAGTCGGGTCACTTGTTCGCCGA	681
QY	141	AspAspGlnGlyHisValHisValLeuLeuGlyPheValLeuGluAlaArdLeuGlyVal	160
DB	680	GATGACCAGGGGCACGTCCAGTCTCTCTTGGTTTTGTCTTGAGCGAAGACTTGTGTCT	621
QY	161	GluAspLeuLeuProGluProLeuHisLeuLeuGluGlyValAlaValValGlnThrGlu	180
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QY	181	HisGlnAspGluAsnValSerCyeGluAspGlyGluAlaProHisGlyGlyGluArgVal	200
DB	560	CACCAGGATGAACGTCCTCTGTGAGGATGGAGCGCGCGCATGGCGGGGACCGGTG	501
QY	201	ValAlaGlyArgValGluAspValGluLeuValAspLeuAlaAlaAspGlyValGluLeu	220
DB	500	GTTGCCGAGCGTCTCAGGATGTCAGCTGGTAGACCTCGCCCGGATGGAGTAGAACCTT	441
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DB	440	CGGTGGNAGTCTCGATGTTAGCGCTGTGAGCGTCTCGAAGCGCGCGGTGAGNAGCG	381
QY	241	ArgHisAspGlyArgLeuAlaHisLeuGlyArgAlaGluAspAspHisAlaIleAlaVal	260
DB	380	CGACACGATGGCGCTCTTGCCCACTTTGACGCGCCGAGGATGACCATGCGATAGCAGTT	321
QY	261	LeuGlyArgAspThrGlnLeuArgValAlaArgAlaHisLeuLeuAspHisArgGlyGln	280
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QY	281	PheHis	282
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RESULT 2

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US-09-053-374A-3/C
; Sequence 3, Application US/09053374A
; Patent No. 6462177
; GENERAL INFORMATION:
; APPLICANT: YEN, KWANG-MU
; TITLE OF INVENTION: MAMMALIAN BLOOD LOSS-INDUCED GENE, KD312
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: US
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/053,374A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-514
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3986 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-053-374A-3

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Percent Similarity:	79.89%	Mismatches:	0
Best Local Similarity:	95.54%	Indels:	71
Query Match:	4	Gaps:	1
DB:			

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Db	1770 GATGTACATGAGGTGCCTGTGTACCTGGCGCGCGCGAAGGGTGCCACGATGCCAAA 1711
QY	41 GlyValAlaArgValAlaAlaAlaAlaAlaAlaGlyProGlnGlnLeuLeuValPro 60
Db	1710 GGCGTGC CGCGGTGCGCGCGCGCGCGCTCCCGCGCGCGACGAGCTCTTGTTCGG 1651
QY	61 GlnArgLeuLeuValGlnHisValAlaValLeuHisArgAspLeuAlaValGlnValTrp 80
Db	1650 CAGCGCCTCTTTGTGCAGCACGCTCCAGTACTGTACCAGACCTTGGCGGTGCAGGTCGG 1591
QY	81 AlaHisLeuAlaGlyGlnLeuGlyHisGlyGluGluArgAlaGluHisLeuValGlnAla 100
Db	1590 GCTCATCTCGCTGGCAGCTTGGCATGTCGANGAGCGCGGGAACATCTGGTCCAGGCT 1531
QY	101 AlaValLeuLeuGlyArgAspLeuGluValGlyAlaLeuGlyValValAlaHisGln 120
Db	1530 GCTGTCTCTTTTGCGCCGAGATCTCGAAGTAGCGCAGCGCTGGGGGTCTGCCCCACCG 1471
QY	121 LeuLeuAspLeuAlaLeuValHisLeuAlaValGluValAlaValThrLeuValAlaAla 140


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Qy 161 GluAspLeuLeuProGluProLeuHisLeuLeuGlnGlyValAlaValGlnThrGlu 180
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RESULT 3
US-09-053-374A-4/C
; Sequence 4, Application US/09053374A
; Patent No. 6462177
; GENERAL INFORMATION:
; APPLICANT: YEN, KWANG-MU
; TITLE OF INVENTION: MAMMALIAN BLOOD LOSS-INDUCED GENE, KD312
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSER: AMGEN INC.
; STREET: ONE AMGEN CENTER DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: US
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/053,374A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.

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; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-514
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 132..971
; US-09-053-374A-4

Alignment Scores:
Pred. No.: 2,81e-83
Score: 963.50
Percent Similarity: 79.79%
Best Local Similarity: 70.92%
Query Match: 68.28%
DB: 4 Gaps: 1

US-09-709-103-1f4 (1-282) x US-09-053-374A-4 (1-1689)

Qy 1 LeuAlaAspAspAlaAlaLeuValLeuAlaAlaGlyLeuAlaAlaGlyLeuAlaAla 20
Db 974 CTACTGATGACACAGCGCTCTTGTCTTACGCTGCTGACACTGGTTTTCACAG 915
Qy 21 AspValHisGlnValAlaValAlaValAlaGlyProAlaArgGlnGlyGlyHisAspAlaVal 40
Db 914 AATGACATGAGGCGCGCTATGACAGCTAGCTGCGAGCAAGGGGCCCAAGATGCCAA 855
Qy 41 GlnValAlaArgValAlaAlaAlaAlaAlaAlaAlaGlyProGlnGlnLeuValPro 60
Db 854 GGCATCTCC--GGGTCGCGCCCGCCACCTCGCGTCCGCGCAGCAGAGAGCTTCTTCT 798
Qy 61 GlnArgLeuLeuValGlnHisValAlaValLeuHisArgAspLeuAlaValGlnValTrp 80
Db 797 CAGAGCTTTTGTGACGACGTCACAGTACTGACAGCACCTTGCCTGTCAGTCAAG 738
Qy 81 AlaHisLeuAlaGlnLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100
Db 737 GCTCATCTCCCTGAGGAGCTTGGCGCAAGGCGGAGGAGGAGGAGGAGGAGGAGGAGG 678
Qy 101 AlaValLeuLeuGlnValArgAspLeuGlnValAlaAlaAlaLeuGlyValAlaHisGln 120
Db 677 GCTATCTTCTTGGCGGAGATCTCGAAGTGGCACACAGCTGAGGTCATCGCCACAG 618
Qy 121 LeuLeuAspLeuAlaLeuValHisLeuAlaValAlaValAlaValThrLeuValAlaAla 140
Db 617 CTGCTCAATCTCCGCGTCTCCACTCGCGGTAGAAAGTCCCGGTCCCTTGTTCACGCA 558
Qy 141 AspAspGlnGlyHisValHisValLeuLeuGlnGlyPheValLeuGlnAlaArgLeuGlyVal 160
Db 557 AATGACACGCGGACGTCACATCTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 498
Qy 161 GluAspLeuLeuProGlnProLeuHisLeuLeuGlnGlnGlnGlnGlnGlnGlnGlnGln 180
Db 497 TAGGATCTGCTGTTGACGCTTTCACCTCTCCAGAGAGTGGCGTTGTTGTTGTTGTTG 438
Qy 181 HisGlnAspGlnAsnValSerCysGlnAspGlyGlnAlaProHisGlnGlnGlnGlnGln 200
Db 437 CACCAAGATGAAAACGTTCTCTGAGGATGAGAGGCGCGCGCATGCGGGAACGAGATG 378
Qy 201 ValAlaGlyArgValAlaGlnAspValGlnLeuValAspLeuAlaAlaAspGlyValGlnLeu 220
Db 377 ATTGCCAGATGTTGTCAGTATGCTCACTGTTGACTTCCCGCGGATCGACGTAAACTT 318
Qy 221 AlaValGlnValLeuAspGlyArgArgValGlyValLeuGlnAlaAlaGlnGlnGlnGln 240
Db 317 TCGTGGAAGCTTCAATGATGAGGGGTGAAGCGTCTCGAAGCGCGCGTGAAGAGAGG 258
Qy 241 ArgHisAspGlyArgLeuAlaHisLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 260

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Tue Dec 31 15:27:52 2002

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1045 GCTCATCTCGCTAGGAGCGTTGGCCATGGCAAGAGCGCGACGGAACATCTGGTCCAGGCT 986
101 AlalaHisLeuAlaGlyGlnLeuGlyHisGlyGluAlaGlyGlnHisLeuValGlnAla 100
101 AlalaHisLeuAlaGlyGlnLeuGlyHisGlyGluAlaGlyGlnHisLeuValGlnAla 120
985 GCTATTCTCTTGGCGGAGATCTCGAAGTAGGACCAACGCTGAGGGTTCATCGCCACGAG 926
121 LeuLeuAspLeuAlaLeuValHisLeuAlaValGluValAlaValThrLeuValAlaAla 140
925 CTGCTCAATCTCCGCTGCTCCACTTCGCGGTAGAAAGTCCCGGTCCCTTGTGTACCCGA 866
141 AspAspGlnGlyHisValHisValLeuLeuGlyPheValLeuGluAlaAargLeuGlyVal 160
865 AATGACCGAGCGGCACGCTCCACATTTCTTTGGTTTGTCTTGACACAGGACTTGGTGTCT 806
161 GluAspLeuLeuProGluProLeuHisLeuGluGlyValAlaValAlaGlnThrGlu 180
805 TAGGATCTGCTGTTGAGCGCTTTGACCTCTCTGAAGGAGTCCGCGTGTCTTAAGCTGAA 746
181 HisGlnAspGluAsnValSer----- 187
745 CACCAGAAATGAAACGCTCTC-CTACAAGGAACGAGTGTGAAGAGTGAAGGAGTGCCTCAA 687
187 ----- 187
686 GCACGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 627
188 -----CysGluAspGlyGluAlaPro 194
626 GATTCCTCTCCCGACGCTGCTCGTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCT 567
195 HisGlyGlyGluArgValAlaGlyValAlaGlyValAlaGlyValAlaGlyValAla 214
566 CATGCGGGAACCGAGTGTGCGTCCAGTGTGCGTCCAGTGTGCGTCCAGTGTGCGTCCAG 507
215 AlaAspGlyValGluLeuAlaValGluValLeuAspGlyValGlyValGlyValGlyVal 234
506 GCGGATCGAGTAAACTTTTCGTTGGAAGTCTTCAATGTTGAGGGGTGTAAGCGCTCTCGAA 447
235 AlalaGlyGluGluAlaAargHisGlyValGlyValGlyValGlyValGlyValGlyVal 254
446 GCGGCGCGGTGAGGAAGCGCGACACGATGCGCTCTTCCCGCTCTTCCCGCTCTTCCCGCT 387
255 AspHisAlaAlaValLeuGlyArgAspThrGlnLeuArgValAlaAargAlaHisLeu 274
386 GACCATCTCTGAGCAGTCTTGGCGGGATACTCAGTTTCAGAGTCTGCTTGGGACATCTT 327
275 LeuAspHisArgGlyGlnPheHis 282
326 CTTGATCATCGCGCCAGTTTCAT 303

RESULT 5
US-07-951-715A-2/c
; Sequence 2, Application US/07951715A
; Patent No. 5625136
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.

```

```

257 CGACACGATGCGCTCTTGGCCACTTTGGATGAGCGGAGATGACCATCTCTGTAGCAGTT 198
261 LeuGlyArgAspThrGlnLeuArgValAlaAargAlaHisLeuLeuAspHisArgGlyGln 280
197 CTTGGCGGAGATCTAGTTTCAAGTTCAGATGCTTGGGACATCTTCTTGATCATCGCGGAG 138
281 PheHis 282
137 TTTTCAT 132

RESULT 4
US-09-053-374A-6/c
; Sequence 6, Application US/09053374A
; Patent No. 6462177
; GENERAL INFORMATION:
; APPLICANT: YEN, KWANG-MU
; TITLE OF INVENTION: MAMMALIAN BLOOD LOSS-INDUCED GENE, KD312
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: US
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/053.374A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-514
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-053-374A-6

Alignment Scores:
Pred. No.: 6,77e-78 Length: 3079
Score: 911.00 Matches: 199
Percent Similarity: 68.29% Conservative: 25
Best Local Similarity: 60.67% Mismatches: 57
Query Match: 64.56% Indels: 48
DB: 4 Gaps: 2

US-09-709-103-1F4 (1-282) x US-09-053-374A-6 (1-3079)
QY 1 LeuAlaAspAlaAlaLeuLeuValLeuGlyLeuAlaGlyAlaGlyLeuAla 20
DB 1282 CTAACCTGATGACACAGCGCTCTTGTCTTGTAGCTGCTGCTGACACCTGTTCTCAGC 1223
QY 21 AspValHisGluValAlaValAlaGlyProAlaArgGluGlyCysHisAspAlaLys 40
DB 1222 AATGTACATGAGTGCCTATGACGCTAGGTTCTCGAGACAAAGGGCCCAAGATGCCAA 1163
QY 41 GlyValAlaAargValAlaAlaAlaAlaAlaAlaGlyProGlnGlnLeuValPro 60
DB 1162 GGCATCTCC--GTGGTCCGCCCCACCTCCGCTGCCCGCAGCAGAGGCTTCTGTCTCT 1106
QY 61 GlnArgLeuValGlnHisValAlaValLeuHisArgAspLeuAlaValGlnValTyr 80
DB 1105 CAGAGCCTTTTGTGAGCAGCAGCTCAGTACTGACACAGACACCTTGGGTGCAAGTCAAG 1046

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Alignment Scores:	
Pred. No.:	1,72e-06
Score:	166.00
Percent Similarity:	39.44%
Best Local Similarity:	29.97%
Query Match:	11.76%
DB:	1
Gaps:	16

QY	1	LeuAlaAspAspAlaAlaLeuLeuAlaLeuGly-----LeuAla	13
Db	2304	GTAGCGGATCCAGTGAATCTCCAGGCTGGCTCTGTCGATGTAGCGCGAGCTGTGA	2244
QY	14	AlaGlyAlaGlyLeuLeuAlaAspValHisGluValAlaValTyrAlaGlyProAlaIa	33
Db	2244	GCGGGGTGAGGCTTCACGCTTCTCTCGTGAATCTTCGTGACAGTGAAGTGGGGTGA	2185
QY	34	-----GluGlyCysHisAspAlaIaIaValGlyVal-----	42
Db	2184	CTGTGTGAAGGTGCCACAGGAGTCACTGATCTCTTGAACAGTGTGGCGCGCTTG	2125
QY	43	---AlaArgValAlaAlaAlaAlaAlaAlaAlaIaGlyProGlnGlnLeuLeuValProGln	61
Db	2124	GATGTGATGTCTGGTGTCTGGCCGCGCAGGCGGGGTCCAGTGGGGGTATATGCCCGGGA	2065

QY 62 ArgLeuLeuValGlnHisValAlaValLeuNH₂SAKAspSerLeuAlaValGlnValTrrPala 81
 Db 2064 GTTGGGGCTCTCCACAGAGTTGGCGCTCGCTCGCTCAGAGCGCTTGGCGGTG-----CTT 201
 QY 82 HisLeuAlaGlyGlnLeuGlyHisGGIyGlnGlnAArgIuHisIstLeuValGlnAlaAla 101
 Db 2013 CACCTTCTCGCTCAGCTC-----CTTCTTCTCGCTCCAGGAGAGA 1975
 QY 102 ValIstLeuLeuGlyAArgAspLeuLeuGlyValGlyAlaAlaLeuGlyValValAlaHisGlnLeu 121
 Db 1974 CTC-----GTCCCTCAGGACACTCCACAGGTGTCTCAC---CTG 1939
 QY 122 LeuAspLeuAlaLeuValHisIstLeuAlaValGlyValAlaValHisIstLeuValAlaAsp 141
 Db 1938 GTCATGTGGTAAGTACGTGCACGTCCGTCTTAG-----GCCATTTGGTTCTCTCTGGT 1885
 QY 142 AspGln-----GlyHisValHisValIstLeuLeuGlyPheValIstLeuGlu 155
 Db 1884 GAACAGCTGCTTACAGCGCTTCTGGGCGCGCTCCAGGTGCTACTGGC-----CTGAA 1831
 QY 156 AlaArgIstLeuGlyValGlyAspLeuLeuProGlnProLeuHisIstLeuLeuGlnGlyValAla 175
 Db 1830 GGTACACTCGGCGGAGACAGAACTGATGCGGTGATGTAACACTGTTGGCCGCTTGAA 1771
 QY 176 ValVal-----GlnThrGlnHisGlnAspGlnAsnValSerCysGluAspGlyValAla 193
 Db 1770 CAGGTGGGGCTCAGAGGTGAACACGCTGCTGCCGTTGCTGAAGTTGAAGGGGGGTGGAA 1711
 QY 194 ProHisGlyGlyGlnAArgVal-----ValAlaGlyAArgValGlu-----Asp 207
 Db 1710 GCCCAAGCGCGGAAAGCTGCCGCTCGACAGTTGCTGCCCGCTCTAAGTGGCGCTGAA 1651
 QY 208 ValGlnLeuValAspLeuAlaAla-----AspGlyValIstLeuAlaVal----- 222
 Db 1650 GTTGGCCGTGTTAATGGCGGCGCGCTCGATGCTGTGTGGAACTGCAGAGTTGGTGTGCT 1591
 QY 223 GluValIstLeuAspGlyAArgAArgValGlyValIstLeuGlnAlaIstLeuGlnGlnAlaAlaHis 242
 Db 1590 GCGGTAGCGAATGGACGCGCGGTAGCGGTGGCTCAGGGGCGGTATGTTACCGCGCAG 1531
 QY 243 AspGlyAArgLeuAlaHisIstLeuGlyAArgIstLeuGlnAspHisAlaIstLeuAlaValIstLeuGly 262
 Db 1530 GGTGTGATGTGGCGCGGCGGTGTGTGGCGCAGAGAT----- 1495
 QY 263 ArgAspThrGlnLeuAArgValAlaArgAlaHisIstLeuLeuAspHisArgGly 279
 Db 1494 -----GTCCCGCGCGGTGAACCGCGGCGCTTACACAGCTGCT 1456
 RESULT 6
 / Sequence 2, Application US/08459448A
 / Patent No. 5859336
 GENERAL INFORMATION:
 APPLICANT: Kozielec, Michael G.
 APPLICANT: Desai, Nalini M.
 APPLICANT: Lewis, Kelly S.
 APPLICANT: Kramer, Vance C.
 APPLICANT: Warren, Gregory W.
 APPLICANT: Eyola, Stephen V.
 APPLICANT: Crossland, Lytle D.
 APPLICANT: Wright, Martha S.
 APPLICANT: Merilin, Ellis J.
 APPLICANT: Launus, Karen L.
 APPLICANT: Rothstein, Steven J.
 APPLICANT: Bowman, Cindy G.
 APPLICANT: Dawson, John L.
 APPLICANT: Dunder, Erik M.
 APPLICANT: Pace, Gary M.
 APPLICANT: Suttie, Janet L.
 TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
 NUMBER OF SEQUENCES: 94
 TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
 CORRESPONDENCE ADDRESS:

1

RESULT 7
US-08-459-595A-2/C
; Sequence 2, Application US/08459595A
; Patent No. 6018104
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6018104artis Corporation

Alignment Scores:	1.72e-06	Length:	3468
Pred. No.:	166.00	Matches:	95
Score:	39.43%	Conservative:	30
Percent Similarity:	29.97%	Mismatches:	120
Best Local Similarity:	11.76%	Indels:	72
Query Match:	2	Gaps:	16
DB:			
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Qy	1	LeuAlaAspAspAlaAlaLeuLeuValLeuGly	-----LeuAla 13
		:::	
Db	2304	GTAGCGGATCAGGTAGATCTCAGGTCCTGGCTCGATGTAGCGCGCAGCTGGTA	2245
Qy	14	AlaGlyAlaGlyLeuLeuAlaAspValHisGluValAlaValTyrAlaGlyProAlaArg	33
Db	2444	CGGGTGTAGCCTTCAGCTTGCTCTCGTCGATCTTCTGGTACAGGTAGTGGGTAGCA	2185
Qy	34	-----GluGlyCysHisAspAlaValGlyVal	-----42
Db	2184	CTCGTCGAAGTGTCCCGCAGCGGTACAGTAGTCTCTTGAACACGTCTGTCCGCCCGCTG	2125
Qy	43	--AlaArgValAlaAlaAlaAlaAlaAlaGlyProGlnGlnLeuLeuValProGln	61
			:::
Db	2124	GATGTTGATGTCGGTGTCTGCCGCCAGCCGCGTCCAGCTGGCGGTTGATGCCCGGAA	2065
Qy	62	ArgLeuLeuValGlnHisValAlaValLeuHisArgAspLeuAlaValGlnValTrpAla	81

[illegible]

Db	2064	GTTCGGGCTTCGACGAGGTTGGCTGTGCTGCACGGCTTGCGCTC-----CTT	2014
Qy	82	HTsleuAlaAglyGlnleuGlyNHisGlyGlnIuArgAlaGlnHisIleuValGlnAlaA	101
Db	2013	CACCTTCTCGCTCAGCTC-----CTTCTTCTCGCTCAGGCAGA	1975
Qy	102	ValIleuLeuGlyArgAspIleuGluValGlyAlaAlaIleuGlyValValAlaHisGlnIleu	121
Db	1974	CTC-----GTGCTCAGGCACCTCCACAGAGTGTCTAC---CTG	1939
Qy	122	LeuAspIleuAlaIleuValHisIleuAlaValGluValAlaValThrIleuValAlaAlaAsp	141
Db	1938	GTTCGATGTGTGATGCTGCACGTGCGCTTCAG-----GCCAGTCTGGTGTCTCTGCT	1885
Qy	142	AspGln-----GlyHisValHisValIleuLeuGlyPheValIleuGlu	155
Db	1884	GAAACAGCTCTTCCACGGCTTCTGGGGGGCGCTCCAGCTGTACTCTGGC-----CTCGAA	1831
Qy	156	AlaArgIleuGlyValGluAspIleuLeuProGluProLeuHisIleuLeuGluGlyValAla	175
Db	1830	GGTCACCTCGGGCGGGACGAACCTGATGGCGTTCGATGATGACACTTGTGCGCGCTGTGA	1771
Qy	176	ValVal-----GlnThrGluHisGlnAspGluAsnValSerCysGluAspGlyGluAla	193
Db	1770	CACGTGGCGCTCAGGGGTGAACAACGCTGCTGCTGCTGTAAGTTGAAGGGGGGTGTGA	1711
Qy	194	ProHisGlyGlyGluArgVal-----ValAlaGlyArgValGlu-----Asp	207
Db	1710	GCCACCGGTGGGAAGCTGCGCTGTGCAGAGTTGCTGCCGCTCATGTGTGGCGCTGA	1651
Qy	208	ValGluLeuValAspIleuAlaA-----AspGlyValGluLeuAlaVal-----	222
Db	1650	GTTCCTCGGTGATGATGGGGCGGCGCTGCATGCTGTGTGGAACGTGACAGTTGCTGTCT	1591
Qy	223	GluValLeuAspGlyArgArgValGlyValIleuGluAlaAlaGlyGlnGluAlaArgHis	242
Db	1550	GGCTTACCGATGCCAGCCGGAGGCGTGGCTCAGGGGGCGGTGATGTTCACGCCGAG	1531
Qy	243	AspGlyArgIleuAlaHisIleuGlyArgAlaGluAspHisAlaIleuAlaValIleuGly	262
Db	1530	GGTGTGATGTGCGCGGGCTGTGTGCGGCAGAT-----	1495
Qy	263	ArgAspThrGlnLeuArgValAlaArgAlaHisIleuLeuAspHisArgGly	279
Db	1494	-----GTCCCGCGCGGTGAAGCCGGGGCCCTTCACACACGCTGT	1456

RESULT 8
 US-08-459-504B-2/c
 Sequence 2, Application US/08459504B
 Patent No. 6075185
 GENERAL INFORMATION:
 APPLICANT: Kozziel, Michael G.
 APPLICANT: Desai, Nalini M.
 APPLICANT: Lewis, Kelly S.
 APPLICANT: Kramer, Vance C.
 APPLICANT: Warren, Gregory W.
 APPLICANT: Ewola, Stephen V.
 APPLICANT: Crossland, Lyle D.
 APPLICANT: Wright, Martha S.
 APPLICANT: Merlin, Ellis J.
 APPLICANT: Lounis, Karen L.
 APPLICANT: Rothstein, Steven J.
 APPLICANT: Bowman, Cindy G.
 APPLICANT: Dawson, John L.
 APPLICANT: Dunder, Erik M.
 APPLICANT: Pace, Gary M.
 APPLICANT: Suttie, Janet L.
 TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
 NUMBER OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
 CORRESPONDENCE ADDRESSES: 94
 ADDRESSES: No. 6075185artis Corporation
 STREET: 3054 Cornwallis Road

us-09-709-103-1f4.p2n.rni

Tue Dec 31 15:27:52 2002

QY 208 ValGluLeuValAspLeuAlaAala-----AspGlyValGluLeuAlaVal----- 222
 Db 1650 GTTGCCTGTTGATGGCGCGCTCGATGCTGTGTGGAACTCGAGTTGGTGGTCT 1591
 QY 223 GluValLeuAspGlyArgValGlyValLeuGluAlaAalaGlyGluAlaAalaArgHis 242
 Db 1590 GCGGTAGCGGATCGCACCGGTTAGCGTGTCTCAGGGGGGGGTGTGTCTCACGCGCAG 1531
 QY 243 AspGlyArgLeuAlaHisLeuGlyArgAlaGluAspAspHisAlaAlaValLeuGly 262
 Db 1530 GGTCTGATCTGGCGGGCTGTGGTGGCGCGCAGGAT----- 1495
 QY 263 ArgAspThrGlnLeuArgValAlaAalaHisLeuLeuAspHisArgGly 279
 Db 1494 -----GTCCGCGCGGTGAAGCCGCGGCGCTTCACACGCTGGT 1456

RESULT 11

US-09-547-422-2/c

; Sequence 2, Application US/09547422

; Patent No. 6320100

; GENERAL INFORMATION:

; APPLICANT: Koziel, Michael G.

; Desai, Nalini M.

; Lewis, Kelly S.

; Kramer, Vance C.

; Warren, Gregory W.

; Evola, Stephen V.

; Crossland, Lyle D.

; Wright, Martha S.

; Merlin, Ellis J.

; Launis, Karen L.

; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

; INSECTICIDAL ACTIVITY IN MAIZE

; NUMBER OF SEQUENCES: 94

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 6320100artis Agribusiness Biotechnology Research, Inc.

; STREET: 3054 Cornwallis Road

; CITY: Research Triangle Park

; STATE: NC

; COUNTRY: USA

; ZIP: 27709

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/547,422

; FILING DATE: 11-Apr-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/459,595

; FILING DATE: 02-JUN-1995

; APPLICATION NUMBER: US 07/951,715

; FILING DATE: 25-SEP-1992

; APPLICATION NUMBER: US 07/772,027

; FILING DATE: 04-OCT-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Meigs, J. Timothy

; REGISTRATION NUMBER: 38,241

; REFERENCE/POCKET NUMBER: S-18805H

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (919)541-8587

; TELEFAX: (919)541-8689

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3468 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: other nucleic acid

; DESCRIPTION: /desc = "Synthetic DNA"

; HYPOTHETICAL: NO

STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "Synthetic DNA"
 HYPOTHETICAL: NO
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1..3468
 OTHER INFORMATION: /product= "Full-length pure maize
 OTHER INFORMATION: optimized synthetic Bt"
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..3465
 US-09-053-549-3

Alignment Scores:
 Pred. No.: 1.72e-06 Length: 3468
 Score: 166.00 Matches: 95
 Percent Similarity: 39.43% Conservative: 30
 Best Local Similarity: 29.97% Mismatches: 120
 Query Match: 11.76% Indels: 72
 Gaps: 16
 DB:

US-09-709-103-1f4 (1-282) x US-09-053-549-3 (1-3468)

QY 1 LeuAlaAspAlaAlaLeuLeuValLeuGly-----LeuAla 13
 Db 2304 GTACGGATCAGGTAGATCTCCAGGTCCTCGCTGCTCGATGTAGCCGCGAGCTGTA 2245
 QY 14 AlaGlyAlaGlyLeuLeuAlaAspValHisGluValAlaValTyraAlaGlyProAlaArg 33
 Db 2244 GCGGGTGTAGCCCTTCAGTGTCTCTGTCGATCTTCTGTGTACAGGTAGTGGGTAGCA 2185
 QY 34 -----GluGlyCysHisAspAlaLysGlyVal----- 42
 Db 2184 CTCGTGGAAGTGGCCAGCAGGTCACGTAGTCTCTCTGTAACACGTCGTCGCGCCCTG 2125
 QY 43 ---AlaArgValAlaAlaAlaAlaAlaAlaGlyProGlnGlnLeuLeuValProGln 61
 Db 2124 GATGTGTATGTCGTCTGCGCCGCGCCAGCCGCTCCAGCTGGCGGTGTATGTCGCGGAA 2065
 QY 62 ArgLeuLeuValGlnHisValAlaValLeuHisArgAspLeuAlaValGlnValTpAla 81
 Db 2064 GTTGGGTCCTCCAGCAGGTTCGCTGCTGCTCAGCGCTTGTGCTG-----CTT 2014
 QY 82 HisLeuAlaGlyGlnLeuGlyHisGlyGluGluArgAlaGluHisLeuValGlnAlaAla 101
 Db 2013 CACCTTCTCGCTCAGCTC-----CTTCTCTCTCAGCAGGAGAA 1975
 QY 102 ValLeuLeuGlyArgAspLeuGluValGlyAlaAlaLeuGlyValValAlaHisGlnLeu 121
 Db 1974 CTC-----GTCCGTCAGGCACTCCACAGGTTCCTCAC-----CTG 1939
 QY 122 LeuAspLeuAlaLeuValHisLeuAlaValGluValAlaValThrLeuValAlaAlaAsp 141
 Db 1938 GTCGATGTGTAGTCGCTCAGCTGCTCTCTAG-----GCCGATCTGGTGTCTGCTGT 1885
 QY 142 AspGln-----GlyHisValHisValLeuLeuGlyPheValLeuGlu 155
 Db 1884 GAACAGTCGCTTACGGCCCTTCTGGGGCGGCTCCAGGTCTGTA-----CTCGAA 1831
 QY 156 AlaArgLeuGlyValGluAspLeuLeuProLeuHisLeuLeuGlyValAla 175
 Db 1830 GGTACCTCGCGCGGCGCAACTCGATGCGGTGATGACCTCGTCTGCCGCTGTGAA 1771
 QY 176 ValVal-----GlnThrGluHisGlnAspGluAsnValserCysGluAspGlyGluAla 193
 Db 1770 CACGTGGCGGTGAGGTGACACGCTGCTGCCGCTTCTGAACTTGAAGGGGTGTGAA 1711
 QY 194 ProHisGlyGlyGluArgVal-----ValAlaGlyArgValGlu-----Asp 207
 Db 1710 GCCCAGCGTGGGAAGCTGCGCGCTCTGTCAGGTTGCTGCCGCTGCTATGTTGGCGCTGAA 1651


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1      FEATURE:
2      NAME/KEY:  misc feature
3      LOCATION:  1..3468
4      OTHER INFORMATION:  /product= "full-length pure maized
5                          optimized synthetic bc"
6                          /note= "disclosed in Figure 3 as syn117.mze"
7
8      SEQUENCE DESCRIPTION:  SEQ ID NO: 2:
9      US-09-547-422-2

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Pred. No.:	1.72e-06	Length:	3466
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Query Match:	11.76%	Indels:	72
DB:	4	Gaps:	16

US-09-103-1F4 (1-282) X US-09-547-422-2 (1-3468)

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Db	2304	GTAGCGGATCAGGTATGATCTCCAGGCTCCGGCTGCTCCATATGACCGGCGGACGCTGGTA	-----	2245	
Qy	14	AlaGValAlaGValLeuLeuAlaAspValHisGluValAlaValTyrAlaGluProAlaArg	-----	33	
Db	2244	GCGGGGTGTAGGCGCTTACAGCTTGGCTCTGCATCTTGGTACAGGATGGGGGAGACA	-----	2185	
Qy	34	-----GluGluGluHisAspAlaLeuGluVal	-----	42	
Db	2184	CTGCTGAAAGGTGGCCACAGGCTCAGCTAACTTCTCTTAAACAGTCTGTCGCCCTGG	-----	2125	
Qy	43	-----AlaAspValAlaAlaAlaAlaAlaAlaAlaGluProGlnLeuLeuValProGln	-----	61	
Db	2124	GATGGTATGTGTGGTGTGGTGGCGGCGGACGCGGCTCAGCTGGGTTATGCCCGGAA	-----	2055	
Qy	62	AspLeuLeuValGlnHisValAlaValLeuHisAspAspLeuAlaValGlnValTyrAla	-----	81	
Db	2064	GTTGGGGTCTCCAGACAGTTCGGCTGGCTGTCTCAGGCTGTGGCGCTG	-----	CTT	2014
Qy	82	HisLeuAlaGluGlnLeuGluHisGluGluGluAlaGluHisGluValGlnAlaAla	-----	101	
Db	2013	CACCTTCTCCGCTCAGCTC	-----	CTTCTTCTGCTCCAGGCAAA	1975
Qy	102	ValLeuLeuGluArgAspLeuGluValGluValAlaLeuGluValValAlaHisGlnLeu	-----	121	
Db	1974	CTC-----GTGGCTACGACCTCCACAGGTTGCTCAC	-----	CTG	1939
Qy	122	LeuAspLeuAlaLeuValHisLeuAlaValAlaValAlaValThrLeuValAlaAlaAsp	-----	141	
Db	1938	GTCGATGTGTAATCGGTCAACGTCGCTTCAAC	-----	GCCGATCTGTGGTGGCTGGT	1885
Qy	142	AspGln-----GluHisValHisValLeuLeuGluPheValLeuGlu	-----	155	
Db	1884	GAAACAGCTCTTACCGGCTTCTGGGCGGCGCTCCAGGCTGATCTGGC	-----	CTGAA	1831
Qy	156	AlaArgLeuGluValGluAspLeuLeuProGlnProLeuHisLeuLeuGluValAla	-----	175	
Db	1830	GGTCACTCGCGGCGGACCAACTCATGCGGTGATGATCACTCTGTTGCGCGTGTGAA	-----	1771	
Qy	176	ValVal-----GlnThrGlnHisGlnAspGlnAsnValSerCysGluAspGluValAla	-----	193	
Db	1770	CACGTGGCGCTCAGAGGTAAACAGCTGCTGCCGTGTGAAAGTTGAAGGGGTGGTAA	-----	1711	
Qy	194	ProHisGluGluGlnArgVal-----ValAlaGluArgValGlu-----Asp	-----	207	
Db	1710	GCCACAGGTGGGAAAGCTCCGCTGTGACAGTGTGCTGCCGCTGTCAATGTGTGGCGCTGAA	-----	1651	
Qy	208	ValGluLeuValAspLeuAlaAla-----AspGluValGluLeuAlaVal-----	-----	222	
Db	1650	GTTGGCTGTGTATGATGGCGGCGCTGCATCTGTGTGGAACTGCAGGTTGGTGGTCT	-----	1591	
Qy	223	GluValLeuAspGluArgArgValGluValLeuGluAlaAlaGluGluGluAlaArgHis	-----	242	

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Db      1590  GGCGTACGGATCGCAGCCGGGTACCGCTGCCTCAGGGGGGCGGTATGTCACGCCGAC 1533
Oy      243  AspcIyAArgLeuAlaHisLeuGlyAArgAlaGluAspAspHisAlaIleAlaValLeuGly 262
Db      1530  GGTCGTGATCTGGCGCGGCGTGTGTCGCGCGCAGAT-----1495
Oy      263  ArgAspThrClnLeuAArgValAlaAlaArgAlaHisLeuLeuAspHisArgGly 279
Db      1494  -----GTCGCGCGCGGTGAAGCCGGGGCGCTTTCACCAACCGCTGT 1456

RESULT 12
US-07-951-715A-4/c
Sequence 4, Application US/07951715A
Patent No. 5625136
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Wyola, Stephen V.
APPLICANT: Crossland, Lytle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Lunnis, Karen L.
APPLICANT: Rothenstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/951,715A
FILING DATE: 25-SEP-1992
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8615
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3468 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNA"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..3468

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 243 AACGCTAAGCGCAGGGGGCGGTGATGTTACGCCGAC 1531

OTHER INFORMATION

1495

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; OTHER INFORMATION: maize optimized"
; OTHER INFORMATION: /note="Disclosed in Figure 3 as synfl.mod. This sequence
; OTHER INFORMATION: identical to flsynbt.fin as disclosed in Figure 1."
; OTHER INFORMATION:
US-08-459-595A-4

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Alignment Scores:	8.06e-06	Length:	3468
Pred. No.:	159.00	Matches:	94
Score:	29.12%	Conservative:	30
Percent Similarity:	29.85%	Mismatches:	121
Best Local Similarity:	11.27%	Indels:	72
Query Match:	3	Gaps:	16
DB:			

US-09-709-103-1F4 (1-282) x US-08-459-595A-4 (1-3468)

QY	1	LeuAlaAspAlaAlaLeuLeuValLeuGly	-----LeuAla 13
Db	2304	GTACGGATCAGGTAGATCTCCAGGTCTGGCTGCTCCGATGTAGCGCGCAGCTGGTA	2245
QY	14	AlaGlyAlaGlyLeuLeuAlaAspValHisGluValAlaValTyAlaGlyProAlaArg 33	
Db	2244	GCGGGTGTAGCCCTCAGTTCTCTGCTCGATCTTCTGCTACAGGTAGTGGGTAGCA	2185
QY	34	-----GluGlyCysHisAspAlaValGlyVal-----	42
Db	2184	CTGCTCGAAGGTCCCGCAGGAGTCCAGTGTCTCTTGAACACGCTGCTGCGCGCCCTG	2125
QY	43	---AlaArgValAlaAlaAlaAlaAlaAlaAlaGlyProGlnGlnLeuLeuValProGln 61	
Db	2124	GATGGTATGTTCGGTGTCTGCCGCCGAGCGCGGTCCAGCTGGCGGTGATGCCGCGAA	2065
QY	62	ArgLeuLeuValGlnHisValAlaValLeuHisArgAspLeuAlaValGlnValTrpAla 81	
Db	2064	GTTGGGTCTCTGCAGCAGGTTGCGTCTGCTCAGCGCGCTTGGCGTG-----CTT	2014
QY	82	HisLeuAlaGlyGlnLeuGlyHisGlyGluGluArgAlaGluHisLeuValGlnAlaAla 101	
Db	2013	CACCTTCTCGCTCAGCTC-----CTTCTCTGCTCCAGCGCAGAA 1975	
QY	102	ValLeuLeuGlyArgAspLeuGluValGlyAlaAlaLeuGlyValValAlaHisGlnLeu 121	
Db	1974	CTC-----GTGCTCAGGCACCTCCACAGGTTGCTCAC---CTG 1939	
QY	122	LeuAspLeuAlaLeuValHisLeuAlaValGluValAlaValThrLeuValAlaAlaAsp 141	
Db	1938	ATCGATGTGGTAGTGCCTCAGCTCGCTTCACAG-----GCCATCTGTTGCTGCTGGT	1885
QY	142	AspGln-----GlyHisValHisValLeuLeuGlyPheValLeuGlu 155	
Db	1884	GAACAGCTCGTTACGGCCTTCAGCCCTCTCCAGTCTGTACTCGC-----CTCGAA 1831	
QY	156	AlaArgLeuGlyValGluAspLeuLeuProGluProLeuHisLeuLeuGluGlyValAla 175	
Db	1830	GGTCACTCGCGGCGACGAACTCGATCGGTCGATGATACCTCTGTTCCCTGTTGAA 1711	
QY	176	ValVal-----GlnThrGluHisGlnAspGluAsnValSerCysGluAspGlyGluAla 193	
Db	1770	CACGTGGCGCTCAGGTTGAACGCTGCTGCCCTGCTGAACTTGAAGGGGTGGTGA 1711	
QY	194	ProHisGlyGlyGluArgVal-----ValAlaGlyArgValGlu-----Asp 207	
Db	1710	GCCACGGTCCGGAAGCTCCCGCTCTGCAGGTTGCTGCCCTGCTCATGTGGCGCTGA 1651	
QY	208	ValGluLeuValAspLeuAlaAla-----AspGlyValGluLeuAlaVal-----	222
Db	1650	GTTGCCCTGGTTGATGGGCGCGCGCTCGATGCTGTGTGGAACTCGACGGTTGGTGGTGT	1591
QY	223	GluValLeuAspGlyArgArgValGlyValLeuGluAlaAlaGlyGluGluAlaArgHis 242	
Db	1590	GGCGTACGGATTCGGACCGCGTAGCGTGGCTCAGGGGGCGGTGATGTTCCGCGCAG 1531	
QY	243	AspGlyArgLeuAlaHisLeuGlyArgAlaGluAspHisAlaIleAlaValLeuGly 262	

	Db	1530	GTTGCTGAATCGCCGGGCCTGGTCGCCGCAGGAT-----
	Qy	263	ArgAspThr-GlnLeuArgValAlaAargAlaHisLeuLeuASPHisArgGly 279 ::: GTCAACCGCAGCCCCGGCCCATTACCACGCGTGT 1456

RESULT 15

US-08-459-504B-4/C
Sequence 4, Application US/08459504B
Patent No. 6075185
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6075185artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,504B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: GCG1577/CIP/DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3468 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNA"
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..3468


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; OTHER INFORMATION: /product= "Full length synthetic
; OTHER INFORMATION: maize optimized"
; OTHER INFORMATION: /note= "Disclosed in Figure 3 as synfl.mod. This sequence
; OTHER INFORMATION: identical to f1sybvt.fin as disclosed in Figure 1."
US-00-459-504B-4

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Alignment Scores:
Pred No.

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Fred. NO.:      8.06e-06      Length:      3466
Score:          159.00        Matches:      90
Percent Similarity: 39.12%    Conservative: 34
Best Local Similarity: 29.65% Mismatches:    121
Query Match:    11.27%       Indels:       72
DB:             3            Gaps:       16

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US-09-103-1H4 (1-282) X US-08-459-504B-4 (1-3468)

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Oy      1 LeuAlaAspAspAlaAlaLeuLeuValLeuGly-----LeuAla 13
Db      2304 GTAGCGGAGTCAAGTGAATGATCCAGAGCTCTGGCTGTCTCCATGATGAGCCGCGAGCTGTGA 2245
Oy      14 AlaGlyValaGlyLeuLeuAlaAspValaHnIsglyValaAlaValTyrAlaGlyProAlaAsp 33
Db      2244 GCGGGTGTAGGCGCTTCAGATTGTCTGTCCATCTTGTGTGAACGTAAGGTGGGTAGCA 2185
Oy      34 -----GlnGlyCysHnAspAlaLeuGlyVal-----42
Db      2184 CTCTGTGAAGGAGGCCAGGCGAGGATCAGATGTTCTCTTGAACAGCTGTGCGCGCGCTG 2125
Oy      43 ---AlaArgValaAlaAlaAlaAlaAlaAlaGlyProAlnIleuLeuValProAln 61
Db      2124 GATGGTGAATGTGGTGTGGTGGCGGCCGAGCGAGCTCCAGTGGCGGGTATATGCCAGGA 2065S
Oy      62 ArgLeuLeuValGlnHnIsvAlaValaValLeuHnIAspAspLeuAlaValGlnValTyrAla 81
Db      2064 GTTGGGCTCTGCGACAGAGTTGGCGGCTGTGGTCTGACAGCGCTTGGCGGTG-----CTT 2014
Oy      82 HnIsvAlaGlyGlnLeuGlnHnIsglyGlnGlnArgAlaGlnHnIsvLeuValGlnAlaAla 101
Db      2013 CACCTTCTCGCTACAGCTC-----CTTCTTCTGCTCCAGGACAGA 1975
Oy      102 ValLeuLeuGlyArgAspLeuGlnValaGlyAlaAlaLeuGlyValaValaHnIsglnLeu 121
Db      1974 CTC-----GTGCGTCAAGGACCTCCACAGATTTGCTCAC---CTG 1939
Oy      122 LeuAspLeuAlaLeuValHnIsvAlaValaGlnValaAlaValThLeuValaAlaAsp 141
Db      1938 ATCATGTGTGATGTCGCTCAGCTGTGGTTCAC-----GCCATCTGTGTTGCTGTGTGT 1885
Oy      142 AspGln-----GlnHnIsvAlaHnIsvAlaLeuLeuGlyPheValLeuGln 155
Db      1884 GAAACAAGCTGTTCAACGGCTTTCAGACCCCTTCACAGTGTGTACTGGC-----CTGAA 1831
Oy      156 AlaArgLeuGlyValaGlnAspLeuLeuProGlnProLeuHnIsvLeuLeuGlnGlyValaAla 175
Db      1830 GGTCACTCGCGCGGCGACGAACCTGATGGCGTGAATGAACCTGTTGGCGCGGTGAA 1771
Oy      176 ValVal-----GlnThrGlnHnIsglnAspGlnAsnValserCysGlnAspGlyVala 193
Db      1770 CAGCTGGGCGCTCAGGAGTGAACACGCTGCTGCCCTGTCTGAAGTTGAAGGGGGGTGAA 1711
Oy      194 ProHnIsglyLeuGlnArgVal-----ValaAlaGlyArgValGln-----Asp 207
Db      1710 GCCCAAGCGTCCGAAACCTCCGCTCTGACAGTTTCTGCGCGCTGCTCAATGATGGCGCGA 1651
Oy      208 ValGlnLeuValAspLeuAlaAla-----AspGlyValaGlnLeuAlaVala-----222
Db      1650 GTTGGCTGTGATGGGCGCGCGCTCCATGCTGTGTGTGGAACCTGCAAGTTGGTGTGCT 1591
Oy      223 GlnValLeuAspGlyArgArgValaGlyValaLeuGlnAlaAlaGlyGlnGlnAlaArgHnIsv 242
Db      1590 GGGGTAGCGGATGCCAGCCGCTACCGCTGCTCAGGGGGGCGGTATGTTCACGGCGAG 1531
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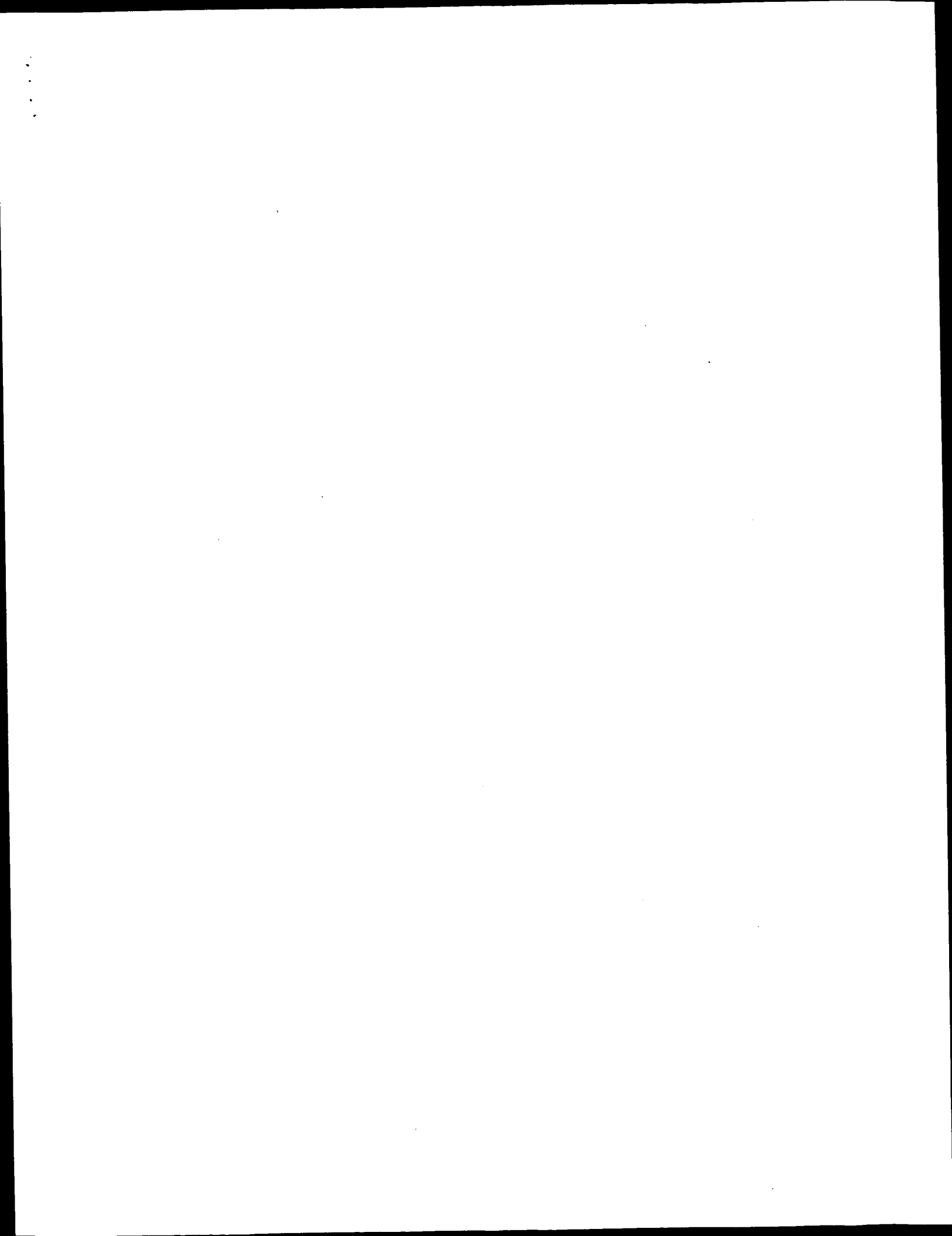
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Search completed: December 30, 2002, 18:05:59
Job time : 93 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on:

December 30, 2002, 15:42:56 / Search time 2179 Seconds
(without alignments)
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Total number of hits satisfying chosen parameters: 32308132

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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12	893	63.3	1160	14	BM805574
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VERSION
BM919341.1 GI:19369720
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1035)
NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found at: <http://www.imgc.org/Consortium/LLNL/>

round image:
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FEATURES
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/lab_host="DH10B"
/note="organ: pooled pancreas and spleen; Vector:
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male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH MGC Library."
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others

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BASE COUNT
ORIGIN

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Score:	1194.00	Matches: 245
Percent Similarity:	92.94%	Conservative: 5
Best Local Similarity:	91.08%	Mismatches: 17
Query Match:	84.62%	Indels: 3
DB:	14	Gaps: 2

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Db	992	GCGGGATGTTCATAAAGTGCCCTGTGTTCGCTGGGCCCGCCGC -CGAAAGGTT 934
QY	36	CysHisASP---AlalysGlyVallalaArg----ValAlaAlaAlaAlaAlaAlaGly 53
Db	933	TGCCACGAATGGCCAAAGGCGTGC GCCGGGTTCGCCCGCCGCCGCGCTTGCCGCG 874
QY	54	ProGlnGlnLeuLeuValProGlnArgLeuLeuValGlnHisValAlaValLeuHisArg 73
Db	873	CCGCAGCAGGTTTTCTGTTCGCACGCTTCTTGTGCAGCACGTCCGCACTACTCCACCGA 814
QY	74	AspLeuAlaValGlnValTrpAlaHisLeuAlaGlyGlnLeuGlyHisGlyVgluGluArg 93
Db	813	GACCTTGGCGTGCAGGTCTCGGGTCACTCGCTGGGCACGCTTGGCATGGCCNAGAGCGC 754
QY	94	AlaGluHisLeuValGlnAlaAlaValLeuLeuGlyArgAspLeuGluValGlyAlaAla 113
Db	753	CGGGHACATCTGGTTCAGGGTGCTGTCTTCTTGGCCGAGATCTCGAAAGTAGGCCACGC 694
QY	114	LeuGlyValValAlaHisGlnLeuLeuAspLeuAlaValHisLeuAlaValGluVal 133
Db	693	CTNGGGGTGTCGCGCCACCAGCTGCTCGATCTTCGCTGTGTCCACCTCGCGTAGAAGTC 634
QY	134	AlaValThrLeuValAlaAlaAspAspGlnGlyHisValHisValLeuLeuGlyPheVal 153
Db	633	GGCGTCA C CCTTGTTCGCCAGATGACAGGGGGCACGTCCACAGTCTCTCTTGGTTTTGTT 574
QY	154	LeuGluAlaArgLeuGlyValGluAspLeuLeuProGluProLeuHisLeuLeuGluGly 173
Db	573	CTTTAGGCCAAGACTTGGTGTTCGAGATCTGCTGCTCGAGCCGCTGCACCTCTCGAAGA 514
Db		

QY	174	ValAlaValValGlnThrGluHisGlnAspGluAsnValSerCysGluAspGlyGluAla	190
Db	513	GTCCGGTGTTCAGACTGACACACACAGGATGAAACCTCTCTGTAGGATGGAGGCG	454
QY	194	ProHisGlyGlyGluArgValValAlaGlyArgValGluAspValGluLeuValAspLeu	213
Db	453	CGCATGGCGGGAAACGGGTGGTTCGCGAGCTGTGCAGGATGTCGAGCTGTGAGACCTC	394
QY	214	AlaAlaAspGlyValGluLeuAlaValGluValLeuAspGlyArgArgValGlyValLeu	233
Db	393	GC CGCGGATGGAGTAGAACTTGC GGTGGAACTCTCTCGATGTGTAGCGCTGTAGCGCTCTC	334
QY	234	GluAlaAlaGlyGluGluAlaArgHisAspGlyArgLeuAlaHisLeuGlyArgAlaGlu	253
Db	333	GAAGCGCGGTGAGGAAGCGCACAGATGGCCGCTCTTGGCCACCTTGGACGAGCCGAG	274
QY	254	AspAspHisAlaIleAlaValLeuGlyArgAspThrGlnLeuArgValAlaAlaArgAlaHis	273
Db	273	GATGACCATGGCATAGACAGTTCTTGGCCCGGGATATCTAGCTCCGAGTCGCTCGGCACAT	214
QY	274	LeuLeuAspHisArgGlyGlnPheHis	282

[illegible]

BM543472
BM543472.1
EST.

SOURCE human.

SOURCE: NCBI
 ORGANISM: Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 962)
 REFERENCE
 AUTHORS: NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE: National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL: Unpublished (1999)
 COMMENT: Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Invitrogen
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA sequencing by: Agencourt Bioscience Corporation
 Clon distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LRAM12719 row: d column: 11
 High quality sequence start: 18
 High quality sequence stop: 692.

FEATURES source

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/clone="IMAGE:5726554"
/clone_lib="NIH MGC 124"
/tissue_type="hippocampus"
/lab_host="DH10B"
/note="organ: brain; Vector: pCMV-SPORT6; Site_1: EcorV
(destroyed); Site_2: NotI; RNA source male hippocampus,
age 27. Library is oligo-dT primed and directionally
cloned (EcorV site is destroyed upon cloning). Average
insert size 1.4 kb, insert size range 0.9-4 kb. Library
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 012."

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	BASE COUNT	- 185 a	363 c	tracking code 012."	141 t	1 others
ORIGIN						

Alignment Scores:	5.68e-99	962
Pred. No.:		Length:

us-09-709-103-1f4.p2n.rst

Tue Dec 31 15:27:53 2002

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Db 612 CGTCCAGTCTCTGTTGTTTCTTGGGCAAGACTTGGTGTGGAGATCTGCTGCC 553
Qy 165 oGluProLeuHisLeuLeuGluGlyValAlaValAlaValGlnThrGluHisGlnAspGluAs 185
Db 552 TGAGCCGCTGCACCTCTCGAAGGAGTACCGTTGTCAGACTGAACACACAGGATGAAA 493
Qy 185 nValSerCysGluAspGlyGluAlaProHisGlyGlyGluArgValAlaGlyArgVa 205
Db 492 CGTCTCTGAGGATGGAGAGGCGCCGATGCGCGGGAACGGGTGTTGCCGGACGTGT 433
Qy 205 lGluAspValGluLeuValAspLeuAlaAspGlyValGluLeuAlaValGluValLe 225
Db 432 CGAGGATGTCAGCTGTGTAGACCTCGCGCGGATGGAGTGAACCTTGGCGTGAAGTCT 373
Qy 225 uAspGlyArgValGlyValLeuGluAlaAlaGlyGluGluAlaAArgHisAspGlyAr 245
Db 372 CGATGTTAGCGTGTAGCGCTCTCGAAGCGCGCGTGGAGAGCGGACACAGATGCCG 313
Qy 245 lGluAlaHisLeuGlyArgAlaGluAspAspHisAlaAlaValLeuGlyArgAspTh 265
Db 312 TCTTGCACCTTGGACGAGCGAGGATGACATGCGATACAGTCTTGGCGGGATAC 253
Qy 265 rGlnLeuArgValAlaAArgAlaHisLeuAspHisArgGlyGlnPheHis 282
Db 252 TCAGCTCCGAGTGGCTCGGGGCACATCTTCTTGATCATCGCGCCAGTTTCAT 201

RESULT 4
AW028127/c 742 bp mRNA linear EST 27-OCT-1999
LOCUS wv26c07.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2530668 3'
DEFINITION similar to TR_035626 035626 RAS, DEXAMETHASONE-INDUCED 1 ;, mRNA
sequence.
ACCESSION AW028127
VERSION AW028127.1 GI:5886883
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 742)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: -400P from Gibco
High quality sequence stop: 445.
Location/Qualifiers
1. 742
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2530668"
/clone_lib="NCI CGAP_Kid11"
/lab_host="pH105"
/note="Organ: kidney; Vector: pTVT3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
plasmid DNA from the normalized library NCI CGAP_Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneID9 132376-132391, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.

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BASE COUNT 149 a 260 c 208 g 122 t 3 others
ORIGIN
Alignment Scores: 3 72e-97 Length: 742
Pred. No.: 1111.00 Matches: 225
Score: 96.19% Conservative: 2
Percent Similarity: 95.34% Mismatches: 9
Best Local Similarity: 78.74% Indels: 1
Query Match: 10 Gaps: 0
DB:
US-09-709-103-1f4 (1-282) x AW028127 (1-742)
Qy 47 AlaAlaAlaAlaAlaAlaGlyProGlnGlnLeuValProGlnArgLeuLeuValGln 66
Db 741 GCACGACCCGCGCTGC -GGACCGCACAGCTTCTGTTTCGCGCAGCGCTTCTGTGCAGG 683
Qy 67 HisValAlaValLeuHisArgAspLeuAlaValGlnValTrpAlaHisLeuAlaGlyGln 86
Db 682 CACGTCAGGTACTGACACAGAGACCTTGGCGTGCAGCTCTGGCTCATCTCGCTGGGCAG 623
Qy 87 LeuGlyHisGlyGluArgAlaGluHisLeuValGlnAlaAlaValLeuLeuGlyArg 106
Db 622 CTTGGCCATGGCGAAGAGCGCGCGAACATCTGCTCGAGCTGCTGTTCTTCTTGGCNGA 563
Qy 107 AspLeuGluValGlyAlaAlaLeuGlyValAlaHisGlnLeuLeuAspLeuAlaLeu 126
Db 562 GATCTCGAAGTGAAGCGGCGCGCTGGGGTCTGTCGCCACACAGCTGCTCGATCTCGCGCTG 503
Qy 127 ValHisLeuAlaValGluValAlaValThrLeuValAlaAlaAlaAspAspGlnGlyHisVal 146
Db 502 GTCCACCTCGCGGTAGAGTCCCGTTCACCTTGTTCGCCAGATGACACAGGGGCAGTCTC 443
Qy 147 HisValLeuLeuGlyPheValLeuGluAlaArgLeuGlyValGluAspLeuLeuProGlu 166
Db 442 CACGTCTCTTGGTTTGTCTTGAGGCAAGACTTGGTGTGAGGATCTGCTGCTGAG 383
Qy 167 ProLeuHisLeuLeuGlyValAlaValValGlnThrGluHisGlnAspGluAsnVal 186
Db 382 CCGCTGCACCTCTCGAAGGAGTCCCGTTCGAGACTGAACACACAGGATGAACAGTCTC 323
Qy 187 SerCysGluAspGlyGluAlaProHisGlyGlyGluArgValAlaAlaGlyArgValGlu 206
Db 322 TCTGTGAGGTGAGAGAGCGCGCATGCGGGGAACGGTGTGCGCGAGTGTGCGAG 263
Qy 207 AspValGluLeuValAspLeuAlaAlaAspGlyValGluLeuAlaValGluValLeuAsp 226
Db 262 GATGTCGAGCTGGTAGACCTCGCGCGGATGGAGTAGAACCTTGGCGTGAAGTCTCTCAT 203
Qy 227 GlyArgArgValGlyValLeuGluAlaAlaGlyGluAlaAlaArgHisAspGlyArgLeu 246
Db 202 GGTAGGCGTGTAGCGTCTTCGAGCGCGAGGTGAGGAAGCGCGACGATGGCGCTCTT 143
Qy 247 AlaHisLeuGlyArgAlaGluAspAspHisAlaAlaValLeuGlyArgAspThrGln 266
Db 142 GCCCACCTTGGACGAGCGCGAGGATGACCATGCGATAGCAGTCTTGGCGCGGATACTCAG 83
Qy 267 LeuArgValAlaAlaArgAlaHisLeuLeuAspHisArgGlyGlnPheHis 282
Db 82 CTCGAGTCTGCTCGGCGACATCTTCTTGATCATTCGCGCGCAGTTTCAT 35

RESULT 5
AL533318/c AL533318 965 bp mRNA linear EST 13-FEB-2001
LOCUS AL533318 LTI_FL015 Brnl Homo sapiens cDNA clone CS0DN003YJ19 5
DEFINITION prime, mRNA sequence.
ACCESSION AL533318
VERSION AL533318.1 GI:12796811
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Source	Features
1	genoscope.cns.fr, web : www.genoscope.cns.fr
2	Location/Qualifiers

Source

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DN003x19"
/clone_lib="LTI_FLO15_Brn1"
/sex="male"
/tissue_type="adult brain"
/note="Vector: pCMVSPORT 6; Site 1: NotI, 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with NotI and
cloned into the NotI and EcoRV sites of the pCMVSPORT 6
vector. Library was constructed by Life Technologies.
Contact : Peng Liang Life Technologies, a division of
Invitrogen 9800 Medical Center Drive Rockville, Maryland
20850, USA Fax : (1) 301 610 8371 Email :
tliang@lifetech.com URL :
http://fulllength.invitrogen.com"

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Alignment Scores:	
Pred. No.:	9,65e-96
Score:	1098.00
Percent Similarity:	92.40%
Best Local Similarity:	92.40%
Query Match:	77.83%
DB:	9
Length:	965
Matches:	231
Conservative:	0
Mismatches:	17
Indels:	4
Gaps:	4

00 05-103-1F4 (1-282) X AL533318 (1-965)

[illegible]

Db	459	GGCGC-CATGGCGGGGAAACGGCTGTTGTCGGACGTCGTGAGANTGTCAGCTGGAGAC	401
Qy	213	LeuAlaAlaaspGlyValGluLeuAlaValGluValLeuaspGlyArgArgValGlyVal	232
Db	400	CTCGCCCGCGAATGAGTAGAATCTTCGCGTAGAGTCTCGATGTAGGCGGTAGAGCTC	341
Qy	223	LeuGluAlaAlaGlyGluGluAlaArgHisaspGlyArgLeuAlaHisLeuGlyArgVala	252
Db	340	CTCGAAGGCGCGGTGGAGAGCGACACGATGGCGGCTTGGCCACCTTGGAGAGCC	281
Qy	253	GluaspAspHisAlaAlaLeuAlaLeuGlyArgaspThrGluLeuArgValAlaArgVala	272
Db	280	GAGATGACCATGAGTAGCAGTCTTTCGCCGGGATCTACGCTCCGAGTGGCTGGGCA	221
Qy	273	HisLeuLeuaspHisArgGlyGluPheHis	282
Db	220	CATCTCTTGATCATCGCGCCAGTTTCAT	191

[illegible]

ORGANISM	<i>Homo sapiens</i>
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo; 1 (bases 1 to 958)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
JOURNAL	
COMMENT	Contact: Robert Strassburg ph.D

FEATURES
SOURCE

High quality sequence stop: 514.
Location/Qualifiers
1. .958

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/sex="male"
/tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
/notes="Vector: PCMV-SPORT6 (Life Technologies) ; Site 1:
NotI ; Site 2 : SalI ; cDNA made by oligo-dT priming.
5'-TGACCCAGCGTCGCG-3' and
5'-GACTAGTTCCTAATCGCGAGCGGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.9 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) ; available through Life
Technologies."
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Alignment Scores:				
Orig	185 a	339 c	275 g	159 t
Length:	3,336-94			956
Pred. No.:	1052.00			Matches:
Score:	83.75%			Conservative: 4
Percent Similarity:				23

[illegible]


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5', mRNA sequence.
BM543630
VERSION BM543630.1 GI:18774186
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1023)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12719 row: m column: 05
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            /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: EcoRV
            (destroyed); Site 2: NotI: RNA source male hippocampus,
            age 27. Library is oligo-dT primed and directionally
            cloned (EcoRV site is destroyed upon cloning). Average
            insert size 1.4 kb, insert size range 0.9-4 kb. Library is
            normalized and enriched for full-length clones and was
            constructed by C. Gruber (Invitrogen). Research Genetics
            tracking code 012."
            196 a 378 c 281 g 168 t
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ORIGIN
Alignment Scores:
Pred. No.: 9,6e-87 Length: 1023
Score: 1005.00 Matches: 206
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Best Local Similarity: 97.63% Mismatches: 3
Query Match: 71.23% Indels: 3
DB: 13 Gaps: 0
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Qy 75 LeuAlaValGlnValTrpAlaHisLeuAla--GlyGlnLeuGlyHisGlyGluAla 94
Db 775 TTGCGGTGTCAGGTCCTGGGCTCATCTTCGCGGGGCGAGCTTGGCCATGGAAAGAGCGG 716
Qy 94 laGluHisLeuVal-GlnAlaAlaValLeuLeuGlyArgAspLeuValGlyAla 113
Db 715 CGGAACATCTGGTCCAGGCTGCTGTTCTTCTTGGCGGAGATCTCGAAGTAGCGGAGCG 656
Qy 114 LeuGlyValValAlaHisGlnLeuLeuAspLeuAlaLeuValHisLeuAlaValGluVal 133
Db 655 CTGGGGTCTGTCGGCCACCGAGCTCTCGATCTCGCGTGTCTCACCTCGCGGTAGAGTC 596
Qy 134 AlaValThrLeuValAlaAlaAspAspGlnGlyHisValHisValLeuLeuGlyPheVal 153
Db 595 GCGGTACCTTGTTCGCGGAGATGATGACGAGGCGCACCTCCACGCTTCTCTGGTTTGT 536
Qy 154 LeuGluAlaArgLeuGlyValGluAspLeuProGluProLeuHisLeuLeuGly 173
Db 535 CTTGAGGCAAGACTTGGTGTGAGGATCTGCTGCTGAGCGCTGACCTCTCTCGAAGA 476
Qy 174 ValAlaValGlnThrGluHisGlnAspGluAsnValSerCysGluAspGlyGluAla 193

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Db 475 GTCCGGTGTTCAGACTGAACACAGGATGAAACAGTCTCTGTGAGGATGGAGGCG 416
Qy 194 ProHisGlyGlyGluArgValValAlaGlyArgValGluAspValGluLeuValAspLeu 213
Db 415 CCGCATGGCGGGAACGGGTGGTGGTCCGAGACGTGTCGAGGATGTCGAGCTGGTAGACCTC 356
Qy 214 AlaAlaAspGlyValGluLeuAlaValGluValLeuAspGlyArgArgValGlyValLeu 233
Db 355 GCCCGGATGGAGTAGAAGTTCCTCGGTGGAAGTCTCTGATGTTAGCGGTAGGCGTCTC 296
Qy 234 GluAlaAlaGlyGluGluAlaAlaArgHisAspGlyArgLeuAlaHisLeuGlyArgAlaGlu 253
Db 295 GAAGCGCGCGGTAGGAAGCGGACACGATGCCCTCTTCCACCTTGGACGAGCGAG 236
Qy 254 AspAspHisAlaAlaAlaValLeuGlyArgAspThrGlnLeuArgValAlaAargAlaHis 273
Db 235 GATGACCATGCGATAGCAGTCTTGGCCGGGATCTCAGCTCCGAGTCGTCGGGCACAT 176
Qy 274 LeuLeuAspHisArgGlyGlnPheHis 282
Db 175 CTTCTTGATCATCGCGGCCAGTTTCAT 149
RESULT 10
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LOCUS 603190722F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5262101 5',
DEFINITION mRNA sequence.
ACCESSION BI553776
VERSION BI553776.1 GI:15441088
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 758)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11660 row: 1 column: 06
High quality sequence stop: 738.
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            /note="Organ: brain; Vector: pBluescriptR (modified
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            ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
            size-selected for average insert size 2.5 kb and
            normalized to 5. This is a primary library enriched
            for full-length clones and constructed using the
            Cap-trapper method (Carninci, in preparation). Library
            constructed by M. Brownstein (NHGRI, National
            Institutes of Health). Note: this is a NIH_MGC Library."
            155 a 252 c 249 g 102 t
BASE COUNT
ORIGIN
Alignment Scores:
Pred. No.: 2e-76 Length: 758

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http://image.llnl.gov
Plate: LLAM11722 row: k column: 15
High quality sequence stop: 803.
Location/Qualifiers
1..814

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[illegible]

Tue Dec 31 15:27:53 2002

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RESULT 12
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
BASE COUNT 207 a 473 c 279 g 201 t
ORIGIN
Alignment Scores:
Pred. No.: 7,12e-76 Length: 1160
Score: 893.00 Matches: 208
Percent Similarity: 76.49% Conservative: 10
Best Local Similarity: 72.98% Mismatches: 49
Query Match: 63.29% Indels: 18
DB: 14 Gaps: 6
US-09-709-103-1f4 (1-282) x BM805574 (1-1160)
QY 8 LeuValLeuGlyLeuAlaAlaGlyAlaGlyLeuLeuAlaAlaGlyValHisGluValAlaVal 27
Db 1019 CTTTGGTTAGGGAGTACCGGGGGGGTGGTGG-----GTT 984
QY 28 TyraAlaGlyProAlaArgGluGly----CysHisAspAlaGlyValAlaAlaArg----- 44
Db 983 ACCGTGGGGCCGAAAAAAGGGTTCGCGGAATCCAAAGAGGGGGCGCGGGGTAA 924
QY 45 ValAlaAlaAlaAlaAlaAlaAlaGlyProGlnGlnLeuLeu---ValProGlnArgLeu 63
Db 923 ACACCAACCAACCGCGGGGGGGCCAAAGCACTGTGGGTTTCAGCAGGGGCTTT 864
QY 64 LeuValGlnHisVal-AlaVal---LeuHisArgAspLeuAlaValGlnValTrrAlaHi 82
Db 863 TTGGTCAGCATGTTGGCAGTGGGGGGCCCGGACCCCTGCGGGGGCAGGTTCTGGGGTCA 804

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BM805574 1160 bp mRNA linear EST 05-MAR-2002
 AGENCOURT_6498388 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5729129
 5', mRNA sequence.
 BM805574
 EST.
 BM805574.1 GI:19122397
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1160)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Invitrogen
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM12725 row: 0 column: 18
 High quality sequence start: 23
 High quality sequence stop: 501.
 Location/Qualifiers
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 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: EcoRV
 (destroyed); Site_2: NotI; RNA source male hippocampus,
 age 27. Library is oligo-dT primed and directionally
 cloned (EcoRV site is destroyed upon cloning). Average
 insert size 1.4 kb, insert size range 0.9-4 kb. Library is
 normalized and enriched for full-length clones and was
 constructed by C. Gruber (Invitrogen). Research Genetics
 tracking code 012."
 207 a 473 c 279 g 201 t

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QY 82 sleuAla---GlyGlnLeuGlyHisGlyGluGluArg-AlaGluHisLeuVal-GlnAla 100
Db 803 TCTCCGCTGGGGCCAGCTTGACCAATGACAAAGAGCGCCGGGAGCATGGGTTCCAGGT 744
QY 101 AlaValLeuLeuGlyArgAspLeuGluValGlyAlaAlaLeuGlyValAlaAlaHisGln 120
Db 743 GGTGTTTCTGGGCGGAGATCTCGAGTAGCGACGCTGGGGGTCGTCCGCCACAG 684
QY 121 LeuLeuAspLeuAlaLeuValHisLeu-AlaValGluValAlaValThrLeuValAlaAl 140
Db 683 CTGTGATCTCGCTGCTGCCTCCACCTTCGCGTGGAAGTCGCGGTTCACCTTGGTTGGGC 624
QY 140 aspaspGlnGlyHisValHisValLeuGlyPheValLeuGluAlaArgLeuGlyVa 160
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QY 260 lLeuGlyArgAspThrGlnLeuArgValAlaAlaHisLeuLeuAspHisArgGlyGl 280
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QY 280 nPheHis 282
Db 203 GTTTCAT 197
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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

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BM821656 1137 bp mRNA linear EST 12-MAR-2002
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 EST.
 BM821656.1 GI:19372035
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 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1137)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM12788 row: 1 column: 23
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 Location/Qualifiers
 1..1137

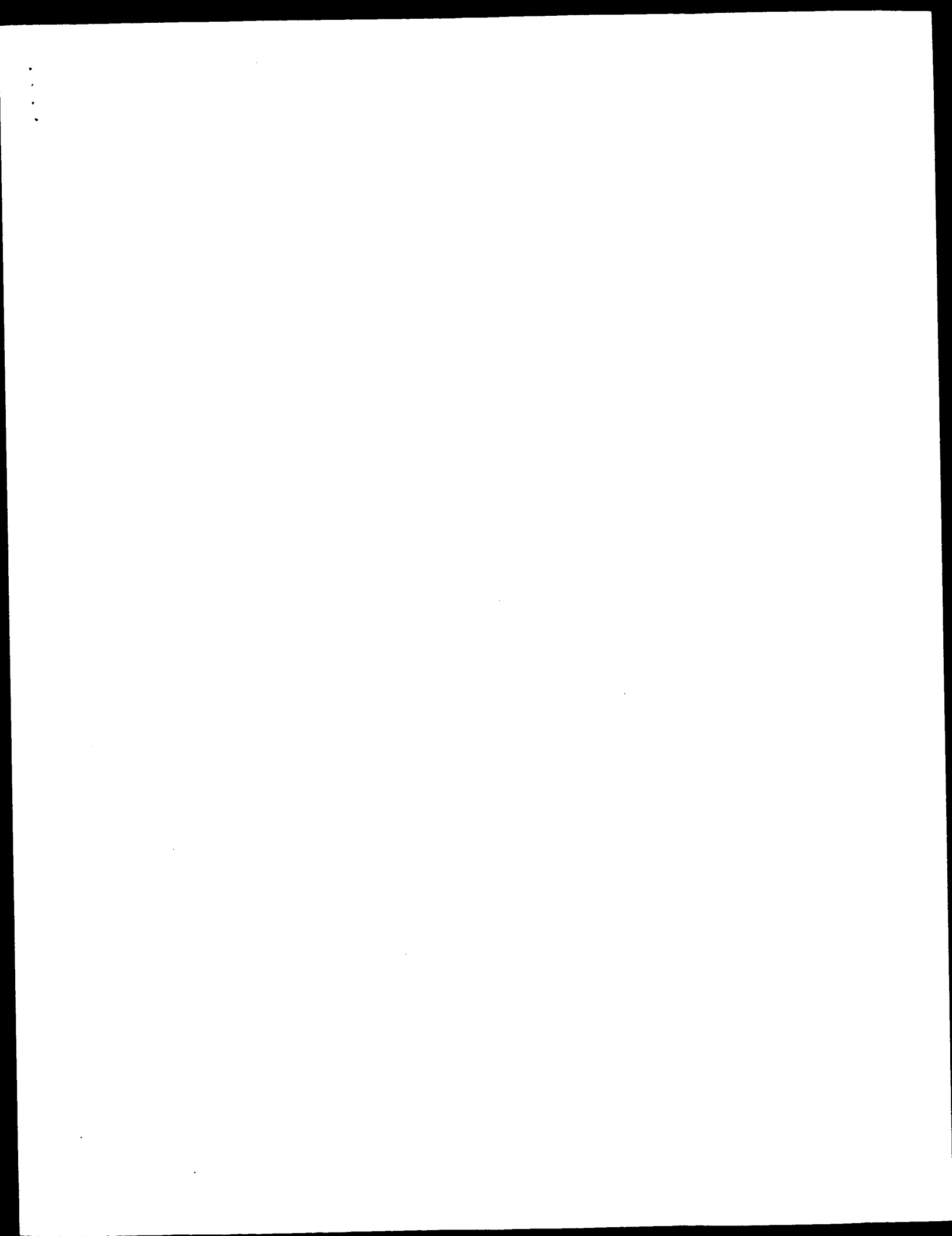
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DB:	13
IS-09-709-103-1F4 (1-282) x B1506637 (1-831)	
Length:	832
Matches:	193
Conservative:	20
Mismatches:	10
Indels:	7
Gaps:	1

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us-09-709-103-1f4.p2n.rst

Job time : 2185 secs



GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus.p2n model

Run on: December 30, 2002, 14:46:00 ; Search time 355 Seconds

(without alignments)
1788.911 Million cell updates/sec

Title: US-09-709-103-1f4

Sequence: 1 LADDAALLVGLAAGAGLLA.....RDTQLRVARALHDLRGQFH 282

Scoring table:

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-USBR=SULLVAVL1F4 @CGN 1.1 79 @runat_30122002.144046.21490 -NCPU=6 -ICPU=3
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
C 1	1411	100.0	846	21	AAZ36892	CDNA encoding an a
C 2	1411	100.0	1740	21	AAZ36914	CDNA encoding an a
C 3	1411	100.0	1776	21	AAZ36917	CDNA encoding an a
C 4	1411	100.0	1801	21	AAZ36893	CDNA encoding an a
C 5	1411	100.0	1841	20	AAZ36922	Human kd312 polyom
C 6	1348	95.5	3986	20	AAZ36923	Human kd312 polyom
C 7	963.5	68.3	1689	20	AAZ36924	Rat kd312 polyom
C 8	911	64.6	3079	20	AAZ36925	DNA encoding a hom
C 9	579.5	41.1	837	21	AAZ36913	Human Tumour Endot
C 10	579.5	41.1	2832	24	ABL92076	Human Tumour Endot
C 11	579.5	41.1	2973	24	ABL92087	Human d1cnp polyu
C 12	579.5	41.1	3427	24	ABK71553	Human d1cnp polyu
C 13	498.5	35.3	3020	24	ABJ92134	Mouse Tumour Endot
C 14	478.5	33.9	951	23	AAJ90571	DNA encoding novel
C 15	422	29.9	624	24	ABQ28318	Oligonucleotide fo
C 16	422	29.9	624	24	ABQ28319	Oligonucleotide fo
C 17	321	22.7	624	24	ABQ28320	Oligonucleotide fo
C 18	321	22.7	624	24	ABQ28321	Oligonucleotide fo
C 19	267	18.9	1305	23	ABJ07789	Drosophila melanog
C 20	244.5	17.3	3061	24	ABQ72648	Human MDR1 encodin
C 21	228.5	16.2	1249	24	ABQ72525	Human MDR1 encodin
C 22	219	15.5	368	22	ABA51382	Human breast cell
C 23	219	15.5	368	22	ABA69388	Human foetal liver
C 24	219	15.5	368	22	ABA69383	Human foetal liver
C 25	219	15.5	368	22	AAK17661	Probe #14789 for g
C 26	219	15.5	368	22	AAK43477	Human brain expres
C 27	219	15.5	368	22	AAI24259	Human bone marrow
C 28	219	15.5	368	22	AAI49541	Probe #14192 for g
C 29	219	15.5	368	22	AAI49541	Probe #18227 used
C 30	219	15.5	368	22	ABJ17600	Probe #9809 used t
C 31	188.5	13.4	1144	22	AAH90075	Human genome-deriv
C 32	188.5	13.4	4933	22	AAK81235	Human bone marrow
C 33	188.5	13.4	4933	22	AAK81234	Human immune/haema
C 34	184.5	13.1	1087	22	AAI60838	Human immune/haema
C 35	184.5	13.1	1108	22	AAI59052	Human polynucleoti
C 36	184.5	13.1	4167	24	AAD37605	Human polynucleoti
C 37	166.5	11.8	702	23	ABL14159	Human intracellular
C 38	166	11.8	3474	14	AAO39018	Drosophila melanog
C 39	166	11.8	3474	18	AAT74012	Sequence of pure m
C 40	166	11.8	3474	19	AAV16191	Maize optimised-B.
C 41	161	11.4	6338	24	ABK91481	Modified HIV prote
C 42	161	11.4	6610	24	ABK91514	Modified HIV prote
C 43	161	11.4	7819	24	ABK91496	Modified HIV prote
C 44	159.5	11.3	2322	21	AAA51961	Modified HIV-1 Env
C 45	159.5	11.3	2565	24	ABL40018	Synthetic Env gp16

ALIGNMENTS

RESULT 1
ID AAZ36892/c
AAZ36892 standard; CDNA: 846 BP.

AC AAZ36892;
DT 13-MAR-2000 (first entry)

DE CDNA encoding an activator of G protein signalling (AGS) protein.

KW Activator of G protein signalling; AGS; ras-related G protein;

KW GTP hydrolysis; G protein activity; pheromone response pathway;

KW G protein-coupled signal transduction; G-gamma selectivity;

KW cellular signal transduction; ss.

OS Homo sapiens.
XX Location/Qualifiers
FH Key

Tue Dec 31 15:27:52 2002

CC Human cDNA libraries from various tissues were screened for GTPase
CC associated proteins (GTPAP). The present sequence is cDNA encoding
CC human GTPAP-7. This sequence was derived from a cDNA library of the
CC brain tumour tissue from the parietal lobe of a female.
CC This protein is expressed in reproductive, nervous and
CC gastrointestinal tissue. The GTPAP proteins may be used to define
CC agonists and antagonists of GTPAP activity and to generate antibodies
CC to GTPAP. This means the GTPAP proteins may be useful for treatment or
CC prevention of diseases associated with GTPAP such as cell proliferation
CC disorders, autoimmune disorders, inflammatory disorders, immune system
CC disorders, cancer, AIDS, asthma, atherosclerosis, arthritis, systemic
CC lupus erythematosus and psoriasis.

XX SQ Sequence 1776 BP; 430 A; 565 C; 490 G; 291 T; 0 other;

Alignment Scores: Length: 1776
Pred. No.: 141.00 Matches: 282
Score: 100.00% Conservatives: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 21 Gaps: 0
DB: 21

US-09-709-103-1f4 (1-282) x AAA49177 (1-1776)

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DB	1025	CTAGCTGATGACGACGCTCTTGTCTTGGCTTGGCTGGCGCGTGGCGCTTCTCGCG	966
QY	21	AspValHisGluValAlaValTyAlaGlyProAlaArgGluGlyCysHisAspAlaLys	40
DB	965	GATGTACATGAGTGTCTGTGTACCTGGCGCGCGCGGCGGAGGTCACGATGCGCAA	906
QY	41	GlyValAlaArgValAlaAlaAlaAlaAlaAlaAlaGlyProGlnGlnLeuValPro	60
DB	905	GGCGTGGCGCGGCTGGCGCGCGCGCGCTGGCGCGCGCGCGCGCGCTTCTGTTCG	846
QY	61	GlnArgLeuValGlnHisValAlaValLeuHisArgAspLeuAlaValGlnValTrp	80
DB	845	CAGCGCTCTTGTGCGACGCTGCGCAGTACTGACCCGAGACCTTGGCGTGCAGGTCTGG	786
QY	81	AlaHisLeuAlaGlyGlnLeuGlyHisGlyGluGluArgAlaGluHisLeuValGlnAla	100
DB	785	GCTCATCTGCTGGCAGCTTGGCCATGGCGAGCGCGCGGAGACATCTGTTCAGGCT	726
QY	101	AlaValLeuLeuGlyArgAspLeuValGlyValAlaAlaLeuGlyValValAlaHisGln	120
DB	725	GCTGTCTCTTGGCGGAGATCTCGAAGTAGGCGGACGCTGGGGTCTGCGCCACCGAG	666
QY	121	LeuLeuAspLeuAlaLeuValHisLeuAlaValGluValAlaValThrLeuValAlaAla	140
DB	665	CTGCTCGATCTCGCGTGGTCCACCTCGCGGTAGAGTCCGCGTCCACCTTGTTCGCCGA	606
QY	141	AspAspGlnGlyHisValHisValLeuLeuGlyPheValLeuGluAlaArgLeuGlyVal	160
DB	605	GATGACGAGGGGACGCTCCACGTTCTTCTTGGTTTGTCTTCTTGAGGCAAGACTTGGTGT	546
QY	161	GluAspLeuLeuProGluProLeuHisLeuLeuGlyValAlaValValGlnThrGlu	180
DB	545	GAGATCTGCTGCTGAGCGCGTCCACCTCGCGGTAGAGTCCGCGTGTTCAGACTGAA	486
QY	181	HisAspGluAenValSerCysGluAspGlyGluAlaProHisGlyGlyGluArgVal	200
DB	485	CACGAGGATGAAACGCTCTCTGTGAGATGAGAGGACCGCATGCGGGGACGGGTG	426
QY	201	ValAlaGlyArgValGluAspValGluLeuValAspLeuAlaAlaAspGlyValGluLeu	220
DB	425	GTTCGCGGACGCTGTCAGAGATGTCGAGTGTGTAGCTGTGTAGCTCGCGCGGATGAGT	366
QY	221	AlaValGluValLeuAspGlyArgArgValGlyValLeuGluAlaAlaGlyGluAla	240
DB	365	GCGGTGGAAGTCTCTCGATGGTAGGCGTGTAGGCGTCTCGAAGCGCGCGGTGAGGAGCG	306

QY	241	ArgHisAspGlyArgLeuAlaHisLeuGlyArgAlaGluAspHisAlaAlaVal	260
DB	305	CGACACGATGGCGCTTGTCCACCTTGGACGAGCCGAGGATGACCATGCGATGACGTT	246
QY	261	LeuGlyArgAspThrClnLeuArgValAlaAlaArgAlaHisLeuLeuAspHisArgGln	280
DB	245	CTTGGCGGGATGACTCAGCTCCGAGTCCGTCCTGGGACACATCTTCTTGATCATCGCGG	186
QY	281	PheHis	282
DB	185	TTTCAT	180

RESULT 4
AAZ36893/c
ID AAZ36893 standard; cDNA; 1801 BP.

XX	AC	AAZ36893;
XX	DT	13-MAR-2000 (first entry)
XX	DE	cDNA encoding an activator of G protein signalling (AGS) protein.
XX	KW	Activator of G protein signalling; AGS; ras-related G protein;
XX	KW	GTP hydrolysis; G protein activity; pheromone response pathway;
XX	KW	G protein-coupled signal transduction; G-gamma selectivity;
XX	KW	cellular signal transduction; ss.
XX	OS	Homo sapiens.
XX	PH	Key
XX	FT	5'UTR
XX	FT	Location/Qualifiers
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XX	FT	/product= "activator of G protein signalling (AGS)
XX	FT	protein"
XX	FT	1000..1801
XX	FT	/*tag= c
XX	PN	WO9958670-A1.
XX	PD	18-NOV-1999.
XX	PF	07-MAY-1999; 99WO-US10151.
XX	PR	08-MAY-1998; 98US-0084842.
XX	PR	07-OCT-1998; 98US-0103355.
XX	PA	(CADU-) CADUS PHARM CORP.
XX	PI	Cismowski M, Duzic E;
XX	DR	WPI: 2000-072337/06.
XX	DR	P-PSDB; AAY53921.
XX	PT	A new activator of G protein signalling used to treat disorders
XX	PT	characterized by an aberrant AGS protein activity -
XX	PS	Claim 3; Page 133-135; 162pp; English.
XX	CC	The present sequence encodes an activator of G protein signalling (AGS)
XX	CC	protein. The cDNA sequence was isolated from a human liver cDNA
XX	CC	library. The AGS protein exhibits homology to ras-related G proteins,
XX	CC	and contains alterations in conserved amino acids consistent with a
XX	CC	deficiency in GTP hydrolysis activity. AGS stimulates G protein
XX	CC	activity, G protein-coupled signal transduction and the pheromone
XX	CC	response pathway in a receptor-independent manner. The AGS protein
XX	CC	also shows G-gamma selectivity, as measured by growth assays in
XX	CC	yeast expressing various mammalian G-gamma constructs, and
XX	CC	tissue-specific expression, as measured by Northern blot analysis.
XX	CC	The AGS protein can be used to screen for compounds that modulate
XX	CC	cellular signal transduction. The protein is used to treat disorders
XX	CC	characterized by an aberrant AGS protein activity or AGS nucleic acid

CC expression.

SQ Sequence 1801 BP; 437 A; 561 C; 500 G; 303 T; 0 other;

Alignment Scores:

Pred. No.:	1,06e-88	Length:	1801
Score:	1411.00	Matches:	282
Percent Similarity:	100.00%	Conservative:	0
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Query Match:	100.00%	Indels:	0
DB:	21	Gaps:	0

US-09-709-103-1f4 (1-282) x AA236893 (1-1801)

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QY 21 AspValHisGlyValAlaValAlaValAlaValAlaValAlaValAlaValAlaValAlaVal 40
Db 939 GATGTACATGAGAGTCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCG 880
QY 41 GlyValAlaArgValAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 60
Db 879 GCGGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 820
QY 61 GlnArgLeuLeuValGlnHisValAlaValLeuHisArgAspLeuAlaValGlnValTyr 80
Db 819 CAGCGCCCTTTCTTTGTCACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 760
QY 81 AlaHisLeuAlaGlyGlnLeuGlyHisGlyGlyGlnArgAlaGlnHisLeuValGlnAla 100
Db 759 GCTCATCTCGCTGGGAGCTTGGCCATGGCGAAGCGCGGGAACCTTGTGTCAGCGCT 700
QY 101 AlaValLeuLeuGlyArgAspLeuGlyValAlaAlaLeuGlyValAlaHisGln 120
Db 699 CCTGTTCTTCTTGGCCAGATCTCGAAGTAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 640
QY 121 LeuLeuAspLeuAlaLeuValHisLeuAlaValGlyValAlaValHisLeuValAlaAla 140
Db 639 CTGCTTCATCTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 580
QY 141 AspAspGlnGlyHisValHisValLeuLeuGlyPheValLeuGlyAlaArgLeuGlyVal 160
Db 579 GATGACCAAGGGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 520
QY 161 GlnAspLeuLeuProGlnProLeuHisLeuLeuGlyValAlaValAlaGlnThrGln 180
Db 519 GAGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 460
QY 181 HisGlnAspGlnAsnValSerCysGlnAspGlyGlyAlaProHisGlyGlyGlnArgVal 200
Db 459 CACCAGAGATGAACCTCTCTGAGTAGAGAGCGCCGCAAGGGGGAACGGGGTG 400
QY 201 ValAlaGlyArgValGlnArgValGlnLeuValAspLeuAlaAspGlyValGlnLeu 220
Db 399 GTTCCCGGACGCTGCTGAGGATGTCAAGCTGTAGACCTGCGCGCGAGTAGGAGAACTT 340
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QY 281 PheHis 282
Db 159 TTTTCAT 154

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RESULT 5

AA23022/C

ID AA23022 standard, cDNA, 1841 BP.

XX AA23022;

AC 17-JAN-2000 (first entry)

DE Human kd312 polypeptide encoding cDNA.

KW kd312 polypeptide; cancer; immunodeficiency disorder; AIDS; stroke;

KW heart attack; head trauma; neurodegenerative disease; human;

KW Parkinson's disease; Alzheimer's disease; ss.

XX Homo sapiens.

PN WO950288-A2.

PD 07-OCT-1999.

PF 30-MAR-1999; 99WO-US06993.

PR 31-MAR-1998; 98US-0053374.

PA (AMGE-) AMGEN INC.

PI Yen K;

DR WPI; 1999-601322/51.

XX P-PSDB; AAY42693.

PT kd312 polypeptides useful for treating diseases and disorders

XX associated with alterations in cell proliferation and cell death

PS Claim 1; Fig 8; 85p; English.

XX The invention provides nucleic acid molecules encoding human and rat

CC kd312 polypeptides. The kd312 polypeptides can be expressed by standard

CC recombinant methodology. The kd312 sequences, and the antibodies against

CC the proteins may be used to treat or diagnose the presence or progression

CC of various diseases, e.g. cancer, immunodeficiency disorders (e.g. AIDS),

CC stroke, heart attack, head trauma, and neurodegenerative diseases (e.g.

CC Parkinson's disease and Alzheimer's disease). The present sequence

XX represents the human kd312 cDNA sequence.

SQ Sequence 1841 BP; 398 A; 605 C; 530 G; 308 T; 0 other;

Alignment Scores:

Pred. No.:	1.09e-88	Length:	1841
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Percent Similarity:	100.00%	Conservative:	0
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DB:	20	Gaps:	0

US-09-709-103-1f4 (1-282) x AA23022 (1-1841)

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QY 21 AspValHisGlyValAlaValAlaValAlaValAlaValAlaValAlaValAlaValAlaVal 40
Db 1040 GATGTACATGAGTCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCG 981
QY 41 GlyValAlaArgValAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 60
Db 980 GCGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 921
QY 61 GlnArgLeuLeuGlnHisValAlaValLeuHisArgAspLeuAlaValGlnValTyr 80
Db 920 CAGCGCTTCTTGTGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCG 861

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Tue Dec 31 15:27:52 2002

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QY 81 AlahisLeuAlaGlyGlnLeuGlyHisGlyGluGluArgAlaGluHisLeuValGlnAla 100
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QY 101 AlavalleuLeuGlyArgAspLeuGluValGlyAlaAlaLeuGlyValValAlaHisGln 120
DB 800 GCTGTTCTTCTGGCCAGATCTCGAAGTAGCGCAGCGCTGGGGTCTGCCCCACCAG 741
QY 121 LeuLeuAspLeuAlaLeuValHisLeuAlaValAlaValThrLeuValAlaAla 140
DB 740 CTGCTCATCTCGCGCTGGTCCACCTCGCGGTAGAAGTCCGGTCACTTGTGGCGCA 681
QY 141 AspAspGlnGlyHisValHisValLeuGlyPheValLeuGluAlaArgLeuGlyVal 160
DB 680 GATGACACAGGGGACGTCACGCTTCTTGGTTTGTCTTGGAGCAAGACTTGGTGT 621
QY 161 GluAspLeuLeuProGluProLeuHisLeuLeuGluGlyValAlaValValGlnThrGlu 180
DB 620 GAGGATCTGCTGCTGAGCGCTGCACCTCTCGAAGGAGTGGCGGTGTCCAGACTGAA 561
QY 181 HisGlnAspGluAsnValSerCysGluAspGlyGluAlaProHisGlyGlyGluArgVal 200
DB 560 CACCAAGGATGAAGATCTCTCTGTTGAGGATGGAGGCGCGCATGGCGGGAACGGGTG 501
QY 201 ValAlaGlyArgValGluAspValGluLeuValAspLeuAlaAlaAspGlyValGluLeu 220
DB 500 GTTCCGCGAGCTGTGAGGATCTGAGCTGTGAGCTCGCGCGGATGGAGTAGAAGTCTT 441
QY 221 AlavalleuValLeuAspGlyArgValGlyValLeuGluAlaAlaGlyGluGluAla 240
DB 440 GCGGTGGAAGTCTCATGTTAGGCGGTGAGCGGTCCTCGAAGCGCGCGGTGAGGAAGCG 381
QY 241 ArgHisAspGlyArgLeuAlaHisLeuGlyArgAlaGluAspAspHisAlaAlaVal 260
DB 320 CTTGGCGGGATATCAGCTCCAGTCCGAGTGGCGGACCTTGGACGAGCGGAGGATGACCATGCGATGACGATT 321
QY 261 LeuGlyArgAspThrGlnLeuArgValAlaArgAlaHisLeuAspHisArgGlyGln 280
DB 281 PheHis 282
QY 260 TTTTAT 255
RESULT 6
AAZ23023/c
ID AAZ23023 standard; DNA; 3986 BP.
XX AC AAZ23023;
XX DT 17-JAN-2000 (first entry)
XX DE Human kd312 genomic DNA sequence.
XX KW kd312 polypeptide; cancer; immunodeficiency disorder; AIDS; stroke;
XX KW heart attack; head trauma; neurodegenerative disease; human;
XX KW Parkinson's disease; Alzheimer's disease; ss.
XX OS Homo sapiens.
XX PN WO9950288-A2.
XX PD 07-OCT-1999.
XX PF 30-MAR-1999; 99WO-US06993.
XX PR 31-MAR-1998; 98US-0053374.
XX PA (AMGE-) AMGEN INC.
XX PI Yen K;
XX

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DR WPI: 1999-601322/51.
DR P-PSDB; AAY42693.
XX kd312 polypeptides useful for treating diseases and disorders
PT associated with alterations in cell proliferation and cell death
XX Claim 1; Fig 5; 85pp; English.
XX The invention provides nucleic acid molecules encoding human and rat
CC kd312 polypeptides. The kd312 polypeptides can be expressed by standard
CC recombinant methodology. The kd312 sequences, and the antibodies against
CC the proteins may be used to treat or diagnose the presence or progression
CC of various diseases, e.g. cancer, immunodeficiency disorders (e.g. AIDS),
CC stroke, heart attack, head trauma, and neurodegenerative diseases (e.g.
CC Parkinson's disease and Alzheimer's disease). The present sequence
CC represents the human kd312 genomic DNA sequence.
XX Sequence 3986 BP; 856 A; 1226 C; 1172 G; 732 T; 0 other;
SQ
Alignment Scores: 5.19e-84 Length: 3986
Pred. No.: 1348.00 Matches: 282
Score: 1348.00 Conservative: 0
Percent Similarity: 79.89% Mismatches: 0
Best Local Similarity: 79.89% Indels: 71
Query Match: 95.54% Gaps: 1
DB: 20
US-09-709-103-1F4 (1-282) x AAZ23023 (1-3986)
QY 1 LeuAlaAspAspAlaAlaLeuLeuValLeuGlyLeuAlaAlaGlyAlaGlyLeuLeuAla 20
DB 1830 CTAGCTGATGACGACGCTCTTGTCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCG 1771
QY 21 AspValHisGluValAlaValTyAlaGlyProAlaArgGluGlyCysHisAspAlaLys 40
DB 1770 GATGTACATGAGTGCCTGTGTACGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1711
QY 41 GlyValAlaArgValAlaAlaAlaAlaAlaAlaAlaGlyProGlnGlnLeuLeuValPro 60
DB 1710 GCGGTGCGCGCGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1651
QY 61 GlnArgLeuLeuValGlnHisValAlaValLeuHisArgAspLeuAlaValGlnValTrp 80
DB 1650 CAGCGCTCTTCTTGTGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1591
QY 81 AlaHisLeuAlaGlyGlnLeuGlyHisGlyGluGluArgAlaGluHisLeuValGlnAla 100
DB 1590 GCTCATCTGCTGGCGAGCTTGGCCATGGCGAAGAGCGCGCGAACAATCTGGTCCAGCT 1531
QY 101 AlavalleuLeuGlyArgAspLeuGluValGlyAlaAlaLeuGlyValValAlaHisGln 120
DB 1530 GCTGTTCTTCTTGGCGAGATCTCGAAGTAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1471
QY 121 LeuLeuAspLeuAlaLeuValHisLeuAlaValGluValAlaValThrLeuValAlaAla 140
DB 1470 CTGCTCATCTGCGCTGGTCCACCTCGCGGTAGAAGTCCGCTCACCTTCTTGTCCGCA 1411
QY 141 AspAspGlnGlyHisValHisValLeuLeuGlyPheValLeuGluAlaArgLeuGlyVal 160
DB 1410 GATGACACAGGGGACGTCACGCTTCTTGGTTTGTCTTGGAGCAAGACTTGGTGTCT 1351
QY 161 GluAspLeuLeuProGluProLeuHisLeuLeuGlyValAlaValValGlnThrGlu 180
DB 1350 GAGGATCTGCTGCTGAGCGCGCTGACCTCTCTCGAAGGAGTCCGCGGTGTGTCAGACTGAA 1291
QY 181 HisGlnAspGluAsnValSer----- 187
DB 1290 CACCAAGGATGAAGCTCTCTAGAGGGGCGACAGAGAGCAAGAGAGAGAGAGAGAGAG 1231
QY 187 ----- 187
DB 1230 TGGCGCGCGCGCGGCAAGTCTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCTC 1171

```


QY 187 ----- 187
 Db 1170 TAAGCGGAAGCGCACTACGCGCGCAGACCGGAGCGGCTCGGGGCGCCCTG 1111
 QY 188 ----- CysGluAs 190
 Db 1110 GCGAGGCTTCCCGCCCTTCCCTCCCGACCTGCCCGGCCCCCGCTCACCTGTAGAGA 1051
 QY 190 pGlyGluAlaProHisGlyGlyGluArgValAlaIleGlyArgValGluAspValGluLe 210
 Db 1050 TGAAGAGCGCCGATGCGCGGAGACGGGTGCTGCCGACCTGTGAGAGATGTGAGCT 991
 QY 210 ValAspLeuAlaAlaAspGlyValGluLeuAlaValGluValLeuAspGlyArgArgVal 230
 Db 990 GGTACCTCTGCGCGAGATGAGTACCTTCCGCTGGAAGTCTCGATGTGAGCGCTG 931
 QY 230 IglValIleuGluAlaAlaGlyGluGluValArgHisAspGlyArgLeuAlaHisIleuG 250
 Db 930 AGCGCTCTCGAAGCGCGCGGTGAGAGACCGGACACGATGGCCGCTTGGCCACCTTGG 871
 QY 250 YArgAlaGluAspAspHisAlaIleAlaValIleuGlyArgAspThrGluLeuArgValAl 270
 Db 870 ACCAGCGCGAGATGACCAATGCGATGACAGTCTTGGCGGGAATCTCAGCTCCAGTCC 811
 QY 270 aArgAlaHisIleuLeuAspHisAspGlyGluPheHis 282
 Db 810 TCGGCGACATCTTCTTGATCATCGCGCCAGTTTCAT 774

RESULT 7
 AA23024/C
 ID AA23024 standard; cDNA; 1689 BP.

XX AC AA23024;
 XX DT 17-JAN-2000 (first entry)
 DE Rat kd312 polypeptide encoding cDNA.
 XX KD kd312 polypeptide; cancer; immunodeficiency disorder; AIDS; stroke;
 KW heart attack; head trauma; neurodegenerative disease; rat;
 KW Parkinson's disease; Alzheimer's disease; ss.
 OS Rattus sp.
 XX PN W09950288-A2.
 XX PD 07-OCT-1999.
 XX PF 30-MAR-1999; 99MO-US06993.
 XX PR 31-MAR-1998; 98US-0053374.
 XX PA (AMGE-) AMGEN INC.
 XX PI Yen K;
 XX PT WPI, 1999-601322/51.
 XX DR P-PDB; AAY42694.
 XX PT kd312 polypeptides useful for treating diseases and disorders
 XX associated with alterations in cell proliferation and cell death -
 PS Claim 2; Fig 9; 85pp; English.
 XX CC The invention provides nucleic acid molecules encoding human and rat
 CC kd312 polypeptides. The kd312 polypeptides can be expressed by standard
 CC recombinant methodology. The kd312 sequences, and the antibodies against
 CC the proteins may be used to treat or diagnose the presence or progression
 CC of various diseases, e.g. cancer, immunodeficiency disorders (e.g. AIDS),
 CC stroke, heart attack, head trauma, and neurodegenerative diseases (e.g.
 CC Parkinson's disease and Alzheimer's disease). The present sequence
 CC represents the rat kd312 cDNA sequence.

SQ Sequence 1689 BP; 417 A; 462 C; 434 G; 376 T; 0 other;

Alignment Scores:

Pred. No.:	7 1e-58	Length:	1689
Score:	963.50	Matches:	200
Percent Similarity:	79.79%	Conservative:	25
Best Local Similarity:	70.92%	Mismatches:	56
Query Match:	68.28%	Indels:	1
DB:	20	Gaps:	1

US-09-709-103-1f4 (1-282) x AA23024 (1-1689)

QY 1 LeuAlaAspAspAlaAlaLeuValIleuGlyLeuAlaIleuGlyValIleuGlyLeuAla 20
 Db 974 CTAACTGATGACACACCGCTCTTCTTCTTACCTGGCTGTGACACTGTTTCTTCAAG 915
 QY 21 AspValHisGluValAlaValAlaValArgProAlaArgGluGlyCysHisAspAlaLys 40
 Db 914 AATGTACATGAGGTGCTATGACGCTAGCTCCGAGCAAGGGCGCCAAAGTCCAA 855
 QY 41 GlyValAlaArgValAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 60
 Db 854 GGCATCTCC---GTGGTGGCCCCCACCCTCCGCTCCCGCAGCAGAACTTCTTGTCTCT 798
 QY 61 GlnArgLeuLeuValGlnHisValAlaValIleuHisArgAspLeuAlaValGlnValTyr 80
 Db 797 CAGAGCTTTTGTGCGACAGCTCAGCTAGTGCACGACCTTGGGGTGCAGTCAAG 738
 QY 81 AlaHisIleuAlaGlyGluIleuGlyHisGlyGluGluArgAlaGluHisIleuValGlnAla 100
 Db 737 GCTATCTCGCTAGACAGCTTGGCCATGCGCAAGAGCGCAGCAAGACATCTGTCTCAGGCT 678
 QY 101 AlaValIleuLeuGlyArgAspLeuGluValGlyAlaAlaIleuGlyValAlaHisGln 120
 Db 677 GCTATCTTCTTGGCCGAGATCTCGAAGTAGGCACACGCTAGAGGTCTATGCCACCAAG 618
 QY 121 LeuLeuAspLeuAlaLeuValHisIleuAlaValGluValAlaValThrLeuValAlaAla 140
 Db 617 CTGCTCAATCTCCCGCTGCTCCACTTCCGCGTAGAAGTCCCGCTCCCTTGTTCACCGCA 558
 QY 141 AspAspGlnGlyHisValHisValIleuLeuGlyPheValIleuGluAlaArgLeuGlyVal 160
 Db 557 AATGACCGCGCAGCGCCACATCTCTTGGTTTGTCTTGAAGACAGACTTGGTGTG 498
 QY 161 GluAspLeuLeuProGluProLeuHisIleuLeuGlyValAlaValAlaValGlnThrGlu 180
 Db 497 TAGGATCTGCTGTTAGGCTTTGACCTCTCGAAGGAGTGGCGGTTGTCTAAGCTGAA 438
 QY 181 HisGlnAspGluAsnValSerCysGluAspGlyGluAlaProHisGlyGlyGluArgVal 200
 Db 437 CACCAAGATGAAACCTCTCTGTGAGATAGAGAGGCGCCGATGGGGGAAACCGGATG 378
 QY 201 ValAlaGlyArgValGluAspValGluLeuValAspLeuAlaAlaAspGlyValGluLeu 220
 Db 377 ATTGCCAGATGTGTCAGATATGCCAATGTAAGCTTGGCGGGGATCGAGTAAACTT 318
 QY 221 AlaValGluValLeuAspGlyArgArgValGlyValIleuGluAlaAlaGlyGluGluAla 240
 Db 317 TCGGTGGAAGCTTCAATAGTGGGGGTAAAGCGTCTCGAAGCGCGCGGAGGAAGCG 258
 QY 241 ArgHisAspGlyArgLeuAlaHisIleuGlyArgAlaGluAspAspHisAlaIleAlaVal 260
 Db 257 CGACACGATGGCGCTTGGCCCACTTGTGAGCGCAGATGACCATCTCTGTAGCAGTT 198
 QY 261 LeuGlyArgAspThrGlnLeuArgValAlaArgAlaHisIleuLeuAspHisArgGlyGln 280
 Db 197 CTTGGCGGGATACTCAATTGACAGTGGCTTGGCACATCTTGTATCATCGCGGCGAG 138
 QY 281 PheHis 282
 Db 137 TTTCAT 132

RESULT 8

Tue Dec 31 15:27:52 2002

AAZ23025/c

ID AAZ23025 standard; DNA; 3079 BP.

AC AAZ23025;

DT 17-JAN-2000 (first entry)

XX Rat kd312 genomic DNA sequence.

DE kd312 polypeptide; cancer; immunodeficiency disorder; AIDS; stroke;

XX heart attack; head trauma; neurodegenerative disease; rat;

KW Parkinson's disease; Alzheimer's disease; ss.

XX Rattus sp.

OS WO9950288-A2.

XX 07-OCT-1999.

XX 30-MAR-1999; 99WO-US06993.

XX 31-MAR-1998; 98US-00533374.

XX (AMGE-) AMGEN INC.

XX Yen K;

XX WPI; 1999-601322/51.

XX P-PSDB; AAY42694.

XX kd312 polypeptides useful for treating diseases and disorders

XX associated with alterations in cell proliferation and cell death

XX Claim 2; Fig 7; 85pp; English.

XX The invention provides nucleic acid molecules encoding human and rat

XX kd312 polypeptides. The kd312 polypeptides can be expressed by standard

XX recombinant methodology. The kd312 sequences, and the antibodies against

XX the proteins may be used to treat or diagnose the presence or progression

XX of various diseases, e.g. cancer, immunodeficiency disorders (e.g. AIDS),

XX stroke, heart attack, head trauma, and neurodegenerative diseases (e.g.

XX Parkinson's disease and Alzheimer's disease). The present sequence

XX represents the rat kd312 genomic DNA sequence.

XX Sequence 3079 BP; 708 A; 843 C; 829 G; 699 T; 0 other;

XX Alignment Scores:

XX Pred. No.: 5.39e-54 Length: 3079

XX Percent Similarity: 91.00 Matches: 199

XX Best Local Similarity: 68.29% Conservative: 25

XX Query Match: 60.67% Mismatches: 57

XX DB: 64.56% Indels: 48

XX Gaps: 2

XX US-09-709-103-1F4 (1-282) x AAZ23025 (1-3079)

QY 1 LeuAlaAspAlaAlaLeuLeuValLeuGlyLeuAlaAlaGlyLeuLeuAla 20

DB 1282 CTAAGTATGATGACAGCGCTCTTGTCTCTAGCTGCTGCTGACACTGTTCTCAGC 1223

QY 21 AspValHisGluValAlaValAlaGlyProAlaArgGluGlyCysHisAspAlaLys 40

DB 1222 AATGTATATGAGGTGCTATCAGCTAGGTCTCGAGCAAGGGCCCAAGATGCCAA 1163

QY 41 GlyValAlaArgValAlaAlaAlaAlaAlaAlaGlyProGlnGlnLeuValPro 60

DB 1162 GCACTCTCC--GTGTGCGCCCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1106

QY 61 GlnArgLeuValGlnHisValAlaValLeuHisArgAspLeuAlaValGlnValTrp 80

DB 1105 CAGAGCCTTTTGTGCAGCAGCTCAGTACTGCACACACACCTTGGTGGTGCAGT 1046

QY 81 AlaHisLeuAlaGlyGlnLeuGlyHisGlyGluGluArgAlaGluHisLeuValGlnAla 100

Db 1045 GCTCATCTCGCTAGGACGCTTGGCCATGGCAAGAGCGCCGGAACATCTGGTCCAGGCT 986

QY 101 AlaValLeuGlyArgAspLeuGluValGlyAlaAlaLeuGlyValValAlaHisGln 120

Db 985 GCTATTCTTCTTGGCCGAGATCTCGAAGTAGGCACAACGCTGAGGGTCATCGCCACGAG 926

QY 121 LeuLeuAspLeuAlaLeuValHisLeuAlaValGluValAlaValThrLeuValAlaAla 140

Db 925 CTGCTCAATCTCCGCTGCTCCACTTCGCGTAGAAGTCCCGGTCCTTGTGTACCGCA 866

QY 141 AspAspGlnGlyHisValHisValLeuGlyPheValLeuGluAlaArgLeuGlyVal 160

Db 865 AATGACACGCGGACGCTCCACATCTCTTTGGTTTGTCTTGACAGAGGACTTGGTGTG 806

QY 161 GluAspLeuLeuProGluProLeuHisLeuGlyValAlaValAlaValAlaValGlnThrGlu 180

Db 805 TAGGATCTGCTTTTGAGGCTTTTGACCTCTCTCGAAGGAGTCCGGTTGTCTTAAGCTGAA 746

QY 181 HisGlnAspGluAsnValSer----- 187

Db 745 CACCAGAATGAATAACGCTCTC-CTACAAGGAACGAGTGGAAAGGTCAGGGCAGCTGCCAA 687

QY 187 ----- 187

Db 686 GCACGGAGCAGCAGCAGCAGCCCAAGCACAACACACCGCCCATCCGCTCCCGCA 627

QY 188 -----CysGluAspGlyGluAlaPro 194

Db 626 GATTCTCCCTCCCGACGCTCCCTGTGGTCCCGCTCCTCAGCTGTGAGGATAGAGGCGCG 567

QY 195 HisGlyGlyGluArgValValAlaGlyArgValGluAlaAspValGluLeuValAla 214

Db 566 CATGGCGGGAACCGATGATGTCAGATGTCAGTATGTCCAACTGGTAGACTTTCGCC 507

QY 215 AlaAspGlyValGluLeuAlaValGluValLeuAspGlyArgArgValGlyValLeuGlu 234

Db 506 GCGGATCGAGTAAACTTTCGCTGGAAGTCTTCAATGGTAGGGGTGTAACGCTTCGCA 447

QY 235 AlaAlaGlyGluGluAlaArgHisAspGlyArgLeuAlaHisLeuGlyArgAlaGluAsp 254

Db 446 GCGGCGCGGTGAGGAAGCGGACACAGTGGCGCTCTTCCCACTTGGATGAGCGGAGAT 387

QY 255 AspHisAlaAlaAlaValLeuGlyArgAspThrGlnLeuArgValAlaAlaAlaHisLeu 274

Db 386 GACCATCTCTGTAGAGTCTTGGCGGATACATCAGTTTCAGAGTCGCTTGGGCACATCTT 327

QY 275 LeuAspHisArgGlyGlnPheHis 282

Db 326 CTTGATCATCGCGGCGAGTTTCAT 303

RESULT 9

AAZ236913/c

ID AAZ36913 standard; DNA; 837 BP.

AC AAZ36913;

XX 13-MAR-2000 (first entry)

XX DNA encoding a homologue of activator of G protein signalling AGS1.

XX Activator of G protein signalling; AGS; ras-related G protein;

XX GTP hydrolysis; G protein activity; pheromone response pathway;

XX G protein-coupled signal transduction; G-gamma selectivity;

XX cellular signal transduction; AGS1 homologue; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT 1..837

FT /tag= a

FT /product= "AGS1 homologue"

PN WO958670-A1.
 PD 18-NOV-1999.
 XX
 XX 07-MAY-1999; 99WO-US10151.
 XX
 XX 08-MAY-1998; 98US-0084842.
 PR 07-OCT-1998; 98US-0103355.
 XX
 PA (CADU-) CADUS PHARM CORP.
 XX
 PI Cismowski M, Duzic E;
 DR WPI: 2000-072337/06.
 DR P-PSDB; MAY53923.
 XX
 XX A new activator of G protein signalling used to treat disorders
 PT characterized by an aberrant AGS protein activity -
 XX
 PS Example 15; Page 143-144; 162pp; English.
 XX
 CC The present sequence encodes a homologue of a human AGS1 (activator
 CC of G protein signalling (AGS)) protein. The AGS cDNA sequence was
 CC isolated from a human liver cDNA library. The AGS protein exhibits
 CC homology to ras-related G proteins, and contains alterations in
 CC conserved amino acids consistent with a deficiency in GTP hydrolysis
 CC activity. AGS stimulates G protein activity, G protein-coupled signal
 CC transduction and the pheromone response pathway in a receptor-independent
 CC manner. The AGS protein also shows G-gamma selectivity, as measured by
 CC growth assays in yeast expressing various mammalian G-gamma constructs,
 CC and tissue-specific expression, as measured by Northern blot analysis.
 CC The AGS protein can be used to screen for compounds that modulate
 CC cellular signal transduction. The protein is used to treat disorders
 CC characterized by an aberrant AGS protein activity or AGS nucleic acid
 CC expression.
 XX
 SQ Sequence 837 BP; 177 A; 272 C; 233 G; 155 T; 0 other;
 Alignment Scores:
 Pred. No.: 1.05e-31 Length: 837
 Score: 579.50 Matches: 146
 Percent Similarity: 61.59% Conservative: 24
 Best Local Similarity: 52.90% Mismatches: 93
 Query Match: 41.07% Indels: 13
 DB: 21 Gaps: 5
 US-09-709-103-1f4 (1-282) x AAZ36913 (1-837)
 QY 4 AspAlaAlaLeuValLeu--GlyLeuAlaAlaGlyValGlyLeuLeuAlaAspVal 22
 DB 831 GATGTCGACCTGTCTCCCTGCACGGGCTGGCTTCCCGAAGACCTTGGCTGATGTA 772
 QY 23 HisGluValAlaValAlaGlyProAlaArgGlyGlyCysHisAspAlaLysGlyVal 42
 DB 771 CTTGAGGTCACTGTTACCTGGCGGCGGCGGCGAAGGGCGAGACCATGAGGCTC 712
 QY 43 AlaArgValAlaAlaAlaAlaAlaAlaGlyProGlnGlnLeuLeuValProGlnArg 62
 DB 711 ---CATCTCTTGCACCGCGCATGTCAGAAAGGCGCTGGG----- 676
 QY 63 LeuLeuValGlnHisValAlaValLeuHisAspLeuAlaValGlnValTrpAlaHis 82
 DB 675 -----GTGAAAGCGCTCACCGTACGACGAGATCTTGGATGTCAGGGGGGCTCAT 622
 QY 83 LeuAlaGlyGlnLeuGlyHisGlyGlyGluAlaGlnHisLeuValGlnAlaVal 102
 DB 621 CTCGTGTGCGACCTTGGCCATCTTAAGAGCACGTGAACATCTTCCTCACGTTGTT 562
 QY 103 LeuLeuGlyArgAspLeuGluValGlyAlaAlaLeuGlyValAlaHisGlnLeu 122
 DB 561 CTTCTTGGCGCACCTCGAAGTACGGCGCATCTTC---GTCCGCCGACACACACCTC 505
 QY 123 AspLeuAlaLeuValHisLeuAlaValGluValAla---ValThrLeuValAlaAlaAsp 141

DB 504 GGCCTCGGTGTGGGACACCTGGCGGCACAGCTCGCGTCTTGTTCGACAGAT 445
 QY 142 AspGlnGlyHisValHisValLeuLeuGlyPheValLeuGluAlaArgLeuGlyValGlu 161
 DB 444 GACCATGGGACAGCTCCCGCGCTCTTGTGTCTTCTTACAGACAGATTCAGCTCCAG 385
 QY 162 AspLeuLeuProGluProLeuHisLeuLeuGlyValAlaValAlaGlnThrGlnHis 181
 DB 384 GATCTGCTTCTGAAGGGCGCTTGACCTCATGGAAGACCTCCGGTTATCCAGCGCTGAAC 325
 QY 182 GlnAspGluLeuValSerCysGluAspGlyGluAlaProHisGlyGlyGluArgValAla 201
 DB 324 CAGATGAAGACATCCCTCTTGAGATGACAGACCTCCGATGCGGGAAGGGGTT 265
 QY 202 AlaGlyArgValGluAspValGluLeuValAspLeuAlaAlaAspGlyValGluLeuAla 221
 DB 264 GCCAGAGTATCCAGATGTCTGAGCTGTACATGTGCGCGCGATGTTTACCTTACG 205
 QY 222 ValGluValLeuAspGlyArgArgValGlyValLeuGluAlaAlaGlyGluGluAlaArg 241
 DB 204 GTGGAAGTCTTCATGT 145
 QY 242 HisAspGlyArgLeuAlaHisLeuGlyArgAlaGluAlaAspAspHisAlaAlaValLeu 261
 DB 144 CACGATGAGCTCTTGGCCACCCGAGAGGACACCCAGACACCATTCGGGTATGAGTTT 85
 QY 262 GlyArgAspThrGlnLeuArgValAlaAlaGlnHisLeuLeuAspHis 277
 DB 84 GCGCGGACACTGAGGTGCACTTCCCGCTGGAACAAGCTTCATCAT 37
 RESULT 10
 ID ABL92076/c
 ID ABL92076 standard, cDNA; 2832 BP.
 XX
 AC ABL92076;
 XX
 DT 30-MAY-2002 (first entry)
 XX
 XX Human Tumour Endothelial Marker polynucleotide SEQ ID NO 174.
 XX
 KW Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
 KW normal endothelial marker; pan-endothelial marker; immunostimulant;
 KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
 KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
 KW psoriasis; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200210217-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 01-AUG-2001; 2001WO-US24031.
 XX
 PR 02-AUG-2000; 2000US-222599P.
 PR 11-AUG-2000; 2000US-224360P.
 PR 11-APR-2001; 2001US-282850P.
 XX
 PA (UYGO) UNIV JOHNS HOPKINS.
 XX
 PI St Croix B, Kinzler KW, Vogelstein B;
 XX
 DR WPI: 2002-291856/33.
 XX
 XX An isolated molecule comprising an antibody variable region which
 PT specifically binds to an extracellular domain of a tumor endothelial
 PT marker (TEM) protein, useful for inhibiting tumor growth -
 XX
 PS Disclosure; Page 119-120; 331pp; English.
 XX
 CC The invention relates to an isolated molecule comprising an antibody
 CC variable region which specifically binds to an extracellular domain of a

US-09-709-103-1F4 (1-282) X ABL92087 (1-2973)


```

QY 4 AspAlaAlaLeuLeuValLeu---GlyLeuAlaAlaGlyAlaGlyLeuLeuAlaAspVal 22
Db 1002 GATGGGCACTGTCTCCCTTCACGGGCTGGCTCCCGAGAGACCTTGGCTTGAATGA 943
QY 23 HisGluValAlaValAlaValAlaGlyProAlaArgGluGlyCysHisAspAlaValGlyVal 42
Db 942 CTTGGAGTCACTGTGAGCGTGGGGCGGCGAGAGGCGAGACCATGCGATAGGGGTG 883
QY 43 AlaArgValAlaAlaAlaAlaAlaAlaGlyProGlnGlnLeuLeuValProGlnArg 62
Db 882 ---CATCTCTTGAGCGGGCGGCGATGAGAGGGCTGGG----- 847
QY 63 LeuLeuValGlnHisValAlaAlaValLeuHisArgAspLeuAlaValGlnValAlaHis 82
Db 846 -----GTGGAGAGGCGTACCGTACCGATGACGAGATCTTCGATGACGAGGGGGCTCAT 793
QY 83 LeuAlaGlyGlnLeuGlyHisGlyGlyGluArgAlaGlnHisLeuValGlnAlaAlaVal 102
Db 792 CTCTGTGGGCGAGCTTGGCGACATGCTGAAGAGACGATGACATCTCTGTCGACGTTGGTGT 733
QY 103 LeuLeuGlyArgAspLeuGlyValAlaGlyAlaAlaLeuGlyValAlaHisGlnLeuLeu 122
Db 732 CTTCTTGGCGACACCTCGAAGTGGGCGAGTTCTC---GTCCCGGACACCGACGCTC 676
QY 123 AspLeuAlaLeuValHisLeuAlaValGluValAla---ValThrLeuValAlaAlaAsp 141
Db 675 GGCCTCGGTGGTGGCGACCTGGCGGACAGCTCGCGTGGTCTCTTGTGGCACAGAT 616
QY 142 AspGlnGlyHisValHisValLeuLeuGlyPheValLeuGlnAlaArgLeuGlyValGlu 161
Db 615 GACCATGGGAGCGTCCCGCCCTCTTGGTCTTGTCTTCAAGGACAGATGACCTCCAG 556
QY 162 AspLeuLeuProGluProLeuHisLeuLeuGlyGlyValAlaValAlaGlnThrGlnHis 181
Db 555 GATCTGCTTCTGGAAGCGCTTGACTCATGAGAGGACTCCCGGTTATCCAGGCTGAAC 496
QY 182 GluAspGlyAsnValSerCysGluAspGlyGluAlaProHisGlyGlyGluArgValAla 201
Db 495 CAGAGTGAAGACATCCCTCTGTGAGATGAGACAGCTCCGACATGGCGGAGAGGCTGTG 436
QY 202 AlaGlyArgValGluAspValGluLeuValAspLeuAlaAlaAspGlyValGluLeuVal 221
Db 435 GCCAGAGGTATCCAGAGATGCGAGCTGATGATGCTGCCGCGGATGTTGATACCTTACG 376
QY 222 ValGluValLeuAspGlyArgValGlyValAlaLeuGlnAlaAlaGlyGluGlnValArg 241
Db 375 GTGGAGTCTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 316
QY 242 HisAspGlyArgLeuAlaHisLeuGlyArgAlaGluAspAspHisAlaAlaValLeu 261
Db 315 CACGATGAGAGCTTCTCCACCCGAGAGGACACCCAGACACACCATGCGGTATGATGTTT 256
QY 262 GlyArgAspThrGlnLeuArgValAlaArgAlaHisLeuLeuAspHis 277
Db 255 GGGGGGACACATGAGCGTCACTGTCGGGTGACAAAGTCTTCATCAT 208

RESULT 12
ABK71563/C
ID ABK71563 standard; cDNA, 3427 BP.
XX
XX ABK71563;
XX
XX 30-JUL-2002 (first entry)
XX
XX Human dithp polynucleotide #29.
XX
XX Human, dithp, diagnostic and therapeutic polynucleotide; gene; ss; bone;
XX cell proliferative disorder; cancer; tumour; autoimmune disorder; brain;
XX inflammatory disorder; viral infection; bacterial infection; seizure;
XX fungal infection; parasitic infections; neurological disorder; breast;
XX endocrine disorder; metabolic disorder; developmental disorder; cervix;
XX gastrointestinal disorder; transport disorder; gene therapy; kidney;

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KM adrenal gland; bone marrow; lung; ovary; pancreas; prostate; spleen;
KM skin; testis; thymus.
XX
XX Homo sapiens.
XX
XX WO20020754-A2.
XX
XX 14-MAR-2002.
XX
XX 29-AUG-2001; 2001WO-US27127.
XX
XX 05-SEP-2000; 2000US-229747P.
XX 05-SEP-2000; 2000US-229748P.
XX 05-SEP-2000; 2000US-229749P.
XX 05-SEP-2000; 2000US-229750P.
XX 05-SEP-2000; 2000US-229751P.
XX 05-SEP-2000; 2000US-230583P.
XX 05-SEP-2000; 2000US-230585P.
XX 05-SEP-2000; 2000US-230587P.
XX 05-SEP-2000; 2000US-230589P.
XX 05-SEP-2000; 2000US-230591P.
XX 05-SEP-2000; 2000US-230593P.
XX 05-SEP-2000; 2000US-230595P.
XX 05-SEP-2000; 2000US-230597P.
XX 05-SEP-2000; 2000US-230599P.
XX 05-SEP-2000; 2000US-230601P.
XX 05-SEP-2000; 2000US-230603P.
XX 05-SEP-2000; 2000US-230605P.
XX 05-SEP-2000; 2000US-230607P.
XX 05-SEP-2000; 2000US-230609P.
XX 05-SEP-2000; 2000US-230611P.
XX 05-SEP-2000; 2000US-230613P.
XX 05-SEP-2000; 2000US-231167P.
XX
XX (INCYTE) INCYTE GENOMICS INC.
XX
XX Stuart J, Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman DJ,
XX Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE, Dahl CR,
XX Moriyma MG, Bradley DJ, Rohatgi SD, Harris B, Roseberry AM,
XX Gerstin EH, Peralta CH, David MH, Panzer SR, Flores V, Dafo A,
XX Marwaha K, Chen AJ, Chang SC, Au AP, Inman RR;
XX WPI; 2002-383054/41.
XX P-PSDB; ABG59971.
XX
XX An isolated polynucleotide useful in diagnostics and therapeutics -
XX
XX Claim 1; Page 419-420; 686pp; English.
XX
XX The invention relates to human diagnostic and therapeutic (dithp)
XX polynucleotides and their associated polypeptides (dithp polypeptides).
XX The sequences of the invention are used in the treatment and diagnosis of
XX cell proliferative disorders (e.g. atherosclerosis, cirrhosis), cancers
XX (e.g. tumours of the adrenal gland, bone, bone marrow, brain, breast,
XX cervix, kidney, lung, ovary, pancreas, prostate, skin, spleen, testis or
XX thymus), autoimmune/inflammatory disorders (e.g. asthma, bronchitis,
XX psoriasis, osteoporosis), viral infections, bacterial infections, fungal
XX infections, parasitic infections, developmental disorders (e.g. anaemia,
XX epilepsy), seizure disorders (e.g. cerebral palsy, spina bifida),
XX endocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders
XX (e.g. obesity, diabetes), neurological disorders (e.g. stroke,
XX amyotrophic lateral sclerosis, multiple sclerosis), gastrointestinal
XX disorders (e.g. ulcerative colitis, lysinuria) and transport disorders
XX (e.g. myotonic dystrophy, cataracta, peripheral neuropathy). Sequences
XX ABK71535-ABK71809 represent human dithp polynucleotides of the invention.
XX
XX Sequence 3427 BP; 682 A; 1145 C; 935 G; 665 T; 0 other.
XX
XX Alignment Scores:
XX Pred. No.: 4,29e-31 Length: 3427
XX Score: 579.50 Matches: 146
XX Percent Similarity: 61.59% Conservative: 24
XX Best Local Similarity: 52.90% Mismatches: 93

```


Tue Dec 31 15:27:52 2002

Query Match: 41.07% Indels: 13
DB: 24 Gaps: 5

US-09-709-103-1F4 (1-282) x ABK71563 (1-3427)

Qy 4 AspalalaLeuValLeu---GlyLeuAlaAlaGlyAlaGlyLeuLeuAlaAspVal 22
Db 1438 GATGGTGCACCTTGTCCCTCTCACGGGCTGGCTCCCGAAGGACCTTGGCTTGTATGTA 1379

Qy 23 HisGluValAlaValTyrAlaGlyProAlaArgGluGlyCysHisAspAlaLysGlyVal 42
Db 1378 CTTGAGGTCACTTTGACGCTGGCGGGCGGCGAAGGGCGAGACCATGCATAGGCGTC 1319

Qy 43 AlaArgValAlaAlaAlaAlaAlaGlyProGlnGlnLeuLeuValProGlnArg 62
Db 1318 ---CATCTCTTACGCGCGCGATGCAGAGGGCTTGGG----- 1283

Qy 63 LeuLeuValGlnHisValAlaValLeuHisArgAspLeuAlaValGlnValTrpAlaHis 82
Db 1282 -----GTGGAAGGCGTCACTGCTACCGAGATCTTGCATGCGAGGGGGCTCAT 1229

Qy 83 LeuAlaGlyGlnLeuGlyHisGlyGluGluArgAlaGluHisLeuValGlnAlaVal 102
Db 1228 CTCGTGTGCAGCTTGGCCATCTCTGAAGAGCACGTAGAACATCTCGTCCACGTTGGTGT 1169

Qy 103 LeuGluGlyArgAspLeuValGlyAlaAlaLeuGlyValValAlaHisGlnLeuLeu 122
Db 1168 CTTCTTGGCGGACACCTCGAAGTAGCGGAGTTCTC---GTGCGCGACACCGAGCTC 1112

Qy 123 AspLeuAlaLeuValHisLeuAlaValGluValAla---ValThrLeuValAlaAlaAsp 141
Db 1111 GGCCTCGTGGTGGGCACCTGGCGGCACAGCTCGCGTGTCTTGTGTGCCACAGAT 1052

Qy 142 AspGlnGlyHisValHisValLeuLeuGlyPheValLeuGluAlaArgLeuGlyValGlu 161
Db 1051 GACCATGGGCGAGCTCCGCGCCCTCTTGTGTCTTTCATGCGAGGACTTACCTCCAG 992

Qy 162 AspLeuLeuProGlnProLeuHisLeuLeuGluGlyValAlaValValGlnThrGluHis 181
Db 991 GATCTGCTTCTGAAGGCGCTTGACCTCATCGAAGGACTCCCGTGTATCCAGGCTGAACAC 932

Qy 182 GlnAspGluAsnValSerCysGluAspGlyGluAlaProHisGlyGlyGluArgValVal 201
Db 931 CAGGATGAACACATCCCTGTAGGATGGACACCTGCGCATGGCGGGAAGGGTGGT 872

Qy 202 AlaGlyArgValGluAspValGluLeuValAspLeuAlaAlaAspGlyValGluLeuAla 221
Db 871 GCCAGAGGTATCCAGGATGTCAGCTGGTACATGTCGCGCGGATGTTGTATACCTTACG 812

Qy 222 ValGluValLeuAspGlyArgArgValGlyValLeuGluAlaAlaGlyGluGluAlaArg 241
Db 811 GTGGAAGTCTCGATGTGGTGTGTACTGCTCTCAAGCGGCGCATTTGAGGAAGCGAGA 752

Qy 242 HisAspGlyArgLeuAlaHisLeuGlyArgAlaGluAspAspHisAlaLeuAlaValLeu 261
Db 751 CACGATGGAGCTTGTGCGCCACCGAGAGGACCACGACCCACCATGCGGTATGAGTTT 692

Qy 262 GlyArgAspThrGlnLeuArgValAlaAlaArgAlaHisLeuLeuAspHis 277
Db 691 GCGGGGACACTGAGCGTGCAGTCCCGCTGCGACAAAGTCTTCATCAT 644

RESULT 13
ABL92134/c
ID ABL92134 standard; cDNA; 3020 BP.
XX ABL92134;
XX AC
XX XX
DT 30-MAY-2002 (first entry)
XX Mouse Tumour Endothelial Marker polynucleotide SEQ ID NO 292.
DE Human; mouse; rat; TEM; tumour endothelial marker; pan-endothelial;
KW normal endothelial marker; immunostimulant;

KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
KW psoriasis; gene; ss.
XX Mus musculus.
XX WO200210217-A2.
XX 07-FEB-2002.
XX 01-AUG-2001; 2001WO-US24031.
XX 02-AUG-2000; 2000US-222599P.
XX 11-AUG-2000; 2000US-224360P.
XX 11-APR-2001; 2001US-282850P.
XX (UYJO) UNIV JOHNS HOPKINS.
XX St Croix B, Kinzler KW, Vogelstein B;
XX WPI; 2002-291856/33.
XX P-PSDB; ABB90781.
XX An isolated molecule comprising an antibody variable region which
XX specifically binds to an extracellular domain of a tumor endothelial
XX marker (TEM) protein, useful for inhibiting tumor growth -
XX Disclosure; Page 294-295; 33pp; English.
XX The invention relates to an isolated molecule comprising an antibody
XX variable region which specifically binds to an extracellular domain of a
XX tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
XX ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
XX proteins have cytostatic, immunostimulant and antiangiogenic activity.
XX They are useful for inhibiting tumour growth, neoangiogenesis in
XX subjects bearing a vascularised tumour, polycystic kidney disease,
XX diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse
XX and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and
XX ABB90721-ABB90789) are disclosed, as are marker oligonucleotide
XX sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and
XX ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074;
XX and pan-endothelial markers (PEM) ABL91903-ABL91995.
XX Sequence 3020 BP; 690 A; 848 C; 780 G; 702 T; 0 other;
SQ

Alignment Scores:
Pred. No.: 1.45e-25 Length: 3020
Score: 498.50 Matches: 127
Percent Similarity: 58.42% Conservative: 36
Best Local Similarity: 45.52% Mismatches: 103
Query Match: 35.33% Indels: 13
DB: 24 Gaps: 5

US-09-709-103-1F4 (1-282) x ABL92134 (1-3020)

Qy 1 LeuAlaAspAspAlaAlaLeuLeuValLeu---GlyLeuAlaAlaGlyAlaGlyLeuLeu 19
Db 1179 CTTCTCACTGGATGCTACACTTGTCTCTCGGGCTTGGCCCTCCGCTAGGACCTTGGC 1120

Qy 20 AlaAspValHisGluValAlaValTyrAlaGlyProAlaArgGluGlyCysHisAspAla 39
Db 1119 CTTGATGTACTTGTAGGTCACTGTTGACACTGGGCGCTGGGCAAGGGTGAAGACCATGCC 1060

Qy 40 LysGlyValAlaArgValAlaAlaAlaAlaAlaAlaGlyProGlnGlnLeuLeuVal 59
Db 1059 ATAGGACCTCGACCTT---AGTCGCGCATGTCAGAAAGGCGCGGG--- 1015

Qy 60 ProGlnArgLeuLeuValGlnHisValAlaValLeuHisArgAspLeuAlaValGlnVal 79
Db 1014 -----GTGAAAAGCATCGCGTACTGTCACCGAGATCTTATGTGTGCGAGTGC 970

Qy 80 TrpAlaHisLeuAlaGlyGlnLeuGlyHisGlyGluGluArgAlaGluHisLeuValGln 99
Db 80 TrpAlaHisLeuAlaGlyGlnLeuGlyHisGlyGluGluArgAlaGluHisLeuValGln 99


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Db 969 AGGGCTCATCTATGGGCGACCTTGGCCATGCTGTAACAGCACATGATCTCTTAC 910
QY 100 AAlaAlaValLeuLeuGlyArgAspLeuGluValGlyAlaAlaLeuGlyValAlaHis 119
Db 909 ATTAGTCTCTTCTGGTGAACCTCGAATAGCCGAGTTTC--ATACACAGACAC 853
QY 120 GlnLeuLeuAspLeuAlaLeuValHisValGluValAlaValThr--LeuVal 138
Db 852 CAGCAGCTCAGCTCCATGAGGAGGAGCCTGGCGCAGCTCAGCTGATGATCTTCTT 793
QY 139 AAlaAlaAspAspGlnGlyHisValHisValLeuLeuGlyPheValLeuGluValArgLeu 158
Db 792 CCCACAGATACCCATGAGGAGCTGCTGCTCTCTGTTTATCTTTCAGGACGACTT 733
QY 159 GlyValGluAspLeuLeuProGlnProLeuHisLeuLeuGluGlyValAlaValAlaGln 178
Db 732 GACCTCCAGGATCTGTTCTGAGGCGCTTGAACCTCAAGAGACCTCCGCGCATTCAG 673
QY 179 ThrGluHisGlnAspGluAsnValSerCyseGluAspGlyGluAlaProHisGlyGlu 198
Db 672 GCTGACACCCAGATGAAGACATCTCTGTAGAGATGAGAGCCGCGCATGCGAGGAA 613
QY 199 ArgValAlaAlaGlyArgValGluValGluValGluValAspLeuAlaAlaAspGlyVal 218
Db 612 TGGGTGTTGCGCAGAGGTGTCAGGATATCCAGCTGTATCATGCTCCCGGATGTTGA 553
QY 219 GluLeuAlaValGluValLeuAspGlyArgArgValGlyValLeuGluAlaAlaGlyGlu 238
Db 552 CACCTTGATGAAGAACTCTGATATGAGGCGGTGATCTGCTCAAGAGCGCATTTAG 493
QY 239 GluAlaArgHisAspGlyArgLeuAlaHisLeuGlyArgAlaGluAspHisAlaAla 258
Db 492 GAACCGGAGACATGAGCTCTTGGCCACTCGGAGGACCCAGAGACACCATGCGGTA 433
QY 259 AlaValLeuGlyArgAspTrpGlnLeuArgValAlaArgAlaHisLeuLeuAspHis 277
Db 432 GGAATCTTTCAGGAGGACATTTAGTGTGTCAGTTCCACCTGGAAGAAGTCTTATCAT 376

```

RESULT 14
ID AAS90571/c
AAS90571 standard; cDNA, 951 BP.

```

XX AC AAS90571;
XX DT 13-FEB-2002 (first entry)
XX DE DNA encoding novel human diagnostic protein #26375.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX OS Homo sapiens.
XX PN MO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001MO-US08631.
XX PR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX DR MPI: 2001-639362/73.
XX DR P-PSDB; ABG26384.
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensic, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity.

```

XX Claim 1; SEQ ID No 26375; 103bp; English.

PS The invention relates to isolated polynucleotide (I) and
 XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polypeptide chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 951 BP; 202 A; 291 C; 293 G; 165 T; 0 other;

Alignment Scores:
 Pred. No: 1.1e-24 Length: 951
 Score: 478.50 Matches: 133
 Percent Similarity: 57.85% Conservative: 18
 Best Local Similarity: 50.96% Mismatches: 87
 Query Match: 33.91% Indels: 23
 DB: Gaps: 8

US-09-709-103-1f4 (1-282) x AAS90571 (1-951)

```

QY 4 AspAlaAlaLeuLeuValLeu---GlyLeuAlaAlaGlyValGlyLeuAlaAspVal 22
Db 876 GATGTCGACCTTGTCCCTTTCACGGGCTTCCGGAAGACCTTGGCTTGAATGTA 817
QY 23 HisGluValAlaValTyrAlaGlyProAlaArgGluGlyCysHisAspAlaGlyVal 42
Db 816 CTGAGGTCAGCTTGAAGCTGCGGCGGCGGAGGCGGAGGACCATGAGCGCTC 757
QY 43 AlaArgValAlaAlaAlaAlaAlaAlaGlyProGlnGlnLeuLeuValProGlnArg 62
Db 756 ---CATCTCTTTCAGCGCGGCGCATGACAGAGGCGCTGG----- 721
QY 63 LeuLeuValGlnHisValAlaValLeuHisArgAspLeuAlaValGlnValTrpAlaHis 82
Db 720 -----GTGGAAGGCGTCAACCGTATCTGACGAGATCTTGGATGCGAGGCGGCGTCA 667
QY 83 LeuAlaGlyGlnLeuGlyHisGlyGlnGluArgAlaGluHisLeuValGlnAlaValAla 102
Db 666 CTCGTGTGCGACGCTTGGCGCATGCGAAGACGACGACATCTCGTCCAGCTTGGTGT 607
QY 103 LeuLeuGlyArgAspLeuGluValGlyAlaAlaLeuGlyValValAlaHisGlnLeuLeu 122
Db 606 CTTCTTGGCGCAGCCTTGAAGTGAAGGCGCAGTTTC---GTGCGCCGACACAGCAGCTC 550
QY 123 AspLeuAlaLeuValHisLeuAlaValGluValAla---ValThrLeuValAlaAlaAsp 141
Db 549 GGCCTCGGTGCGGCGACCTGCGGCGACAGTCCCGTGTCTTGTGGCCACAGAT 490
QY 142 AspGlnGlyHisValHisValLeuLeuGlyPheValLeuGluAlaArgLeuGlyValGln 161
Db 489 GACCATGCGGACCTCCGCGCGCTTGTGTTCTTTCAGCAGAGACATTGACCTCCAG 430
QY 162 AspLeuLeu-----ProGluProLeuHisLeuLeuGluGlyValAlaVal 176
Db 429 GATCTGTAACTGCCAGACACATCTCCGACCCA-----TGCCTTGCCCTGCGGCC 379

```


CC types and for investigating cell differentiation. The method allows the
 CC methylation status of many C residues to be determined simultaneously.
 CC ABQ3410-ABQ54121 represent genomic DNA sequences used to illustrate the
 CC method for determining the degree of cytosine methylation described in
 CC the disclosure of the invention.

XX Sequence 624 BP; 127 A; 68 C; 206 G; 223 T; 0 other;
 SQ

Alignment Scores: 5.65e-21 Length: 624
 Pred. No.: 422.00 Matches: 81
 Score: 80.15% Conservativity: 28
 Percent Similarity: 59.56% Mismatches: 27
 Best Local Similarity: 29.91% Indels: 1
 Query Match: 24 Gaps: 0
 DB:

US-09-709-103-1F4 (1-282) x ABQ28318 (1-624)

QY 1 LeuAlaaspAlaAlaAlaLeuValLeuGlyLeuAlaAlaGlyAlaGlyLeuAla 20
 Db 409 CTAACCTAATTAACGACGCTCTTATCTTAACCTAATTAACGACGCTAACCCTTCGCG 350
 QY 21 AspValHisGluValAlaValTyAlaGlyProAlaArgGluGlyCysHisAspAlaLys 40
 Db 349 AATATACATAAAATCGTATATACGCTAAACCGACGCGGAAATAATACCATGATACCAA 290
 QY 41 GlyValAlaArgValAlaAlaAlaAlaAlaAlaAlaGlyProGlnGlnLeuValPro 60
 Db 289 AA-ATCGCCGGAATCGCGCGCGCGCGCGCTACCGACCGCGCAACACTTCTTATTCG 231
 QY 61 GlnArgLeuValGlnHisValAlaValLeuHisArgAspLeuAlaValGlnValTrp 80
 Db 230 CAACGCTTCTTATACAAACGCTCGCAATACTACACGGAACCTTACGATACAAATCTAA 171
 QY 81 AlaHisLeuAlaGlyGlnLeuGlyHisGlyGluArgAlaGluHisLeuValGlnAla 100
 Db 170 ACTCATCTCGCTAAACAACTTAACCAATAACGAAAAACGCGGAAACATCTAATCCAACT 111
 QY 101 AlaValLeuLeuGlyArgAspLeuGluValGlyAlaAlaLeuGlyValValAlaHisGln 120
 Db 110 ACTATCTTCTTAACCGAATCTCGAATAAATACGCAACGCTAAATAATCGTCGCCACCA 51
 QY 121 LeuLeuAspLeuAlaLeuValHisLeuAlaValGluValAlaValThr 136
 Db 50 CTACTCGATCTCGGCTAATCCACCTCGGATATAAATAATCGCGATCACC 3

Search completed: December 30, 2002, 16:35:28
 Job time : 375 secs

QY 177 ValGlnThrGluHisGlnAspGluAseValSerCysGluAspGlyGluAlaProHisGly 196
 Db 378 -----CCAGCCACAGGACAGTGGGCTCCTACCTGTGAGATGGACAGCTCGCATGGC 325
 QY 197 GlyGluArgValValAlaGlyArgValGluAspValGluValAspLeuAlaLasp 216
 Db 324 GGGAGGGGTGGTTGCCAGAGGTATCCAGGATGTCGAGCTGTGTATCATCTGCCGCGGAT 265

QY 217 GlyValGluLeuAlaValGluValLeuAspGlyArgArgValGlyValLeuGluAlaLa 236
 Db 264 GTTGTATACCTTACCGTGGAGTCTCGATGGTGGTGTACTGTCTCTAAAGCGGCC 205
 QY 237 GlyGluGluAlaArgHisAspGlyArgLeuAlaHisLeuGlyArgAlaGluAspHis 256
 Db 204 ATTGAGGAGGACGACACGATGGAGCTTGTGCCACCGGAGGACCCAGCACCATCAT 145

QY 257 Ala 257
 Db 144 GCG 142

RESULT 15
 ABQ28318/c
 ID ABQ28318 standard; DNA; 624 BP.
 XX
 AC ABQ28318;

DT 12-JUL-2002 (first entry)
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 14909.
 KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
 KW drug; side effect; cancer; central nervous system; cardiovascular;
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;
 KW SNP; cell differentiation; ds.

XX Homo sapiens.
 XX WO200218632-A2.
 XX PD 07-MAR-2002.
 XX 01-SEP-2001; 2001WO-EP10074.
 XX 01-SEP-2000; 2000DE-1043826.
 PR 05-SEP-2000; 2000DE-1044543.
 XX
 PA (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K, Guetig D;
 PI WPI; 2002-371829/40.
 XX
 XX Determining the degree of cytosine methylation in genomic DNA, useful
 PT for diagnosis and prognosis, comprises selective hybridization of
 PT amplicons from chemically treated DNA -
 XX
 XX Claim 12; 56pp + Sequence Listing; 56pp; German.

XX This invention describes a novel method for determining the degree of
 XX methylation of a particular cytosine in a motif 5'-CpG-3', present in a
 CC genomic sample of DNA. The sample is treated chemically to convert
 CC cytosine (C) but not methylated C to uracil, then part of the genomic
 CC DNA that contains the target C is amplified to form a labeled amplicon.
 CC The amplicon is hybridised to two classes, each with at least one
 CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
 CC and the degree of hybridisation to both classes is determined from the
 CC label on the amplicon. From the ratio of labels hybridised to the two
 CC classes of oligomers, the degree of methylation is calculated. The method
 CC is used: (i) for diagnosis and/or prognosis of side effects of
 CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
 CC of the central nervous, cardiovascular, gastrointestinal and respiratory
 CC systems etc., particularly by detecting mutations or single nucleotide
 CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue

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OM protein - nucleic search, using frame_plus.p2n model

Run on: December 30, 2002, 14:47:25 ; Search time 3135 Seconds

(without alignments)
2617.860 Million cell updates/sec

Title: US-09-709-103-1f4
Perfect score: 1411
Sequence: 1 LADDAALVGLAAGGLA.....RDTQRAVARAHLLDRGQFH 282

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=xlp
-Q/cgm2.1/USPTO.spool/SULIVAN14/runat.30122002.144046.21500/app.query.fasta_1.455
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPC=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsun62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pct -NORM=ext -HEADSITE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=SULIVAN14@cgm.1.1.3637 @runat.30122002.144046.21500 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAB -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
GenEmbl:.*
1: gb_ba:.*
2: gb_hlg:.*
3: gb_in:.*
4: gb_om:.*
5: gb_ov:.*
6: gb_pat:.*
7: gb_ph:.*
8: gb_pl:.*
9: gb_pr:.*
10: gb_ro:.*
11: gb_sts:.*
12: gb_sy:.*
13: gb_un:.*
14: gb_vl:.*
15: em_ba:.*
16: em_fun:.*
17: em_hum:.*
18: em_in:.*
19: em_mu:.*
20: em_om:.*
21: em_or:.*
22: em_ov:.*
23: em_pat:.*
24: em_pi:.*
25: em_pl:.*
26: em_ro:.*
27: em_sts:.*
28: em_un:.*

Seg 1 Frame 4

29: em_vl:.*
30: em_hlg_hum:.*
31: em_hlg_inv:.*
32: em_hlg_other:.*
33: em_hlg_mus:.*
34: em_hlg_pln:.*
35: em_hlg_rtd:.*
36: em_hlg_mam:.*
37: em_hlg_vrt:.*
38: em_sy:.*
39: em_higo_hum:.*
40: em_higo_mus:.*
41: em_higo_other:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1411	100.0	846	9 AF498923	AF498923 Homo sapi
2	1411	100.0	979	9 AF172846	AF172846 Homo sapi
3	1411	100.0	1740	9 AF069506	AF069506 Homo sapi
4	1411	100.0	1758	9 BC018041	BC018041 Homo sapi
5	1398	99.1	1746	9 AF177335	AF177335 Homo sapi
6	1392	98.7	1187	9 AF153192	AF153192 Homo sapi
7	1348	95.5	4990	9 AF222979	AF222979 Homo sapi
8	1348	95.5	18334	9 AC020558	AC020558 Homo sapi
9	1338	94.8	5141	9 AF262018	AF262018 Homo sapi
10	1318	93.4	58882	2 AC073621	AC073621 Homo sapi
11	1314	93.1	183598	2 AC090608	AC090608 Homo sapi
12	963.5	68.3	1616	10 AF239157	AF239157 Rattus no
13	949.5	67.3	1612	10 BC034166	BC034166 Mus muscu
14	942.5	66.8	1621	10 AF009246	AF009246 Mus muscu
15	914	64.8	179124	10 AL603710	AL603710 Mouse DNA
16	914	64.8	247899	2 AC025909	AC025909 Mus muscu
17	641	45.4	162504	2 AC122995	AC122995 Rattus no
18	579.5	41.1	2832	6 AX393244	AX393244 Sequence
19	579.5	41.1	2832	6 AF279143	AF279143 Homo sapi
20	579.5	41.1	2973	6 AX393267	AX393267 Sequence
21	579.5	41.1	3058	9 BC013419	BC013419 Homo sapi
22	547	38.8	2639	9 HSM803172	HSM803172 Homo sapi
23	498.5	35.3	3020	6 AX393362	AX393362 Sequence
24	456.5	32.4	3469	10 AF134409	AF134409 Rattus no
25	371.5	26.3	114771	9 HS569D19	HS569D19 Human DNA
26	329.5	23.4	211071	10 AC076974	AC076974 Mus muscu
27	249.5	17.7	3391	9 BC030660	BC030660 Homo sapi
28	247.5	17.5	597	9 AY056037	AY056037 Homo sapi
29	247.5	17.5	597	9 AY059641	AY059641 Homo sapi
30	247.5	17.5	774	9 AB076888	AB076888 Homo sapi
31	247.5	17.5	2827	9 AK096600	AK096600 Homo sapi
32	247.5	17.5	17540	9 AC006538	AC006538 Homo sapi
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34	228.5	16.2	1249	6 AX430295	AX430295 Sequence
35	226	16.0	66031	2 AC118046	AC118046 Mus muscu
36	222.5	15.8	153386	2 AC103000	AC103000 Rattus no
37	217.5	15.4	2294	10 BC026377	BC026377 Mus muscu
38	201.5	14.3	3670	3 AY129454	AY129454 Drosophila
39	197.5	14.0	126901	2 AC091518	AC091518 Mus muscu
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42	190	13.5	2145	9 HSM803027	HSM803027 Homo sapi
43	188.5	13.4	1913	9 BC012362	BC012362 Homo sapi
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RESULT 1

ALIGNMENTS


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AF498923/c
LOCUS      AF498923      846 bp      mRNA      linear      PRI 01-MAY-2002
DEFINITION Homo sapiens activator of G protein signaling (RASD1) mRNA, complete cds.
ACCESSION  AF498923
VERSION     AF498923.1  GI:20379021
KEYWORDS
SOURCE      Homo sapiens.
ORGANISM    Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 846)
AUTHORS     Puh.H.L., Ikeda,S.R. and Aronstam,R.S.
TITLE       Direct Submission
JOURNAL     Submitted (05-APR-2002) cDNA Resource Center, Guthrie Research
            Institute, One Guthrie Square, Sayre, PA 18840, USA
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CDS         1..846
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BASE COUNT 176 a 288 c 252 g 130 t
ORIGIN
Alignment Scores:
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Score: 1411.00           Matches: 282
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%           Indels: 0
DB: 9                     Gaps: 0

US-09-709-103-1f4 (1-282) x AF498923 (1-846)
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Db 786 GATGTACATGAGTCTGCTGTGACCTGGCGCGCGCGCGGAGGTGCCAGATGCCAAA 727
Qy 41 GlyValAlaArgValAlaAlaAlaAlaAlaAlaAlaGlyProGlnGlnLeuValPro 60
Db 726 GCGCGTCCCGGGTCCCGCGCGCGCGCGCGCTGGCGCGCGCGAGCAGCTTCTGTTCG 667
Qy 61 GlnArgLeuLeuValGlnHisValAlaValLeuHisArgAspLeuAlaValGlnValTrp 80
Db 666 CAGCGCTCTTCTGTGACGACGCTGCAGTACTGCACCGAGACCTTGGCGTGCAGTCTGG 607
Qy 81 AlaHisLeuAlaGlyGlnLeuGlyHisGlyGluGluArgAlaGluHisLeuValGlnAla 100
Db 606 GCTCATCTCTGGGAGCTTGGCCATGGCGAGAGCGCGCGGACATCTGGTCCAGGCT 547
Qy 101 AlaValLeuLeuGlyArgAspLeuGluValGlyAlaAlaLeuGlyValAlaAlaHisGln 120
Db 546 GCTGTCTCTTCTGGCGAGATCTCGAAGTAGCGGAGCGCTGGGGGTCTGCGCCACCAG 487

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Qy 121 LeuLeuAspLeuAlaLeuValHisLeuAlaValGluValAlaValThrLeuValAlaAla 140
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Db 426 GATGACACAGGCGCAGCTCCAGTCTCTCTGTTTCTTGTGAGCAAGACTTGGTGTCT 367
Qy 161 GluAspLeuLeuProGluProLeuHisLeuLeuGluGlyValAlaValValGlnThrGlu 180
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Qy 181 HisGlnAspGluAsnValSerCysGluAspGlyGluAlaProHisGlyGlyGluArgVal 200
Db 306 CACCAAGATGAAACCTCTCTGTGAGATGAGAGGCGCGCATGGCGGGGAACGGGTG 247
Qy 201 ValAlaGlyArgValGluAspValGluLeuValAspLeuAlaAlaAspGlyValGluLeu 220
Db 246 GTTCCCGGACGCTGTCGAGGATGTCTGAGCTGTAGACCTCGCGCGGATGAGTAGAACTT 187
Qy 221 AlaValGluValLeuAspGlyArgValGlyValLeuGluAlaAlaGlyGluGluAla 240
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Qy 281 PheHis 282
Db 6 TTTCAT 1

RESULT 2
AF172846/c
LOCUS      AF172846      979 bp      mRNA      linear      PRI 05-JAN-2000
DEFINITION Homo sapiens ras-related protein (DEXRAS1) mRNA, complete cds.
ACCESSION  AF172846
VERSION     AF172846.1  GI:6014488
KEYWORDS    Homo sapiens.
SOURCE      Homo sapiens.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            Tu,Y. and Wu,C.
            Cloning, expression and characterization of a novel human
            Ras-related protein that is regulated by glucocorticoid hormone
            Biochim. Biophys. Acta 1489 (2-3), 452-456 (1999)
            20135605
            PUBMED 10673050
REFERENCE   2 (bases 1 to 979)
AUTHORS     Tu,Y. and Wu,C.
TITLE       Direct Submission
JOURNAL     Submitted (27-JUL-1999) Department of Cell Biology, University of
            Alabama at Birmingham, 1670 University Blvd., Birmingham, AL 35294,
            USA
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Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk
Email: cgabbs@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-shgc.stanford.edu>

Contact: (Dickson, Mark) mcdgpaxil@stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 32 Row: f Column: 11.

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BASE COUNT	387 a	576 c	501 q	294 t
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Alignment Scores:

Pred. No.:	2.33e-58	Length:	1758
Alignment scores:		Matches:	282
Score:	1411.00	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	100.00%	Gaps:	0
DG:	9		

UUS-09-709-103-1F4 (1-282) x BC018041 (1-1758)

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Qy	21	AspValHisGluValAlaValTyrAlaGlyProAlaArgGluGlyCysHisAspAlaLys	40
Db	998	GATGTACATGAGTTCGCTGTGTACGCTGGCGCGCGCGAAGGTGCCACGATGCCAA	939
Qy	41	GlyValAlaArgValAlaAlaAlaAlaAlaGlyProGlnGlnLeuLeuValPro	60
Db	938	GGCGTCGCCCGGTCGCCCGCGCGCGCTGCCGCGCCGAGCAGCTTCTGTGTCCG	879
Qy	61	GlnArgLeuLeuValGlnHisValAlaValLeuHisArgAspLeuAlaValGlnValTyr	80
Db	878	CAGCGCCCTTCTGTGCAGCAGCTGCAGTACTGCACCGAGACCTTGGCGTGCAGGCTCG	819
Qy	81	AlaHisLeuAlaGlyGlnLeuGlyHisGlyGluGluArgAlaGluHisLeuValGlnAla	100
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871	Db	GGCGTGGCCGGGTGGCGCGCGCGCGTGGCGGCCGCGAGCAGCTTCTGTTCGG812
61	Qy	GlnArgLeuLeuValGlnHisValAlaValLeuHisArgAspLeuAlaValGlnValTrp80
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81	Qy	AlaHisLeuAlaGlyGlnLeuGlyHisGlyGluGluArgAlaGluHisLeuValGlnAla100
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181	Qy	HisGlnAspGluAsnValSerCysGluAspGlyGluAlaProHisGlyGlyGluArgVal200
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331	Db	GGCGTGGAAAGTCTTCGATGTGTAGGCGGTGTCGAAAGCGCGCGGTGAGGAAGCG272
241	Qy	ArgHisAspGlyArgCgLeuAlaHisLeuGlyArgAlaGluAspHisAlaIleAlaVal260
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261	Qy	LeuGlyArgAspThrGlnLeuLeuArgValAlaArgAlaHisLeuLeuAspHisArgGlyGln280
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nb 157 TTTTCAT 146

DECIII.T A

RESULT 4
BC018041/0

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LOCUS					

LOCUS BC018041 1758 bp
DEFINITION Homo sapiens. RAS. dexamethasone-i-

DEFINITION

ACCESSION BC018041
IMAGE: 475, 482, 488a, 488b, 488c, 488d, 488e, 488f, 488g, 488h, 488i, 488j, 488k, 488l, 488m, 488n, 488o, 488p, 488q, 488r, 488s, 488t, 488u, 488v, 488w, 488x, 488y, 488z, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000, 1001, 1002, 1003, 1004, 1005, 1006, 1007, 1008, 1009, 1010, 1011, 1012, 1013, 1014, 1015, 1016, 1017, 1018, 1019, 1020, 1021, 1022, 1023, 1024, 1025, 1026, 1027, 1028, 1029, 1030, 1031, 1032, 1033, 1034, 1035, 1036, 1037, 1038, 1039, 1040, 1041, 1042, 1043, 1044, 1045, 1046, 1047, 1048, 1049, 1050, 1051, 1052, 1053, 1054, 1055, 1056, 1057, 1058, 1059, 1060, 1061, 1062, 1063, 1064, 1065, 1066, 1067, 1068, 1069, 1070, 1071, 1072, 1073, 1074, 1075, 1076, 1077, 1078, 1079, 1080, 1081, 1082, 1083, 1084, 1085, 1086, 1087, 1088, 1089, 1090, 1091, 1092, 1093, 1094, 1095, 1096, 1097, 1098, 1099, 1100, 1101, 1102, 1103, 1104, 1105, 1106, 1107, 1108, 1109, 1110, 1111, 1112, 1113, 1114, 1115, 1116, 1117, 1118, 1119, 1120, 1121, 1122, 1123, 1124, 1125, 1126, 1127, 1128, 1129, 1130, 1131, 1132, 1133, 1134, 1135, 1136, 1137, 1138, 1139, 1140, 1141, 1142, 1143, 1144, 1145, 1146, 1147, 1148, 1149, 1150, 1151, 1152, 1153, 1154, 1155, 1156, 1157, 1158, 1159, 1160, 1161, 1162, 1163, 1164, 1165, 1166, 1167, 1168, 1169, 1170, 1171, 1172, 1173, 1174, 1175, 1176, 1177, 1178, 1179, 1180, 1181, 1182, 1183, 1184, 1185, 1186, 1187, 1188, 1189, 1190, 1191, 1192, 1193, 1194, 1195, 1196, 1197, 1198, 1199, 1200, 1201, 1202, 1203, 1204, 1205, 1206, 1207, 1208, 1209, 1210, 1211, 1212, 1213, 1214, 1215, 1216, 1217, 1218, 1219, 1220, 1221, 1222, 1223, 1224, 1225, 12

VERSION BC018041.1 G

KEYWORDS: MGC.

SOURCE Homo sapiens.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele-

Mammalia; Eutheria;

REFERENCE 1 (bases 1 to 175

AUTHORS **Strausberg, R.**

TITLE	Direct Submission	Submitted (02 DEC 2001)	National Institute of Health	Mammalian
<p> TITLE Direct Submission Submitted (02 DEC 2001) National Institute of Health Mammalian </p>				

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QY	121	LeuLeuAspLeuAlaLeuValHisLeuAlaValAlaGIuValAlaValThrLeuValAlaAla	140
Db	698	CTGCTCGACTCGCGCTGGTCCACCTCGCGGTAAGAATCGCGGTACCTTTGTGCCGA	639
QY	141	AAPAspGlnGlyHisValHisValLeuLeuGIYpHeValLeuGlnAlaArgLeuGIYAla	160
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QY	161	GIUAAPLeuLeuProGlnProLeuHisLeuLeuGIuGlyValAlaValValGlnThrGIu	180
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Db	398	GGGCTGGAAATCTCTGATGATGTAAGGCTGTAGGCGCTCTGAAGCGCGGTAGGAAGG	339
QY	241	ArgHisAspGIYArgLeuAlaHisLeuGIYArgAlaGIuAspAspHisAlaIleAlaVal	260
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ACCESSION	AF177335		
VERSION	AF177335.1	GI:10503968	
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REFERENCE			
AUTHORS	1 (bases 1 to 1746)		
	Gu,J.-R., Wan,D.-F., Zhao,X.-T., Zhou,X.-M., Jiang,H.-Q., Zhang,P.-P.,		
	Qin,W.-X., Huang,Y., Qiu,X.-K., Qian,L.-F., He,L.-P., Li,H.-N., Yu,Y.,		
	Yu,J., and Han,L.-H.		
TITLE	Novel human cDNA clone with function of inhibiting cancer cell growth		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1746)		
AUTHORS	Gu,J.-R., Wan,D.-F., Zhao,X.-T., Zhou,X.-M., Jiang,H.-Q., Zhang,P.-P.,		
	Qin,W.-X., Huang,Y., Qiu,X.-K., Qian,L.-F., He,L.-P., Li,H.-N., Yu,Y.,		
	Yu,J., and Han,L.-H.		
TITLE	Direct Submission		
JOURNAL	Submitted (06-AUG-1999) National Laboratory For Oncogenes & Related Genes, Shanghai Cancer Institute, 25/Ln 2200 Xie Tu Road, Shanghai 200032, P.R. China		
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ORIGIN					
Alignment Scores:					
Pred. No.:		9.4e-58	Length:	1746	
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Query Match:		99.08%	Indels:	1	
DB:		9	Gaps:	0	
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Qy	1	LeuValASPAPSAAlAAlALeuLeuValLeuGlyLeuAlAAlAGlyValAGlyLeuLeuAlA	20		
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Qy	21	ASPValHISGLIValAlAValATYrAlAGlyProAlAArgGlyUGlyCysHisASPAlAlys	40		
Db	979	GATGTACATGAGAGGTGCGTGTGTACGCTGGGCGCGCGGAGAGGTGCCACATGCCAA	920		
Qy	41	GLYValAlAArgValAlAAlAAlAAlAAlAAlAGlyProGInGInLeuLeuValPro	60		
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Qy	61	GLAArgLeuLeuValGInHISValAlAValLeuHISArgASPLeuAlAValGValTyr	80		
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Qy	121	LeuLeuASPLeuAlALeuValHISLeuAlAValGInValAlAThrLeuValAlAAlA	140		
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Qy	141	ASPAPSGInGlyHISValHISValLeuLeuGlyPheValLeuGlyAlAArgLeuGlyVal	160		
Db	619	GATGACCAAGGGGACAGTCCAGGTTCTCTTGTTGTTCTTGAAGCAAGACTTGGTGTC	560		
Qy	161	GLAASPLeuLeuProGInProLeuHISLeuLeuGInGlyValAlAValAlGInThrGlu	180		
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Qy	181	HISGInASPGLuASPAlAserCysGlyASPGLyGluAlAProHISGLYGLIuArgVal	200		
Db	499	CACAGAGATGAAGAAAGTCTCTCTGAGAGATGGAGAGCGCCCATGGCGGGAACGGGTG	440		
Qy	201	ValAlAGlyArgValAGluASPValGluLeuValASPLeuAlAAlAASPGLyValGlyLe	220		
Db	439	GTTGGCGGAGCTGTGAGAGATGTGAAGCTGGTAGACTCTGGCGGGATGGAGTAGA	380		
Qy	220	uAlAValGluValLeuASPGLYArgArgValAGlyValLeuGInAlAAlAGlyGluAlA	240		
Db	379	TGGGATGGAAGTCCCATGTGTAGGCTGAAGCGTCCCGAAGCGCGGTGAGGAAGC	320		
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Db	319	GCGACACGATGGCGCTTGTGCCACCTTGGACGAGCGGAGATGACATGTGATAGCA	260		

Contact: sapiens@watson.wustl.edu
 ----- Summary Statistics
 Center Project name: H_NH0524F11

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPL11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frenken, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.rsgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is AC073621. Actual start of this clone is at base position 1 of RPL1-524F11; actual end is at base position 18334 of RPL1-524F11.

The sequence from position 1987 to 2253 was derived from PCR

product of RPL1-524F11 BAC DNA.

FEATURES

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Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Sogniez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE

JOURNAL

Submitted (03-MAR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE

3 (bases 1 to 183598)

AUTHORS

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barina, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Collangelo, M., Collins, S., Collamore, A., Cooke, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Fardo, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Navlor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE

JOURNAL

Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT

On Mar 22, 2002 this sequence version replaced gi:1645176. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L11985

Center clone name: 524_F_11

* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 178215: contig of 178215 bp in length

* 178216 178315: gap of 100 bp

* 178316 183598: contig of 5283 bp in length.

Location/Qualifiers

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/db_xref="taxon:9606"

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/clone.lib="RPC1-11 Human Male BAC"

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BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.:

5.69e-52 Length: 183598

Score: 1314.00 Matches: 280
Percent Similarity: 78.87% Conservative: 0
Best Local Similarity: 78.87% Mismatches: 2
Query Match: 93.13% Indels: 73
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US-09-709-103-1f4 (1-282) x AC090608 (1-183598)

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QY 81 AlaHisLeuAlaGlyGlnLeuGlyHisGlyGluGluArgAlaGluHisLeuValGlnAla 100
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QY 121 LeuLeuAspLeuAlaLeuValHisLeuAlaValGluValAlaValThrLeuValAlaAla 140
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QY 180 luhisGlnAspGluAsnValSer----- 187
Db 182026 AACACCAGGATGAACAGTCTCTCTAGAGGGGCGCAGAGAGCAGAAAGAGAGTGAG 181967

QY 187 ----- 187

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QY 187 ----- 187

Db 181906 TCTAAGCGGAAGCGCACTACTTCGCGCGCGCGCAGCGCGCTCGCGGGCGGCC 181847

QY 188 -----CysGlu 189
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus
 REFERENCE 1 (bases 1 to 1616)
 AUTHORS Fang, M., Jaffrey, S.R., Sawa, A., Ye, K., Luo, X. and Snyder, S.H.
 TITLE Dextrast: a G protein specifically coupled to neuronal nitric oxide
 synthase via CAPON
 JOURNAL Neuron 28 (1), 183-193 (2000)
 MEDLINE 20537828
 PUBMED 11086993
 REFERENCE 2 (bases 1 to 1616)
 AUTHORS Fang, M., Jaffrey, S.R., Sawa, A., Ye, K. and Snyder, S.H.
 TITLE Direct Submission
 JOURNAL Submitted (24-FEB-2000) Neuroscience, Johns Hopkins University, 725
 N. Wolfe St. Baltimore, MD 21205, USA
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 DB: 10 Gaps: 1
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 QY 21 AspValHisGlnValAlaAlaValTyrAlaGlyProAlaArgGlnGlyCysHisAspAlaLys 40
 Db 900 AATGTAACATGAGAGTGTATGACACGCTAGTCTGCGACGAAGGGCGCCAAAGATGCCAA 841

QY 41 GlyValAlaArgValAlaAlaAlaAlaAlaAlaGlyProGlnGlnLeuLeuValPro 60
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 QY 201 ValAlaGlyArgValAlaGlyAspValGlnLeuValAspLeuAlaAlaAspGlyValGlnLeu 220
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 QY 221 AlaValGlnValLeuAspGlyArgArgValGlyValLeuGlnAlaAlaGlyGlnGlnAla 240
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 QY 281 PheHis 282
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 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1612)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (02-JUL-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 REMARK NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
 COMMENT Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 58 Row: 9 Column: 5
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 6677672.

FEATURES

source

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1. .1612
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  /note="Vector: pCMV-SPORT6"
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  EQLVGDPPQRCAYFISAKNSLDPQFALFAMAKLPSEMSPLHRKVSVOYCDVLH
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  CVIS"

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CDS

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BASE COUNT 417 a 424 c 420 g 351 t
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Alignment Scores:
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 Best Local Similarity: 70.92% Mismatches: 57
 Query Match: 67.29% Indels: 1
 DB: 10 Gaps: 1

US-09-709-103-1P4 (1-282) x BC034166 (1-1612)

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QY 21 AspValHisGluValAlaValTyrAlaGlyProAlaArgGlyCysHisAspAlaLys 40
Db 890 AATGTACATGAGTCTGCTGTGACCTGGTCTGCACCAAGGCGCCACAGATGCCAA 831
QY 41 GlyValAlaArgValAlaAlaAlaAlaAlaAlaGlyProGlnGlnLeuValPro 60
Db 830 GGCACTCGCC--GTGGTGGCCCGCCCTCCGCTGGCCGACGACAGCTTCTTGTCTCT 774
QY 61 GlnArgLeuValGlnHisValAlaValLeuHisArgAspLeuAlaValGlnValTrp 80
Db 773 CAGACCTCTTGTGACGATGCTGCAGTACTGCACATACCTTGGCGGTGCAAGTCGGG 714
QY 81 AlaHisLeuAlaGlyGlnLeuGlyHisGlyGluGluArgAlaGluHisLeuValGlnAla 100
Db 713 GCTCATCTCGCTAGGACGCTTGGCCATGGCAAGAGCGCACGGAACATCTGTTCCAGCT 654
QY 101 AlaValLeuLeuGlyArgAspLeuValGlyAlaAlaLeuGlyValValAlaHisGln 120

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Db 653 GCTGTTCTTCTTGGCTGAGATCTCGAAGTAGGCACAAACGCTGAGGTCGTCAACCCACAG 594
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QY 141 AspAspGlnGlyHisValHisValLeuLeuGlyPheValLeuGluAlaArgLeuGlyVal 160
Db 533 AATGACACAGCGGACGCTCCACATCTCTTGTGTTTCTTCTTGTGACAGAGACTTGGTGT 474
QY 161 GluAspLeuLeuProGluProLeuHisLeuLeuGlyValAlaValValGlnThrGlu 180
Db 473 TAGATCTGCTGTTTGTAGCCCTTTCACCTCTTCGAATGAGTCCGGTGTCTAAGCTGAA 414
QY 181 HisGlnAspGluAsnValSerCysGluAspGlyCyluAlaProHisGlyGlyGluArgVal 200
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QY 201 ValAlaGlyArgValGluAspValGluLeuValAspLeuAlaAlaAspGlyValGluLeu 220
Db 353 ATTCCCGGATGTCTCCAGTATGTCACCTGTTAGCTGTTAGCTTCCGCGGATCGAGTAAACTT 294
QY 221 AlaValGluValLeuAspGlyArgValGlyValLeuGluAlaAlaGlyGluGluAla 240
Db 293 TCGGTGAAGTCTTCGATGTGAGGTTGTAAGCATCTCTGAAACGCGCCGTGAGGAAGCG 234
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Db 233 CGACACAATGGCGCTCTTCCCTCTTGGATGAGCGGATGACCATCTCTGTAGCAGTT 174
QY 261 LeuGlyArgAspThrGlnLeuArgValAlaAlaArgAlaHisLeuLeuAspHisArgGlyGln 280
Db 173 CTTGGCGGGATACCTCAGTTTTCAGATCGCTTGGGCACATCTTCTTGTATCATCGCGCCAG 114
QY 281 PheHis 282
Db 113 TTTTAT 108

RESULT 14
AF009246/c
LOCUS
DEFINITION Mus musculus ras-related protein (DEXRAS1) mRNA, complete cds.
ACCESSION AF009246
VERSION AF009246.1 GI:2253712
KEYWORDS
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1623)
AUTHORS Kempainen,R.J. and Behrend,E.N.
TITLE Dexamethasone rapidly induces a novel ras superfamily
JOURNAL member-related gene in AtT-20 cells
MEDLINE J. Biol. Chem. 273 (6), 3129-3131 (1998)
PUBMED 9452419
REFERENCE 2 (bases 1 to 1623)
AUTHORS Kempainen,R.J. and Behrend,E.N.
TITLE Direct Submission
JOURNAL Submitted (18-JUN-1997) Physiology & Pharmacology, Auburn
University College of Veterinary Medicine, 213 Greene Hall, Auburn,
AL 36849, USA
FEATURES
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CVIS"
BASE COUNT      412 a      437 c      417 g      357 t
ORIGIN
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Score:      942.50      Matches:      199
Percent Similarity:      79.08%      Conservative:      24
Best Local Similarity:      70.57%      Mismatches:      58
Query Match:      66.80%      Indels:      1
DB:      Gaps:      1
US-09-709-103-1F4 (1-282) x AF009246 (1-1623)
QY      1 LeuAlAspAspAlaAlaLeuLeuValLeuAlaAlaGlyAlaGlyLeuLeuAla 20
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QY      21 AspValHisGlyValAlaValAlaGlyProAlaArgGlyGlyCysHisAspAlaLys 40
DB      924 AATGTACATGAGTGGCTGTGCACGCTGGGTCTGGCAGCAAGGGCCCAACATCCAAA 865
QY      41 GlyValAlaArgValAlaAlaAlaAlaAlaGlyProGlnGlnLeuLeuValPro 60
DB      864 GGCATCGCC---GTGGTCCCGCCCGCTCCGCTCCGCCACGACAGAGCTTGTTCCT 808
QY      61 GlnArgGlyLeuValGlnHisValAlaValLeuHisArgAspLeuAlaValGlnAlaTrp 80
DB      807 CAGAGCTTCTTGTGACAGTACCTGCGAGTACACAGTACCTTGGCGGTGCAATCGAG 748
QY      81 AlaHisLeuAlaGlyValLeuGlyHisGlyGlyValArgAlaGlyHisLeuValGlnAla 100
DB      747 GCTCATCTCGTAGGACGCTTGGCCATGCAAGCGGACGGAACATCTGTGTCACAGCT 688
QY      101 AlaValAlaLeuGlyArgAspLeuGlyValAlaAlaLeuGlyValAlaHisGln 120
DB      687 GGTGTCTCTTCTGGCTGACATCTCGAAGTAGGACACACGCTGAGGGGTGTCACCCACAG 628
QY      121 LeuLeuAspLeuAlaLeuValHisLeuAlaValGlyValAlaValThrLeuValAlaAla 140
DB      627 CTGCTCAATCTCCCGCTGCTCTTACTTCCCGGTAGAAGTCCCGGTCCCTTGTATCCGCA 568
QY      141 AspAspGlnGlyHisValHisValLeuLeuGlyPheValLeuGlyAlaArgLeuGlyVal 160
DB      567 AATGACACACGCGGACGCTCCATCTCTTGTGTTTGTCTTGAACAGAGATTGTGTGTC 508
QY      161 GlnAspLeuLeuProGlnProLeuHisLeuLeuGlyValAlaValAlaGlnThrGln 180
DB      507 TAGGATCTGCTCTTGGAGGCTTGGACCTTCCGATGAGTGGCGGTTGTCTTAAGCTGAA 448
QY      181 HisGlnAspGlnAsnValSerCysGlnAspGlyGlnAlaProHisGlyGlyGlnArgVal 200
DB      447 CACCGAAGTGAAGAGCTCTCTGTGTAGTAGAGAGCGCCCGCATGGCGGGAAGGAGATG 388
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DB      387 ATTGGCGGATGTGTCCAGATGTCCACATCGTAGACTTCCGCCGCGATCGATTAACACTT 328
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DB      327 TCGGTGGAGTCTCGATGTAGGGGTGTAAAGATCTCGAAACGCGCCGTGAGGAACGCG 268
QY      241 ArgHisAspGlyArgLeuAlaHisLeuGlyArgAlaGlnAspHisAlaAlaLeuAlaVal 260
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QY      261 LeuGlyArgAspThrGlnLeuArgValAlaAlaArgAlaHisLeuLeuAspHisArgGlyGln 280
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QY      281 PheHis 282
DB      147 TTTCAT 142
RESULT 15
LOCUS      AL603710      179124 bp      DNA      linear      ROD 05-APR-2002
DEFINITION      Mouse DNA sequence from clone Rp23-247B13 on chromosome 11,
complete sequence.
ACCESSION      AL603710
VERSION      AL603710.8      GI:20068514
KEYWORDS      HTG.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Almeida, J.
Direct Submission
Submitted (04-APR-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Apr 7, 2002 this sequence version replaced gi:18070899.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., paired quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em: EMBL; Sw:
SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
from the R6C1-23 Mouse PAC Library
constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBAC3.6.
FEATURES
source
1..179124
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/db_xref="taxon:10090"
/clone="RP23-247B13"
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BASE COUNT      46162 a      43228 c      43736 g      45998 t
ORIGIN

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Alignment Scores:      2.98e-33      Length:      179124
Score:      914.00      Matches:      200
Percent Similarity:      67.27%      Conservative:      24
Best Local Similarity:      60.06%      Mismatches:      57
Query Match:      64.78%      Indels:      52
DB:      Gaps:      2
US-09-709-103-1F4 (1-282) x AL603710 (1-179124)

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QY      1 LeuAlaAspAspAlaAlaLeuLeuValLeuAlaAlaGlyAlaGlyLeuLeuAla 20
DB      121430 CTAACTGATGACACACGCTCTTGTCTTACCTGGCTGCCGACACTGTTTTCACG 121489

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 30, 2002, 14:39:35 / Search time 737 Seconds

(without alignments)
155.438 Million cell updates/sec

Title: US-09-709-103-1f1

Perfect score: 1450
Sequence: 1 MKLAMIRKMPDSELSIP.....REKASAGSQANDKRCVLS. 282

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 363474 segs, 203117208 residues

Total number of hits satisfying chosen parameters: 726948

Minimum DB seg length: 0
Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame.p2n.model -DEV=xl1p
-Q=/cgn2_1/USFTO.spool/TRANSUS09709103/runatc.30122002.143926.20706/app.query.fasta_1.455
-DB=Published_Applications_NA -QFMT=fastcap -SUFFIX=p2n.rmpb -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blousum62
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000
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-WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:

Published_Applications_NA.*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
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6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match Length	DB ID	Description
1	883 60.9	3082 10	US-09-778-963A-1	Sequence 1, Appl1
2	526 36.3	11221 10	US-09-778-963A-3	Sequence 3, Appl1
3	485 33.4	405 10	US-09-960-352-10273	Sequence 10273, A

4	370	25.5	368	10	US-09-864-761-21643	Sequence 21643, A
5	300	20.7	3346	9	US-09-764-868-67	Sequence 67, Appl
6	291	20.1	688	9	US-09-764-868-490	Sequence 490, Appl
7	283.5	19.6	2040	12	US-10-044-090-336	Sequence 336, App
8	278.5	19.2	197997	10	US-09-822-246-3	Sequence 3, Appl1
9	276.5	19.1	570	12	US-10-104-484-1	Sequence 1, Appl1
10	276.5	19.1	570	12	US-10-104-484-3	Sequence 3, Appl1
11	275.5	19.0	551	10	US-09-765-298A-25	Sequence 25, Appl1
12	272.5	18.8	570	10	US-09-765-298A-27	Sequence 27, Appl1
13	264.5	18.2	930	10	US-09-801-368-285	Sequence 285, App
14	259.5	17.9	536	10	US-09-867-701-5566	Sequence 5566, Ap
15	255.5	17.6	1271	12	US-10-044-090-110	Sequence 110, App
16	254	17.5	942	10	US-09-962-832-256	Sequence 256, App
17	249	17.2	847	10	US-09-822-849A-40	Sequence 40, Appl
18	245.5	16.9	969	10	US-09-801-368-287	Sequence 287, App
19	244	16.8	952	10	US-09-917-800A-1389	Sequence 1389, Ap
20	237	16.3	2418	9	US-09-764-868-84	Sequence 84, Appl
21	237	16.3	2479	9	US-09-764-868-69	Sequence 69, Appl
22	236.5	16.3	1085	9	US-10-067-813-3	Sequence 3, Appl1
23	236	16.3	1119	9	US-10-067-813-1	Sequence 1, Appl1
24	231.5	16.0	452	10	US-09-960-352-4253	Sequence 4253, Ap
25	226	15.6	1088	10	US-09-917-800A-1616	Sequence 1616, Ap
26	225.5	15.6	4454	10	US-09-960-352-5830	Sequence 5830, Ap
27	225	15.5	1151	12	US-10-044-090-111	Sequence 111, App
28	214.5	14.8	1296	9	US-09-954-531-983	Sequence 983, App
29	214.5	14.8	1296	9	US-09-954-531-1378	Sequence 1378, Ap
30	208	14.3	412	10	US-09-960-352-6794	Sequence 6794, Ap
31	206	14.2	1199	10	US-09-794-257-10	Sequence 10, Appl
32	203	14.0	1224	10	US-09-972-529-1	Sequence 1, Appl1
33	203	14.0	3192	10	US-09-788-654A-1	Sequence 1, Appl1
34	200.5	13.8	612	10	US-09-972-529-3	Sequence 3, Appl1
35	194.5	13.4	836	10	US-09-770-445-674	Sequence 674, App
36	194	13.4	1274	10	US-09-925-102-91	Sequence 91, Appl
37	193	13.3	1752	9	US-09-764-868-501	Sequence 501, Appl
38	193	13.3	1157	9	US-10-108-605-44	Sequence 44, Appl
39	192	13.2	401	10	US-09-960-352-6793	Sequence 6793, Ap
40	192	13.2	552	10	US-09-794-257-12	Sequence 12, Appl
41	190.5	13.1	884	10	US-09-770-445-515	Sequence 515, App
42	190	13.1	774	10	US-09-919-580-42	Sequence 42, Appl
43	187	12.9	666	9	US-09-938-442A-40	Sequence 420, App
44	185.5	12.8	2734	9	US-09-764-868-489	Sequence 489, App
45	185.5	12.8	2964	9	US-10-091-613-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-09-778-963A-1
Sequence 1, Application US/09778963A
Parent No. US20020115172A1
GENERAL INFORMATION:
APPLICANT: NEELAM, Beena et al
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
FILE REFERENCE: C0001112
CURRENT APPLICATION NUMBER: US/09/778, 963A
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 3082
TYPE: DNA
ORGANISM: Homo sapiens
US-09-778-963A-1

Alignment Scores:

Pred. No.:	Length:	Matches:
883.00	6,21e-102	3082
Percent Similarity: 77.78%		173
Best Local Similarity: 62.01%		44
Query Match: 60.90%		46
		16
		4


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TYPE: DNA
ORGANISM: Bos taurus
FEATURE:
NAME/KEY: unsure
LOCATION: (3), (23), (31)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: clone ID: 44-LIB3058-050-Q1-K1-C8
US-09-960-352-10273

Alignment Scores:
Pred. No.: 9,15e-53 Length: 405
Score: 485.00 Matches: 95
Percent Similarity: 89.19% Conservative: 4
Best Local Similarity: 85.59% Mismatches: 12
Query Match: 33.45% Indels: 0
DB: 10 Gaps: 0

US-09-709-103-1F1 (1-282) x US-09-960-352-10273 (1-405)
QY 1 MetLysLeuAlaAlaMetIleLysLysMetCysProSerAspSerGluLeuSerIlePro 20
DB 72 ATGAAACGTGCGCGGATGATCAAGAAATGTGCCCGAGCGACTCCGATGTGAGATCCCG 131
QY 21 AAlaLysAsnCySTyrArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIle 40
DB 132 GCCAAGAACTCTCCATGCCCATGTGTCTCTCGCTCGTCCAGAGGTGGCAAGCGCCATC 191
QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
DB 192 GTGTGGCCTTCCTGACGGCGCGCTACAGAGAGCGCTACACGCCCATCGAAGACTTCC 251
QY 61 HisArgLysPheTyrSerTleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSer 80
DB 252 CACCCCAAGTCTCTACTGTCATTCGAGCGAGAGGATCACAGTGCATCTTCGACACGTAC 311
QY 81 GlyAsnHisProPheProAlaMetArgArgLeuSerTleLeuThrGlyAspValPheIle 100
DB 312 GGCAACCGCGCATTCGCCCATCGACGCTCTGCATCTTACCGAGACGTTCATC 371
QY 101 LeuValPheSerLeuAspAsnArgSerPhe 111
DB 372 CTAGGGTTCAGACAGTACAACCGCGCATCTTCC 404

RESULT 4
US-09-864-761-21643
Sequence 21643, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30

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[illegible]

RESULT 5

US-09-764-868-67
 ; Sequence 67, Application US/09764868
 ; Patent No. US20020168711A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PT232
 ; CURRENT APPLICATION NUMBER: US/09/764,868
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - refer to PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 1510
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 67
 ; LENGTH: 3346
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (2787)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: SITE
 ; LOCATION: (2795)
 ; OTHER INFORMATION: n equals a,t,g, or c
 US-09-764-868-67

Alignment Scores:
 Pred. No.: 7.13e-28 Length: 3346
 Score: 300.00 Matches: 68
 Percent Similarity: 59.28% Conservative: 31
 Best Local Similarity: 40.72% Mismatches: 52
 Query Match: 20.69% Indels: 16
 DB: 9 Gaps: 3

US-09-709-103-1f1 (1-282) x US-09-764-868-67 (1-3346)

QY 25 TyrArgMetValIleLeuGlySerLysValGlyLysThrAlaIleValSerArgPhe 44
 Db 201 TACAAGGTAGTGTGGAGGTGGAGGGTTGGCAATCTGCCCTTACTGTGCAGTTT 260
 QY 45 LeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPheHisArgLysPhe 64
 Db 261 GTCACTGGGACTTTCATTGAGAAATATGACCCCACTTGAAGATTCTACCGCAAGAG 320
 QY 65 TyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisPro 84
 Db 321 ATCGAAGTGGACTCTTCCCTCCGCTGCTGGAATTTCTGGACACCGCAGCACTGAGCAG 380
 QY 85 PheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSer 104
 Db 381 TTTCCTCCATGAGAGATCTTACATCAAAACCGCCCAAGGTTTCATCTCTGTTTATAGC 440
 QY 105 LeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGlnIleLeuAspThr 124
 Db 441 CTGGTTAATCAACAGTCTTTTCAGATATCAAGCAATGAGAGATCAAAATGTGC----- 494
 QY 125 LysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeuValIleCysGly 144
 Db 495 -----AGAGTGAAGAGATATGAAAAAGTCCCACTAATCTCTAGTAGCA 536
 QY 145 AsnLysGlyAspArgAspPheTyrArgGluVal-----AspIleGluGluVal 161
 Db 537 AATAAGTGGATCTGGACACAGAAAGAGAGTTATGTCTTCAGAGGCGAGAGCTCTGGCT 596
 QY 162 GlnLeuValGlyAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLysAsn 181
 Db 597 CAAGAATGGGC-----TGTCCTTTCATGAGACATCGCAAAAAGTAAA 641
 QY 182 SerSerLeuAspGlnMetPhe 188
 Db 642 TCAATGTGGATGAATCTTTT 662

RESULT 6

US-09-764-868-490
 ; Sequence 490, Application US/09764868
 ; Patent No. US20020168711A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PT232
 ; CURRENT APPLICATION NUMBER: US/09/764,868
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - refer to PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 1510
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 490
 ; LENGTH: 688
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (579)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: SITE
 ; LOCATION: (610)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: SITE
 ; LOCATION: (669)
 ; OTHER INFORMATION: n equals a,t,g, or c
 US-09-764-868-490

Alignment Scores:
 Pred. No.: 8.72e-28 Length: 688
 Score: 291.00 Matches: 67
 Percent Similarity: 57.93% Conservative: 28
 Best Local Similarity: 40.85% Mismatches: 59
 Query Match: 20.07% Indels: 10
 DB: 9 Gaps: 2

US-09-709-103-1f1 (1-282) x US-09-764-868-490 (1-688)

QY 25 TyrArgMetValIleLeuGlySerLysValGlyLysThrAlaIleValSerArgPhe 44
 Db 194 TACAAGGTAGTGTGGAGGTGGAGGGTTGGCAATCTGCCCTTACTGTGCAGTTT 253
 QY 45 LeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPheHisArgLysPhe 64
 Db 254 GTCACTGGGACTTTCATTGAGAAATATGACCCCACTTGAAGATTCTACCGCAAGAG 313
 QY 65 TyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisPro 84
 Db 314 ATCGAAGTGGACTCTTCCCTCCGCTGCTGGAATTTCTGGACACCGCAGCACTGAGCAG 373
 QY 85 PheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSer 104
 Db 374 TTTCCTCCATGAGAGATCTTACATCAAAACCGCCCAAGGTTTCATCTCTGTTTATAGC 433
 QY 105 LeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGlnIleLeuAspThr 124
 Db 434 CTGGTTAATCAACAGTCTTTTCAGATATCAAGCAATGAGAGATCAAAATGTGC----- 487
 QY 125 LysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeuValIleCysGly 144
 Db 488 -----AGAGTGAAGAGATATGAAAAAGTCCCACTAATCTCKAGTAGGA 529
 QY 145 AsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIleGluGlnLeuVal 164
 Db 530 AATAAGTGGATCTGGACACAGAAAGAGAGTTATGTCTTCAGAGGCGAGAGCTCTGGCT 589
 QY 165 GlyAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLysAsnSerSerLeu 184
 Db 590 CAAGAA-----TGGGGCTGCTCTTTTATGAGACATCGCAAAAAGTAAATCAATGGTG 643
 QY 185 AspGlnMetPhe 188
 Db 644 GATGAATCTTTT 655

RESULT 7
 US-10-044-090-336
 ; Sequence 336, Application US/10044090
 ; Patent No. US20020137081A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Olga Bandman
 ; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
 ; FILE REFERENCE: PA-0028 US
 ; CURRENT APPLICATION NUMBER: US/10/044,090
 ; CURRENT FILING DATE: 2002-01-09
 ; NUMBER OF SEQ ID NOS: 850
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 336
 ; LENGTH: 2040
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20020137081A1 3110662CB1
 US-10-044-090-336

Alignment Scores:
 Pred. No.: 4,14e-26 Length: 2040
 Score: 283.50 Matches: 66
 Percent Similarity: 55.21% Conservative: 40
 Best Local Similarity: 34.38% Mismatches: 69
 Query Match: 19.55% Indels: 17
 DB: 12 Gaps: 3

US-09-709-103-1f1 (1-282) x US-10-044-090-336 (1-2040)

QY 25 TyrArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIleValSerArgPhe 44
 Db 202 TATAGCTAGTCTCTTGGCTCAGAGCGCTTGAAAGCTCTTGACTGACATTT 261
 QY 45 LeuThrGlyArgPheGluAspAlaIleThrProThrIleGluAspPheHisArgLysPhe 64
 Db 262 GTTCAGAGAAATTTTGTGAAATAATGATCTTCAATGAAATCTTATGAAAGCAA 321
 QY 65 TyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisPro 84
 Db 322 GTTGAAGTAGATGACACAGCTGTATCTTGAATCTTGGATCTCCAGAAACGAGCAA 381
 QY 85 PheProAlaMetArgArgLysSerIleLeuThrGlyAspValPheIleLeuValPheSer 104
 Db 382 TTTCACGACATGAGGATTTATACATGAAATAATGACAAAGATTGCAATGATTATTC 441
 QY 105 LeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnIleLeuAspThr 124
 Db 442 ATCACACGACAGCTCCATTTTACATGAAATAATGACCTTGAAGAACAGATTCTT 495
 QY 125 LysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeuValIleCysGly 144
 Db 496 -----CGAGTTAAAGACACTGATGATCTTCAATGATCTTGTGGT 537
 QY 145 AsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIleGluGlnLeuVal 164
 Db 538 AATTAATGTGACTTGGA-----GATGAAGAAGTTGTAGCGAAGAACAA 582
 QY 165 GlyAspAspProGlnArg-----CysAlaTyrPheGluIleSerAlaLysLys 180
 Db 583 GGTCAAAATCTTACAGACAAATGAAACAACTGTGATCTTGAATCTTGGCAAAATCA 642
 QY 181 AsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGlu 200
 Db 643 AAAATTAATGTATAGATCTTTATGACCTAGCGCGCAATTAACGAAAAACTCCA 702
 QY 201 MetSerProAspLeuHisArgLysValSerValGln 212
 Db 703 GTGCTGGAGAGCTCGCAAAAGTCATCATGTCTAG 738
 RESULT 8

US-09-822-246-3/c
 ; Sequence 3, Application US/09822246
 ; Patent No. US20020142383A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MERKULOV, Gennady et al.
 ; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
 ; FILE REFERENCE: C0001149
 ; CURRENT APPLICATION NUMBER: US/09/822,246
 ; CURRENT FILING DATE: 2001-04-02
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 197997
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1) - (197997)
 ; OTHER INFORMATION: n = A, T, C or G
 US-09-822-246-3

Alignment Scores:
 Pred. No.: 2.01e-22 Length: 197997
 Score: 278.50 Matches: 65
 Percent Similarity: 55.21% Conservative: 41
 Best Local Similarity: 33.85% Mismatches: 69
 Query Match: 19.21% Indels: 17
 DB: 10 Gaps: 3

US-09-709-103-1f1 (1-282) x US-09-822-246-3 (1-197997)

QY 25 TyrArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIleValSerArgPhe 44
 Db 43187 TATAGCTAGTCTCTTGGCTCAGAGCGCTTGAAAGCTCTTGACTGACATTT 42128
 QY 45 LeuThrGlyArgPheGluAspAlaIleThrProThrIleGluAspPheHisArgLysPhe 64
 Db 43127 GTTCAGAGAAATTTTGTGAAATAATGATCTTCAATGAAATCTTATGAAAGCAA 43068
 QY 65 TyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisPro 84
 Db 43067 GTTGAAGTAGATGACACAGCTGTATCTTGAATCTTGGATCTCCAGAAACGAGCAA 43008
 QY 85 PheProAlaMetArgArgLysSerIleLeuThrGlyAspValPheIleLeuValPheSer 104
 Db 43007 TTTCACGACATGAGGATTTATACATGAAATAATGACCTTGAAGAACAGATTCTT 42948
 QY 105 LeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnIleLeuAspThr 124
 Db 42947 ATCACACGACAGCTCCATTTTACATGAAATAATGACCTTGAAGAACAGATTCTT 42894
 QY 125 LysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeuValIleCysGly 144
 Db 42893 -----CGAGTTAAAGACACTGATGATCTTCAATGATCTTGTGGT 42852
 QY 145 AsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIleGluGlnLeuVal 164
 Db 42851 AATTAATGTGACTTGGA-----GATGAAGAAGTTGTAGCGAAGAACAA 42807
 QY 165 GlyAspAspProGlnArg-----CysAlaTyrPheGluIleSerAlaLysLys 180
 Db 42806 GGTCAAAATCTTACAGACAAATGAAACAACTGTGATCTTGAATCTTGGCAAAATCA 42747
 QY 181 AsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGlu 200
 Db 42746 AAAATTAATGTATAGATCTTTATGACCTAGCGCGCAATTAACGAAAAACTCCA 42687
 QY 201 MetSerProAspLeuHisArgLysValSerValGln 212
 Db 42686 GTGCTGGAGAGCTCGCAAAAGTCATCATGTCTAG 42651



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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 30, 2002, 14:39:31 / Search time 77 Seconds

(without alignments)
1123.154 Million cell updates/sec

Title: US-09-709-103-1f1

Perfect score: 1450

Sequence: 1 MKLAMIKMCPDSELSIP.....REKASAGSQAKDKRCVTS. 282

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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Issued Patents NA -QFMT=fastap -SUFIX=p2n.m1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:

Issued Patents NA:
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6: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1449	99.9	1841	4	US-09-053-374A-1
2	1399.5	96.5	1689	4	US-09-053-374A-4
3	1387	95.7	1396	4	US-09-053-374A-3
4	1343	92.6	3079	4	US-09-053-374A-6
5	300	20.7	615	1	US-08-247-946A-5
6	300	20.7	615	1	PCT-US95-06420-5
7	279	19.2	5775	5	US-08-306-691B-15
8	279	19.2	5775	5	PCT-US93-06251-29
9	277.5	19.1	570	4	US-08-884-866A-2
10	277.5	19.1	570	4	US-08-884-866A-11
11	276	19.0	607	4	US-08-429-964-85
12	275.5	19.0	480	4	US-08-884-866A-9

13	271.5	18.7	4480	4	US-09-167-322-12	Sequence 12, Appl
14	266.5	18.4	450	4	US-08-884-866A-10	Sequence 10, Appl
15	266.5	18.4	574	2	US-08-429-964-83	Sequence 83, Appl
16	265.5	18.3	2436	1	US-08-306-691B-16	Sequence 16, Appl
17	237	16.3	2309	3	US-09-078-317-3	Sequence 3, Appl
18	237	16.3	2309	4	US-09-454-819-3	Sequence 3, Appl
19	234.5	16.2	600	3	US-09-078-317-1	Sequence 1, Appl
20	234.5	16.2	600	4	US-09-454-818-1	Sequence 1, Appl
21	219.5	15.1	563	4	US-09-385-982-426	Sequence 426, App
22	219.5	15.1	3497	4	US-09-503-505A-2	Sequence 2, Appl
23	186	12.8	6453	1	US-08-306-691B-14	Sequence 14, Appl
24	186	12.8	6453	3	US-09-209-668-10	Sequence 10, Appl
25	186	12.8	6453	3	US-09-356-952-8	Sequence 8, Appl
26	185.5	12.8	2964	2	US-08-846-790A-2	Sequence 2, Appl
27	185.5	12.8	2964	3	US-08-935-333-2	Sequence 2, Appl
28	180	12.4	702	3	US-08-842-976-2	Sequence 2, Appl
29	180	12.4	702	3	US-09-213-397-2	Sequence 2, Appl
30	180	12.4	702	3	US-09-416-489-2	Sequence 2, Appl
31	177.5	12.2	1166	5	PCT-US96-12129B-1	Sequence 1, Appl
32	175.5	12.1	603	4	US-09-325-932A-29	Sequence 29, Appl
33	175.5	12.1	932	4	US-09-325-932A-28	Sequence 28, Appl
34	175	12.1	1175	4	US-09-387-341-215	Sequence 215, App
35	173	11.9	1175	2	US-08-773-423-6	Sequence 6, Appl
36	172	11.9	897	2	US-09-006-535-2	Sequence 2, Appl
37	172	11.9	1443	1	US-08-076-089-1	Sequence 1, Appl
38	172	11.9	1443	2	US-08-707-200-1	Sequence 1, Appl
39	172	11.9	1443	4	US-08-996-565-1	Sequence 1, Appl
40	172	11.9	1443	5	PCT-US93-05643-1	Sequence 1, Appl
41	172	11.9	1525	2	US-09-006-535-1	Sequence 1, Appl
42	167	11.5	897	2	US-09-006-535-7	Sequence 7, Appl
43	166.5	11.5	5197	4	US-09-293-170-6	Sequence 6, Appl
44	166	11.4	890	4	US-09-075-454-14	Sequence 14, Appl
45	165	11.4	240	4	US-08-884-866A-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-09-053-374A-1
Sequence 1, Application US/09053374A
Patent No. 6462177
GENERAL INFORMATION:
APPLICANT: YEN, KWANG-MU
TITLE OF INVENTION: MAMMALIAN BLOOD LOSS-INDUCED GENE, KD312
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER DRIVE
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: US
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/053,374A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-514
INFORMATION FOR SEQ ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1841 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:

NAME/KEY: CDS
LOCATION: 255..1097
US-09-053-374A-1

Alignment Scores:

Pred. No.: 5,33e-166 Length: 1841
Score: 1449.00 Matches: 281
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.93% Indels: 0
DB: 4 Gaps: 0

US-09-709-103-1f1 (1-282) x US-09-053-374A-1 (1-1841)

QY 1 MetLysLeuAlaMetIleLysLysMetCysProSerAspSerGluLeuSerIlePro 20
DB 255 ATGAACACTGGCCGATGATCAAGAGATGTCCCGAGCGACTCGGAGTATCCCG 314
QY 21 AlaLysAsnCysTyrArgMetValIleLeuGlySerLysValGlyLysThrAlaIle 40
DB 315 GCCAAGAACTGCTATCGCATGCTCTCGGCTGTCTCAAGGTGGGCAAGCGCCATC 374
QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
DB 375 GTGTGCGGCTTCTCACCAGCGCTTCGAGGACGCTACAGCGCTTACCATCGAGGACTTC 434
QY 61 HisArgLysPheTyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSer 80
DB 435 CACCCGAAGTTCTCTCCATCCGCGGAGGTCTACCGAGCTCGACATCTCCGACACGTCC 494
QY 81 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIle 100
DB 495 GGCAACACCCGCTTCCCGCCATCGCGGCTCTCCATCTCTCACAGGAGAGCTTTTCATC 554
QY 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGln 120
DB 555 CTGGTGTTCAGTCTGACAAACCGGAGCTCTCTCGAGGAGGTGCGAGCGGCTCAGGCGAG 614
QY 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeu 140
DB 615 ATCTCTGACACCAAGTCTTGCTCAGAACAAACCAAGGAGAGACGTGGAGCTGCCCGCTG 674
QY 141 ValIleCysGlyAsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIle 160
DB 675 GTCTATCTCGGCAACAAAGGGTGACCGGACTTCTACCGCGAGGTGGACCGCGGAGATC 734
QY 161 GluGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLys 180
DB 735 GAGCAGCTGGTGGGCGACGACCCCGCGCTGCGCTCTCTCGAGATCTCGGCCAAGAG 794
QY 181 AsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGlu 200
DB 795 AACAGCAGCTTGGACCATGTTCTCGCGGCTCTCTCGCCATGGCCAGAGCTGCCCGCGAG 854
QY 201 MetSerProAspLeuHisArgLysValSerValGlnTyrCysAspValLeuHisLysLys 220
DB 855 ATGAGCCAGACCTGCAACCGCAAGTCTCGGTGCGTACTGCGACGCTGCTGCACAGAG 914
QY 221 AlaLeuArgAsnLysLysLeuLeuArgAlaGlySerGlyGlyGlyGlyAspProGly 240
DB 915 GCGTTCGGAACAAGAGCTCTCGGCGCGGCGAGCGCGCGCGCGCGCGCGCGCGCGCG 974
QY 241 AspAlaPheGlyIleValAlaProPheAlaArgArgProSerValHisSerAspLeuMet 260
DB 975 GACGCTTTGGCATCTGGCACCTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1034
QY 261 TyrIleArgGluLysAlaSerAlaGlySerGlnAlaLysAspLysGluArgCysValIle 280
DB 1035 TACATCGCGAGAGGCG 1094
QY 281 Ser 281
DB 1095 AGC 1097

RESULT 2

US-09-053-374A-4
; Sequence 4, Application US/09053374A
; Patent No. 6462177
; GENERAL INFORMATION:
; APPLICANT: YEN, KWANG-MU
; TITLE OF INVENTION: MAMMALIAN BLOOD LOSS-INDUCED GENE, KD312
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: US
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/053,374A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-514
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 132..971
; US-09-053-374A-4

Alignment Scores:

Pred. No.: 4,74e-160 Length: 1689
Score: 1399.50 Matches: 273
Percent Similarity: 98.22% Conservative: 3
Best Local Similarity: 97.15% Mismatches: 4
Query Match: 96.52% Indels: 1
DB: 4 Gaps: 1

US-09-709-103-1f1 (1-282) x US-09-053-374A-4 (1-1689)

QY 1 MetLysLeuAlaAlaMetIleLysLysMetCysProSerAspSerGluLeuSerIlePro 20
DB 132 ATGAACACTGGCCGATGATCAAGAGATGTCCCGAGCGACTCTGAACTGAGTATCCG 191
QY 21 AlaLysAsnCysTyrArgMetValIleLeuGlySerLysValGlyLysThrAlaIle 40
DB 192 GCCAAGAACTGCTACAGATGCTCTCGGCTCATCTCCAGTGGGCAAGCGCCATC 251
QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
DB 252 GTGTGCGGCTTCTCAGCGCGCTTCGAGGAGCTTACACCCCTACCATTTGAGACTTC 311
QY 61 HisArgLysPheTyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSer 80
DB 312 CACCGAAAAGTTTACTCGATCCGCGGCGAGTCTACCATCTGGACATCTGACACATCT 371
QY 81 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIle 100
DB 372 GGCATCATCTGTTTCCCGCCATCGCGGCGCTCTCTATCTCTCAGGAGAGCTTTTCAT 431
QY 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGln 120

Db 432 CTGGTGTTCAGCTTAGACACACCGCATCTCTTCGAGAGGTGCAAGGCTTCAACACAGCAG 491
 QY 121 TleleasptThlySerCyseuLeuysAsnlyThrlsGluAnvalAspValProleu 140
 Db 492 ATCTTAGACACCAAGCTCTGTCTCAAGAACCAACCAAGAGATGTGAGCTCCCTG 551
 QY 141 ValileCyseGlyAsnlyGlyAspArgAspPheTyraGluValAspGlnArgGluile 160
 Db 552 GTTCATTTGGCGGTACCAAGGGGACCGGAGCTTCTACCGGAAAGTGAGACGCGGAGATT 611
 QY 161 GluGlnLeuValGlyAspAspProGlnArgCysAlaTyrrPheGluileSerAlaLysLys 180
 Db 612 GAGACACTGTGGCGCATATACCTCAGCGTGTGCTTCTGAGATTCGCGCAAGAG 671
 QY 181 AsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGlu 200
 Db 672 AATAGAGCTTGACCAAGATGTTCCGTGCGCTCTTTGCCATGCGCAAGCTGCTAGCAG 731
 QY 201 MetSerProAspLeuHisArgLysValSerValGlnTyrrCysAspValLeuHisLysLys 220
 Db 732 ATGAGGCTTACTTGACCGCAAGGTGTCTGTGCACTGTGAGCGTGTGCAAAAAAG 791
 QY 221 AlaLeuArgAsnlyLysLysLeuLeuArgAlaGlySerGlyGlyGlyValYsLysAspProGly 240
 Db 792 GCTCTGAGAACAGAGAGCTTGTGCGGCGGAGC--GAGGTGGGGGCGACACGGA 848
 QY 241 AspAlaPheGlyLeuValAlaProPheAlaArgArgProSerValHisSerAspLeuMet 260
 Db 849 GATGCTTGGCATCTTGCGGCGCTTTGCTCGCAGACTAGCGTGCAATGACACTCATG 908
 QY 261 TyrIleArgGlyLysAlaSerAlaGlySerGlnAlaLysAspLysGluArgCysValile 280
 Db 909 TACATTCGTGAGAAACCAAGTGTGACGACGACGAGCTTAAGACAAAGAGCGCTGTGTCATC 968
 QY 281 Ser 281
 Db 969 AGT 971
 RESULT 3
 US-09-053-374A-3
 ; Sequence 3, Application US/09053374A
 ; Patent No. 6462177
 ; GENERAL INFORMATION:
 ; APPLICANT: YEN, KWANG-MU
 ; TITLE OF INVENTION: MAMMALIAN BLOOD LOSS-INDUCED GENE, KD312
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: AMGEN INC.
 ; STREET: ONE AMGEN CENTER DRIVE
 ; CITY: THOUSAND OAKS
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 91320
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/053,374A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: COOK, ROBERT R.
 ; REGISTRATION NUMBER: 31,602
 ; REFERENCE/DOCKET NUMBER: A-514
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3986 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)

US-09-053-374A-3
 Alignment Scores:
 Pred. No.: 5.53e-158 Length: 3986
 Score: 1387.00 Matches: 281
 Percent Similarity: 79.83% Conservative: 0
 Best Local Similarity: 79.83% Mismatches: 0
 Query Match: 95.66% Indels: 71
 DB: 4 Gaps: 1
 US-09-709-103-1f1 (1-282) x US-09-053-374A-3 (1-3986)
 QY 1 MetLysLeuAlaAlaMetLleLysLysMetCysProSerAspSerGluLeuSerLlePro 20
 Db 774 ATGAAACTGGCCGCATGATCAAGAAATGTGGCCGAGCACTCGGAGCTGAGATCCCG 833
 QY 21 AlaLysAsnCyseTyrrArgMetValileLengLysSerLysValGlyLysThrAlaile 40
 Db 834 GCCAAGACCTGCTATCGCATGTGTCATCTCGCTGCTCAAGTGTGGCAACCGGCATC 893
 QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrrThrProThrileGluAspPhe 60
 Db 894 GTTCGCGCTTCTCTCACCGCGCGCTTCGAGAGACGCTACAGCCTACCATGAGAGACTTC 953
 QY 61 HisArgLysPheTyserIleArgGlyGluValTyrrGlnLeuAspLleLeuAspThrSer 80
 Db 954 CACCGAAGTTCTATCCATCCGCGCGAGGTCTACAGCTCGATCATCTTGACAGTGGAGCGGCGC 1013
 QY 81 GlyAsnHisProPheProAlaMetArgArgLeuSerLleLeuThr----- 95
 Db 1014 GGCAAACACCGGTTCCCGCCGATGCGGCGCTCTCATCTTCACAGTGAAGCGGCGGCC 1073
 QY 95 ----- 95
 Db 1074 GGGAGGTGGGGAGGGAAGGCGGGGAACCTCGGACAGGCGCCCGCAGCCCGGT 1133
 QY 95 ----- 95
 Db 1134 CCGGCTGCGCGCGCGAGTAGTGCCTTTCGCTTAGAGAGCTAGCCGCCGCCGCG 1193
 QY 95 ----- 95
 Db 1194 GCTTCAAAATGACGCCGACCTTTCCTCGGCGCGCAACCTCCTTCTCTTCTGCT 1253
 QY 96 -----GlyAspValPheLleLeuValPheSerLeuAspAsnArgAsp 110
 Db 1254 CTCTGTGCCCCCTTAGAGAGACGTTTCATCTCGGTGTTCAGTCTGGAACAACCGGACTC 1313
 QY 110 rPheGluGluValGlnArgLeuArgGlnGlnIleLeuAspThrLysSerCyseLysLysAs 130
 Db 1314 CTTGAGAGAGGTGACGCGCTCAGGCGAGCATCTCGATCTGAGACCAAGCTTGGCTCAAGAA 1373
 QY 130 nlySerThrLysGluAsnValAspValProLeuValileCyseGlyAsnlyGlyAspArgAs 150
 Db 1374 CAAGAACCAAGAGAAAGTGAAGTGCCTCGTGTATCTGGGCAACAAGGGTACCGGCA 1433
 QY 150 rPheTyrrArgGluValAspGlnArgGluileGluGlnLeuValGlyAspAspProGlnArg 170
 Db 1434 CTTTACCGCGAGGTGAGCCAGCGCGAGATCGAGCACTGTGGGCGACGACCCGAGCG 1493
 QY 170 gCyseAlaTyrrPheGluileSerAlaLysLysAsnSerSerLeuAspGlnMetPheArgAl 190
 Db 1494 CTGGCGCTTACTTGAAGTCTGCGCCAGAGAAACAGACGCTGAGCAAGATGTTCCGCGC 1553
 QY 190 AleuPheAlaMetAlaLysLeuProSerGlnMetSerProAspLeuHisArgLysValSe 210
 Db 1554 GCTCTTGGCATGCGCAAGCTGCGCAGAGATGAGCCACACTGACCGCAAGGAGTCTC 1613
 QY 210 rValGlnTyrrCysAspValLeuHisLysLysValAleuArgAsnlyLysLeuLeuArgAl 230
 Db 1614 GGTGAGTACTGCGACGTCGTCACAAAGAGCGCTGGGAAACAAGAGCTGCTGGCGGC 1673
 QY 230 agLysSerGlyGlyGlyGlyGlyAspProGlyAspAlaPheGlyLleValAlaProPheAl 250


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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/247,946A
FILING DATE: 24-MAY-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4150
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 615
TYPE: Nucleic acid
STRANDEDNESS: Double
TOPOLOGY: Unknown
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
FEATURE:
NAME/KEY: TC21 gene
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-247-946A-5

Alignment Scores:
Pred. No.: 2,45e-27 Length: 615
Score: 300.00 Matches: 71
Percent Similarity: 55.32% Conservative: 33
Best Local Similarity: 37.77% Mismatches: 70
Query Match: 20.69% Indels: 14
DB: 1 Gaps: 3

US-09-709-103-1f1 (1-282) x US-08-247-946A-5 (1-615)
QY 25 TyrArgMetValIleLeuGlySerSerIleValGlyIleThrAlaIleValSerArgPhe 44
D 43 TACCGGCTCGGTGGTGGCGGGGGCGGTGGCAAGTCGGCGTCACACATCCAGTTC 102
QY 45 LeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPheHisArgIysPhe 64
D 103 ATCCAGTCCATTGTTGAACGATTAATGATCCACATTAAGATTCTTACACAAAGCAG 162
QY 65 TyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisPro 84
D 163 TGTGTGATAGATGACAGACAGCCCGGTAGATATTTGGATACAGACAGANNNGAAG 222
QY 85 PheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSer 104
D 223 TTGGAGCCATGAGAGAAACATATATGAGACTGCGCAAGGCTTCGTGTGCTTTTCA 282
QY 105 LeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGlnIleLeuAspThr 124
D 283 GTCAACAGTATAGAGCAGTTTGAAGAATCTATAAGTTCAAGACGATTCCTC----- 336
QY 125 LysSerCysLeuLysAsnLysThrIleGlyGluAsnValAspValProLeuValIleCysGly 144
D 337 -----AGAGTAAAGATCGTGTAGTGAAGTTCACCAATGATTATTAATGGT 378

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QY 145 AsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGlnIleGluGlnLeuVal 164
D 379 AATTAAGCACATCTGATCATCAAGACAGGTAAACAGGAAGAAAGCAACAGTTAGCA 438
QY 165 GlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLysAsnSerSerLeu 184
D 439 CGGCAG-----CTTAAGGTAAACATCATGAGCAGTCAGCAAAAGATTGATGAATGTA 492
QY 185 AspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGluMet----- 201
D 493 GATCAAGCTTTCATGAACTGTCCGGGTTATCAGAAATTTCAAGACGAGAAATGCTCT 552
QY 202 ---SerProAspLeuHisArgIys 208
D 553 CTTCAACACAGAACCAACGAGAA 576

RESULT 6
PCT-US95-06420-5
Sequence 5, Application PC/TUS9506420
GENERAL INFORMATION:
APPLICANT: AARONSON, S.A.; CHAN, A.;
APPLICANT: MIKI, T.
TITLE OF INVENTION: NOVEL HUMAN P45-RELATED
TITLE OF INVENTION: ONCOGENES UNMASKED BY EXPRESSION OF CDNA
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06420
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/247,946
FILING DATE: 24-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4150PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 615
TYPE: Nucleic acid
STRANDEDNESS: Double
TOPOLOGY: Unknown
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
FEATURE:

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; NAME/KEY: TC21 gene
 ; LOCATION:
 ; IDENTIFICATION METHOD:
 ; OTHER INFORMATION:
 PCT-US95-06420-5

Alignment Scores:	2.45e-27	Length:	615
Pred. No.:	300.00	Matches:	71
Score:	55.32%	Conservative:	33
Percent Similarity:	37.7%	Mismatches:	70
Best Local Similarity:	20.63%	Indels:	14
Query Match:		Gaps:	3
DB:	5		

US-09-709-103-1F1 (1-282) x PCT-US95-06420-5 (1-615)

QY	25	TyrArgMetValIleLeuLeuGlySerSerLysValGlyLysThrAlaIleValSerArgPhe	44
Dd	43	TACCGCCTCGTGGTGTCGCGCGGGCGCGTGGCAAGTGGCGCTCCACCATCCAGTTCTC	102
QY	45	LeuThrGlyArgPheGluAspAlaTyThrProThrIleGluAspPheHisArgLysPhe	64
Dd	103	ATCCAGTCTATTGTGAACGGATTATGATCCAACCATGAAGATTCTTACACAAGACG	162
QY	65	TyrserIleArgGlyGluValTyGlnLeuLeuAspIleLeuAspThrSerGlyAsnHisPro	84
Dd	163	TGTGTGATAGATGACAGACGCCCGCTAGATAATTTGGATACAGCAGANNNGAAG	222
QY	85	PheProLaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSer	104
Dd	223	TTTTGGAGGCATGACAGAACAAGTAGTATGAGGACTCGCGAAGGCTTCTGTTGGTCTTTTCA	282
QY	105	LeuAspAsnArgspPheGluGluValGlnArgLeuArgGlnGlnIleLeuAspThr	124
Dd	283	GTCACAGATAGGCGAGCTTTTGAAGAAATCTATAAGTTTCAAAGACAGATTCTC-----	336
QY	125	LysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeuValIleCysGly	144
Dd	337	-----AGAGTAAGGATCGTGATGAGTATCCCATGATTAAATGTTTAAATGTT	378
QY	145	AsnLysGlyAspArgaspPheTyArgGluValAspGlnArgGluIleGluGlnLeuVal	164
Dd	379	AATAAACAGCATCTGGATCATCAAGACAGAGTAAACACAGGAAGAAGCACACAGTTAGCA	438
QY	165	GlyAspAspProGlnArgCysalaTyPheGluIleSerAlaIylsLysasnSerSerLeu	184
Dd	439	CGGCAG-----CTTAAGGTACATACATGATGGAGGCATCAGCAAGATTAGGATGATGTA	492
QY	185	AspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGluMet-----	201
Dd	493	GATCAAGCTTTCCATGACTTTGTCGGGGTTATCAGGAATTTCAAGAGCAGGAATGTCTCT	552
QY	202	---SerProAspLeuHisArgLys	208
Dd	553	CTTTCACCAAGCAACCAACCGAAA	576

RESULT 7

US-08-306-691B-15
Sequence 15, Application US/08306691B
Patent No. 5734039
GENERAL INFORMATION:
APPLICANT: Calabretta, Bruno
APPLICANT: Skorski, Tomasz
TITLE OF INVENTION: ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavarigna & Monaco, P.C.
STREET: Two Penn Center, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1

Alignment Scores:		
Pred. No.:	2.37e-23	Length:
Score:	279.00	Matches:
Percent Similarity:	54.59%	Conservative:
Best Local Similarity:	36.22%	Mismatches:
Query Match:	19.24%	Indels:
DB:	1	Gaps:
		4
		5775

US-09-709-103-1F1 (1-282) x US-08-306-691B-15 (1-5775)

QY	25	TyArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIleValSerArgPhe	44
Db	202	TATAAACTTGTGTAGTCTGGCGCTAGGCAAGAGTGCCTTGACGATACAGCTTA	261
QY	45	LeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPheHisArgLysPhe	64
Db	262	AITCAGAAATCATTTGTGGACGAATATGATCCAAACAATAGAGGATTCCTACAGGAAGCAA	321
QY	65	TyrSerIleAArgGlyGluValTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisPro	84
Db	322	GTAGTAATTGATGGAGAAACCTGCTCTCTGGATATTCGCACACAGCAGCTCAAGAGGAG	381
QY	85	PheProAlaMetArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSer	104
Db	382	TACAGTGCATAGGAGCACAGTACATAGAGACTGGGAGGGCTTCTTTGTGTATTGGC	441
QY	105	LeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGlnIleLeuAspThr	124
Db	442	ATATAATTAATCTAAATCATTTGAGAGATATTCACCAATTATAGAGAACAAT	492
QY	125	LysSerCysLeuLysAsnLysThrLysGlnAsnValAspValProLeuValIleCysGly	144
Db	493	-----AAAAGAGTTAAGGACTCTGAAGATGTACCTATGGTCTCTAGTAGGA	537
QY	145	AsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIleGlnLeuVal	164
Db	538	AATAAATGTGATTTGGCCT---TCTAGAACAGTAGACACAAAACAGGCTCAGGACTTAGCA	594
QY	165	GlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLeuAsnSerSerLeu	184
Db	595	AGAGCT-----TATGGGAATCCCTTTTATTGAAACATCAGCAAAACAGACAGCGGTGT	648
QY	185	AspGlnMetPheArgAlaLeuPhe---AlaMetAlaLysLeuProSerGluMetSerPro	203

Db 649 GATGATGCTTCTATACATTACTTGCAGAAATTCGAAAAACATAAGAAAGATGAGCAA 708
 Qy 204 AspleuHisArgLys 208
 Db 709 GATGCTAAAAAGAG 723

RESULT 8

PCT-US93-06251-29
 ; Sequence 29, Application PC/TUS9306251
 ; GENERAL INFORMATION:
 ; APPLICANT: Wickstrom, Eric and Rife, Jason P.
 ; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
 ; TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
 ; NUMBER OF SEQUENCES: 93
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: SCULLY, SCOTT, MURPHY & PRESSER
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent'n Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/06251
 ; FILING DATE: 19930630
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Digilio, Frank S.
 ; REGISTRATION NUMBER: 31,346
 ; REFERENCE/DOCKET NUMBER: 8586
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 516-742-4343
 ; TELEFAX: 516-742-4366
 ; TELE: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 29:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5775 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; PCT-US93-06251-29

Alignment Scores:

Pred. No.: 2.37e-23 Length: 5775
 Score: 279.00 Matches: 67
 Percent Similarity: 54.59% Conservative: 34
 Best Local Similarity: 36.22% Mismatches: 72
 Query Match: 19.24% Indels: 12
 DB: 5 Gaps: 4

US-09-709-103-1f1 (1-282) x PCT-US93-06251-29 (1-5775)

Qy 25 TyrArgMetValIleLeuGlySerSerIysValGlyLysThrAlaIleValSerArgPhe 44
 Db 202 TATAAATCTTGCTGTTGAGACCTTGCGTAGGCAAGAGTCCCTTACCATTCAGCTA 261
 Qy 45 LeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPheHisArgLysPhe 64
 Db 262 ATTCAGATCATTTTGTGAGACGAATATGATCCAAATGAGGATTCCTACAGGAGCAA 321
 Qy 65 TyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisPro 84
 Db 322 GTAGTAATTTGATGAGAAACCTGCTCTTGATATTCGACAGCGAGTCAGAGAG 381
 Qy 85 PheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSer 104
 Db 382 TACACTGCATGAGGACCAAGTACATGAGACTGGGAGGGCTTCTTGTGTATTGGCC 441

Qy 105 LeuAspAsnHisArgSerPheGluGluValGlnArgLeuArgGlnIleLeuAspThr 124
 Db 442 ATAAATATCTAAATCATTTTGAAGATATTCACCATTAATGAGAACAAAT 492
 Qy 125 LysSerCysLeuLysAsnLysThrIysGluAsnValAspValProLeuValIleCysGly 144
 Db 493 -----AAAAGAGTTAAGACTGTAAGATGTACTTATGTTCTTACTAGTGA 537
 Qy 145 AsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIleGluGlnLeuVal 164
 Db 538 AATTAATGATTTGGCT---TCTNAAACAGTAGACACAAAACAGGCTCAGACATTAGCA 594
 Qy 165 GlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLysAsnSerIeu 184
 Db 595 AGAAGT-----TATGAAATTCCTTTATTGAAACATCGACAAAGCAGACAGGCTGT 648
 Qy 185 AspGlnMetPheArgAlaLeuPhe---AlaMetAlaLysLeuProSerGlnMetSerPro 203
 Db 649 GATGATGCTTCTATACATTACTTGCAGAAATTCGAAACATTAAGAAAGATGAGCAA 708
 Qy 204 AspleuHisArgLys 208
 Db 709 GATGCTAAAAAGAG 723

RESULT 9

US-08-884-866A-2
 ; Sequence 2, Application US/0884866A
 ; GENERAL INFORMATION:
 ; APPLICANT: Chien, Shu
 ; APPLICANT: Shyy, John Y-J
 ; TITLE OF INVENTION: GENE THERAPY IN CORONARY ANGIOPLASTY AND
 ; FILE REFERENCE: BYPASS
 ; CURRENT APPLICATION NUMBER: US/08/884,866A
 ; CURRENT FILING DATE: 1997-06-30
 ; PRIOR APPLICATION NUMBER: 60/030,358
 ; PRIOR FILING DATE: 1996-11-08
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 570
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(570)
 ; US-08-884-866A-2

Alignment Scores:

Pred. No.: 1.18e-24 Length: 570
 Score: 277.50 Matches: 73
 Percent Similarity: 53.23% Conservative: 34
 Best Local Similarity: 36.32% Mismatches: 72
 Query Match: 19.14% Indels: 23
 DB: 4 Gaps: 6

US-09-709-103-1f1 (1-282) x US-08-884-866A-2 (1-570)

Qy 25 TyrArgMetValIleLeuGlySerSerIysValGlyLysThrAlaIleValSerArgPhe 44
 Db 10 TATAAATCTTGCTGTTGAGACCTTGCGTAGGCAAGAGTCCCTTACCATTCAGCTG 69
 Qy 45 LeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPheHisArgLysPhe 64
 Db 70 ATTCAGATCATTTTGTGAGACGAATATGATCCAAATGAGGATTCCTACAGGAGCAA 129
 Qy 65 TyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisPro 84
 Db 130 GTGCTATTGATGAGGAGACGTGCTGTTGACATCTCGAATACCGCGGCTGAGAGAG 189
 Qy 85 PheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSer 104
 Db 190 TACAGCGCATGCGGAGCAAGTCAATGCGACCGGAGGGCTTCTGTTGTATTGGCC 249


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Qy 105 LeuAspAsnArgAspSerPheGluValGlnArgLeuArgGlnGlnIleLeuAspThr 124
Db 250 ATCAACAACCAAGTCTTTTGGAGACATCCACCAGTACAGGAGCAGATC----- 300
Qy 125 LysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeuValIleCysGly 144
Db 301 -----AAACGGGTGAAGACTCGGATGACGTGCCATCGCTGGTGGTGGGG 345
Qy 145 AsnLysGlyAspArgAspPheTyArgGluValAspGlnArgGluIleGluGlnLeuVal 164
Db 346 AACAAAGTGTGACCTG---GCTGCACGCACACTGTGGAATCTCGGACGGCTCAGACCTCGCC 402
Qy 165 GlyAspAspProGlnArgCysAlaTyPheGluIleSerAlaLysLysAsnSerSerLeu 184
Db 403 CGAAGC-----TACGGCATCCCTTACATCGAGACCTCGGCCAAGACCCGGCAGGAGTG 456
Qy 185 AspGlnMetPheArgAlaLeu-----PheAlaMetAlaLysLeu--- 197
Db 457 GAGGATGCTTCTACAGTGTGGTGGTGAGATCCGGCAGCACAAGCTCGGAAGCTGAAC 516
Qy 198 ---ProSerGluMetSerProAspLeuHisArgLysValSerValGlnIleTyCysAspVal 216
Db 517 CCTCTGATGAGAGTGGCCCGG-CTGCAT-----GAGCTGCAAGTGTGTCTCTC 566
Qy 217 Leu 217
Db 567 CTG 569

RESULT 10
US-08-884-866A-11
; Sequence 11, Application US/08884866A
; GENERAL INFORMATION:
; APPLICANT: Chien, Shu
; APPLICANT: Shyu, John Y-J
; TITLE OF INVENTION: GENE THERAPY IN CORONARY ANGIOPLASTY AND
; TITLE OF INVENTION: BYPASS
; FILE REFERENCE: UCSD1100-1
; CURRENT APPLICATION NUMBER: US/08/884,866A
; PRIOR FILING DATE: 1997-06-30
; PRIOR APPLICATION NUMBER: 60/030,358
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (49)...(51)
; OTHER INFORMATION: nnn = Any nucleic acid triplet, except for UCA,
; OTHER INFORMATION: UCC, UCG, UCU, AGC, or AGU
; OTHER INFORMATION: Variation of SEQ ID NO.:2
US-08-884-866A-11

Alignment Scores:
Pred. No.: 118e-24 Length: 570
Score: 277.50 Matches: 73
Percent Similarity: 53.23% Conservative: 34
Best Local Similarity: 36.32% Mismatches: 72
Query Match: 19.14% Indels: 23
DB: 4 Gaps: 6

US-09-709-103-1f1 (1-282) x US-08-884-866A-11 (1-570)
Qy 25 TyrArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIleValSerArgPhe 44
Db 10 TATAAGCTGGTGGTGGCGCGCGGTGTGGCAANNNGCGCTGACCATCCAGCTG 69
Qy 45 LeuThrGlyArgPheGluAspAlaTyThrProThrIleGluAspPheHisArgLysPhe 64
Db 70 ATCCAGAACCACTTTGTGCGACGATACGACCCCTATAGAGGATTCCTACCGGAAGCAG 129

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```

Qy 65 TyrSerIleArgGlyGluValTyrcInleuAspIleLeuAspThrSerGlyAsnHisPro 84
Db 130 GTGGTCAVTGTGGGAGGACGTGCTGTGGATCCTCGGATCCCGCGGCTCGAGAG 189
Qy 85 PheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSer 104
Db 190 TACACGGCATGCGGACCACTGATGCGCACCGGGAGGGCTTCTCTGTGTGTGGCC 249
Qy 105 LeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGlnIleLeuAspThr 124
Db 250 ATCAACAACCAAGTCTTTTGGAGACATCCACCAGTACAGGAGCAGATC----- 300
Qy 125 LysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeuValIleCysGly 144
Db 301 -----AAACGGGTGAAGACTCGGATGACGTGCCATCGCTGGTGGTGGGG 345
Qy 145 AsnLysGlyAspArgAspPheTyArgGluValAspGlnArgGluIleGluGlnLeuVal 164
Db 346 AACAAAGTGTGACCTG---GCTGCACGCACACTGTGGAATCTCGGACGGCTCAGACCTCGCC 402
Qy 165 GlyAspAspProGlnArgCysAlaTyPheGluIleSerAlaLysLysAsnSerSerLeu 184
Db 403 CGAAGC-----TACGGCATCCCTTACATCGAGACCTCGGCCAAGACCCGGCAGGAGTG 456
Qy 185 AspGlnMetPheArgAlaLeu-----PheAlaMetAlaLysLeu--- 197
Db 457 GAGGATGCTTCTACAGTGTGGTGGTGAGATCCGGCAGCACAAGCTCGGAAGCTGAAC 516
Qy 198 ---ProSerGluMetSerProAspLeuHisArgLysValSerValGlnIleTyCysAspVal 216
Db 517 CCTCTGATGAGAGTGGCCCGG-CTGCAT-----GAGCTGCAAGTGTGTCTCTC 566
Qy 217 Leu 217
Db 567 CTG 569

RESULT 11
US-08-429-964-85
; Sequence 85, Application US/08429964
; Patent No. 5962243
; GENERAL INFORMATION:
; APPLICANT: BROWN, MICHAEL S.
; APPLICANT: GOLDSTEIN, JOSEPH L.
; APPLICANT: REISS, YUVAL
; APPLICANT: JAMES, GUY L.
; TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF FARNESYL
; TITLE OF INVENTION: TRANSFERASE INHIBITORS
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/429,964
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/021,625
; FILING DATE: 16-FEB-1993
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 07/822,011
; FILING DATE: ABANDONED
; CLASSIFICATION: 435
; APPLICATION NUMBER: PCT/US/91/02650

```


FILING DATE: 18-APR-1991
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/615,715
FILING DATE: 20-NOV-1990
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/510,706
FILING DATE: 18-APR-1990 (ABANDONED)
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 607 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-429-964-85

Alignment Scores:
Pred. No.: 1,966-24 Length: 607
Score: 276.00 Matches: 66
Percent Similarity: 54.59% Conservative: 35
Best Local Similarity: 35.68% Mismatches: 72
Query Match: 19.03% Indels: 12
Gaps: 4

US-09-709-103-1f1 (1-282) x US-08-429-964-85 (1-607)

QY 25 TYRARGMETVALILEUENGLYSESERLYSVALIGLYSTHRALEVALSERARGPHE 44
DB 10 TATTAACCTGTGTGAGCTGTGGCGTGAAGAGGCTTACCATGACATGACGTA 69
QY 45 LEUTHRGLYARGPHEGLUASPALATYRTHRPROTHRIEGLUASPHEHISARGLYSPHE 64
DB 70 ATTGAACATCATTTTGTGACGATATGATCCACATATAGAGATTTCTTACGAGAACAA 129
QY 65 TYRSERIEARGGLYGLUVALTYRGLINLEUASPILLEUASPHTHSERGLYASNHSIPRO 84
DB 130 GTAGTAAATTGAGGAGAACTGTCTGTGATATTCGACACAGACGATCAAGAGAG 189
QY 85 PHEPROLAMETARGARGLEUSERILEUTHRGLYASPVALPHEILEUVALPHESE 104
DB 190 TACAGTGCATAGAGGACCCAGTACATGAGAGCTGGGAGGCTTCTGTGATTTGCC 249
QY 105 LEUASPASNARGASPSERPHEGLUGLUALGINARGLEUARGINGLINILEUASPHTHR 124
DB 250 ATTAATTAATACATAATTCATTGAGATATTCACATTAAGAGAACAAATT----- 300
QY 125 LYSSERCYSEULEYASNULYSTRHLYSGULSENVALASPVALPROLEUVALILECYSGLY 144
DB 301 -----AAAAGAGTTAAGGACTCTGGAAGATGTAACATGCTGCTGAGTAA 345
QY 145 ASNLYSGLYASPARGASPPHETRYRARGGLUVALASPGLINARGGLINILEUVAL 164
DB 346 AATAATGATGATTTGCCCT---TCTAGAACAGTAGACACAAACAGGCTCAGACTTACA 402
QY 165 GLYASPARPROGLINARGCYSAATYRPHEGULISESERIALYSLYASNSESERLEU 184
DB 403 AGAAGT-----TATGGAATTCCTTTATTTCAACATAGCAAGACAAAGAGGTCTT 456
QY 185 ARGGLINMETPHEARGALALEUPHE---ALAMETALYSLYEUPROSEGLIMETSE 203
DB 457 GATGATGCCCTTCTATATACATTAGTTCGAGAAATTCGAAACATAAAGATAATGACAAA 516
QY 204 ASPLEUHSISARGLYS 208
DB 517 GATGGTAAAAAGAG 531

RESULT 12

US-08-884-866A-9
Sequence 9, Application US/0884866A
GENERAL INFORMATION:
APPLICANT: Chien, Shu
APPLICANT: Shyu, John Y-J
TITLE OF INVENTION: GENE THERAPY IN CORONARY ANGIOPLASTY AND
TITLE OF INVENTION: BYPASS
FILE REFERENCE: US08100-1
CURRENT APPLICATION NUMBER: US/08/884,866A
CURRENT FILING DATE: 1997-06-30
PRIOR APPLICATION NUMBER: 60/030,358
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 480
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
NAME/KEY: misc_feature
LOCATION: (49)...(51)
OTHER INFORMATION: mm = Any nucleic acid triplet, except for UCA,
OTHER INFORMATION: UCC, UCG, UCU, AGC, or AGU
US-08-884-866A-9

Alignment Scores:
Pred. No.: 1,596-24 Length: 480
Score: 275.50 Matches: 63
Percent Similarity: 56.29% Conservative: 31
Best Local Similarity: 37.72% Mismatches: 62
Query Match: 19.00% Indels: 11
Gaps: 3

US-09-709-103-1f1 (1-282) x US-08-884-866A-9 (1-480)

QY 25 TYRARGMETVALILEUENGLYSESERLYSVALIGLYSTHRALEVALSERARGPHE 44
DB 10 TATTAACCTGTGTGAGCTGTGGCGGCGGTGCGCAANNNGCGTGAACATCCAGCTG 69
QY 45 LEUTHRGLYARGPHEGLUASPALATYRTHRPROTHRIEGLUASPHEHISARGLYSPHE 64
DB 70 ATCCAGAACCATTTTGTGACGATATGACACCCCATATAGAGATTCATACCGAAGCAG 129
QY 65 TYRSERIEARGGLYGLUVALTYRGLINLEUASPILLEUASPHTHSERGLYASNHSIPRO 84
DB 130 GTGCTCATTTGATGGGAGAGAGCTGCTGTGACATCTCGATACCCCGCTGAGAGAG 189
QY 85 PHEPROLAMETARGARGLEUSERILEUTHRGLYASPVALPHEILEUVALPHESE 104
DB 190 TACAGCGCCATGCGGAGCCAGTATATGCGCACCGGAGAGGCTTCTGTGATTTGCC 249
QY 105 LEUASPASNARGASPSERPHEGLUGLUALGINARGLEUARGINGLINILEUASPHTHR 124
DB 250 ATCAACACACCAAGCTTTTGAAGACATCCACAGTACAGGAGAGAGATC----- 300
QY 125 LYSSERCYSEULEYASNULYSTRHLYSGULSENVALASPVALPROLEUVALILECYSGLY 144
DB 301 -----AAACGGGTGAAGAGCTCGAGTGAAGTCCCATGTGCTGTGGGG 345
QY 145 ASNLYSGLYASPARGASPPHETRYRARGGLUVALASPGLINARGGLINILEUVAL 164
DB 346 AACAGATGATCTG---GCTGACCGCATGTGGAATCTCGGACAGCTTACAGACTTCGCC 402
QY 165 GLYASPARPROGLINARGCYSAATYRPHEGULISESERIALYSLYASNSESERLEU 184
DB 403 CGAAGC-----TACGCACTCCCTTACATCAGAGACCTCGGCAAGACCGGAGGAGTG 456
QY 185 ASPGLINMETPHEARGALALEU 191
DB 457 GAGAGTGCCTTCTTACAGCTTG 477

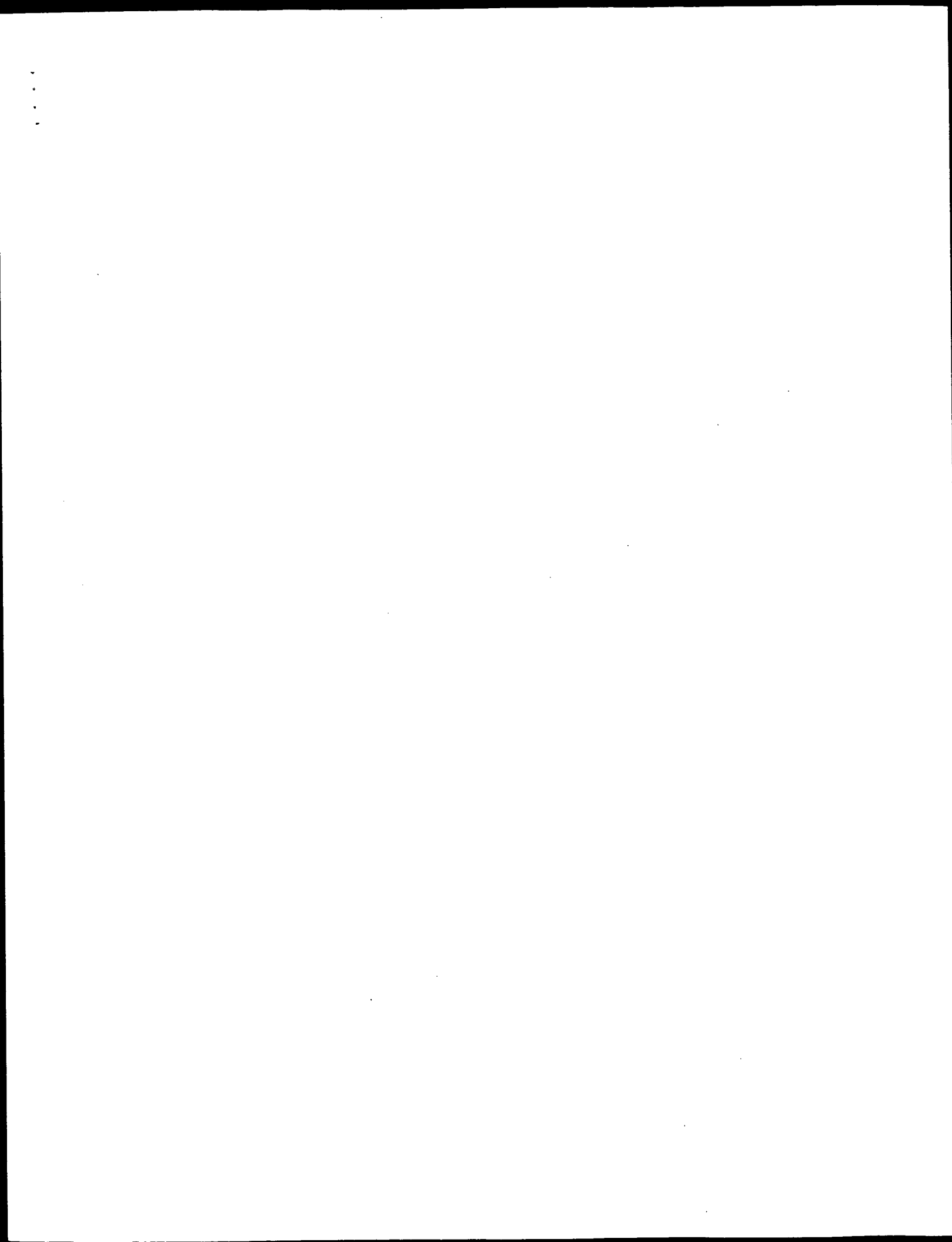
Db 1488 TTCCTCTGTGTAATTGGCCATCAACACACAGTCCTTTTGAAGACATCCATCAGTACAGG 154:
 Qy 119 GInGinIleLeuAepThrLysSerCysLeuLysAsnLysThrLysGluAenValaspVal 138
 ::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
 Db 1548 GAGCAGATC-----AAGCGGCTGAAAGATTCCAGATGATGTG 1583
 Qy 139 ProLeuValIleCysGlyAsnLysGlyAspArgAspPheTyrgGluValaspGlnAtg 158
 |||||:::|||||:::|||||:::|||||:::|||||:::|||||
 Db 1584 CCAATGGTGCTGTGGCGAACAAAGTGACCTGCCCGCTCAC---ACTGTTGAGTCTCGG 1640
 Qy 159 GluIleGluInLeuValcilyAspProGlnArgCysAlaTyrPheGluIleSerAla 178
 ::|||:::|||||:::|||||:::|||||:::|||||:::|||||
 Db 1641 CAGGCCAGGACCTTGCTCGAGC-----TATGGCATCCCTACATTGAACATCAGCC 1694
 Qy 179 LysLysAsnSerSerLeuAspGlnMetPheArgAlaLeu-----Phe 192
 ::::|||||:::|||||:::|||||:::|||||:::|||||
 Db 1695 AAGACCCGACCAGGTGTGGAGGATGCCTTCTACACACTAGTAGCTGAGATTCGGCAGCAT 1754
 Qy 193 AlaMetAlaLyLeUe-----ProSerGluMetSerProAspLeuHisAgLyasValser 210
 ::::|||||:::|||||:::|||||:::|||||:::|||||
 Db 1755 AAACCTCGGGAACATAACCCGCTGATGAGAGTGCCCTGG-CTGCAT-----GAG 1804
 Qy 211 ValGlnTyrCyaspValLeu 217
 ::::|||||:::|||||:::|||||:::|||||
 Db 1805 CTCGAAGTGTGTGCTCTCTG 1825

RESULT 14
 US-08-884-866A-10
 ; Sequence 10, Application US/08884866A
 ; GENERAL INFORMATION:
 ; APPLICANT: Chien, Shu
 ; APPLICANT: Shyu, John Y-J
 ; TITLE OF INVENTION: GENE THERAPY IN CORONARY ANGIOPLASTY AND
 ; TITLE OF INVENTION: BYPASS
 ; FILE REFERENCE: UCSD1100-1
 ; CURRENT APPLICATION NUMBER: US/08/884,866A
 ; CURRENT FILING DATE: 1997-06-30
 ; PRIOR APPLICATION NUMBER: 60/030,358
 ; PRIOR FILING DATE: 1996-11-08
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 10
 ; LENGTH: 450
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (49)...(51)
 ; OTHER INFORMATION: nnn = Any nucleic acid triplet, except for UCA,
 ; OTHER INFORMATION: UCC, UCG, UCU, AGC, or AGU
 US-08-884-866A-10

Alignment Scores:		
Pred. No.:	1,79e-23	Length: 450
Score:	266.50	Matches: 61
Percent Similarity:	58.06%	Conservative: 29
Best Local Similarity:	39.35%	Mismatches: 54
Query Match:	18.38%	Indels: 11
DB:	4	Gaps: 3

US-09-709-103-1F1 (1-282) x US-08-884-866A-10 (1-450)

Qy 25 TyrArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIleValSerArgPhe 44
 |||:::|||||:::|||||:::|||||:::|||||:::|||||
 Db 10 TATAAGCTGTGTGTGGCGCGCGCGGTGTGGGCAANNNGCGCTCACCATCCAGCTG 69
 Qy 45 LeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPheHisArgLysPhe 64
 ::::|||||:::|||||:::|||||:::|||||:::|||||
 Db 70 ATCCAGAACCATTTTGTGACGNATHAGACCCCATATAGAGATTCTTACCGGNAAGCAG 129
 Qy 65 TyrsertileargGlyGluValTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisPro 84
 |||||:::|||||:::|||||:::|||||:::|||||:::|||||
 Db 130 GTGTGTCATTGATGGGAGACGTCCTGTTGGACATCTTGATACCGCGCGCTGGAGGAG 189



GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus.p2n model

Run on: December 30, 2002, 14:39:31 ; Search time 2190 Seconds
(without alignments)

2085,446 Million cell updates/sec

Title: US-09-709-103-1f1

Perfect score: 1450
Sequence: 1 MKLAMIKRCPSDELSIF.....REKASAGSQAQKXRCVYS. 282

Scoring table: BLOSUM62

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Xgapop 10.0 , Xgapext 0.5
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Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-O/cgpt 1/USPTO.spool/TRANSUS09709103/runat.30122002.143926.20664/app.query.fasta.1.455
-DB=EST -OPMT=fastlap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
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-ICPU=3 -NO_XLPHY -NO_MMWP -LANG=QUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAEXT=7 -XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELTEXT=7

Database :

EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
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7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1210.5	83.5	1035	14	BM919341 AGENCOURT
2	1165	80.3	962	13	BM543472 AGENCOURT
3	1144	78.9	1103	14	BM920514 AGENCOURT
4	1121	77.3	965	9	AL533318
5	1120	77.2	742	10	AM028127
6	1114.5	76.9	958	14	BQ719566
7	1100.5	75.9	1053	14	BM921737
8	1064	72.4	649	12	BG085090
9	1038	71.6	1023	13	BM543630
10	1033	71.2	1032	14	BQ067637
11	991.5	68.4	726	12	BF613135
12	987	68.1	655	12	BG711792
13	926	63.9	758	13	BI553776
14	918.5	63.3	1137	14	BM921656
15	917	63.2	814	13	BI596688
16	896.5	61.8	1160	14	BM805574
17	892	61.5	644	13	BG969048
18	890.5	61.4	831	13	BI596637
19	885.5	61.0	710	13	BJ526038
20	884	61.0	1006	14	BQ073742
21	869	59.9	506	13	BM311047
22	867	59.8	1300	11	AK015898
23	862	59.4	947	14	BQ954076
24	859	59.2	648	10	BB636889
25	859	59.2	689	10	BB632699
26	854	58.9	904	14	BQ947936
27	850	58.6	617	13	BI393669
28	832.5	57.4	640	13	BI7490945
29	825	56.9	699	12	BG709229
30	812	56.0	699	13	BI596509
31	812	55.8	700	13	BI596509
32	809	55.0	589	13	BM426066
33	807.5	54.7	888	13	BI754083
34	785.5	54.2	1332	13	BM460899
35	767	52.9	674	13	BI601563
36	748	51.6	675	13	BI545172
37	745	51.4	666	13	BI549939
38	741	51.1	571	13	BI682922
39	732.5	50.5	456	12	BF555822
40	730	50.3	509	10	AW915326
41	703.5	48.5	505	13	BI391213
42	685	47.2	542	9	AA790463
43	674.5	46.5	1438	14	BM807669
44	660.5	45.6	435	10	AW990252
45	655.5	45.2	461	13	BU489219

ALIGNMENTS

RESULT 1
BM919341
LOCUS BM919341 1035 bp mRNA linear EST 12-MAR-2002
DEFINITION AGENCOURT_6715681 NIH_MGC_120 Homo sapiens CDNA clone IMAGE:5748585
5' mRNA sequence.
ACCESSION BM919341
VERSION BM919341.1 GI:19369720
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1035)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12719 row: j column: 10
High quality sequence stop: 658.

FEATURES

source

1..1035
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5748585"
/clone_lib="NIH MGC_120"
/lab_host="DH10B"
/note="Organ: pooled pancreas and spleen; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male.. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."
BASE COUNT 209 a 386 c 293 g 146 t 1 others
ORIGIN

Alignment Scores:

Pred. No.: 1,27e-141 Length: 1035
Score: 1210.50 Matches: 244
Percent Similarity: 95.02% Conservative: 4
Best Local Similarity: 93.49% Mismatches: 8
Query Match: 83.48% Indels: 5
DB: 14 Gaps: 2

US-09-709-103-1F1 (1-282) x BM919341 (1-1035)

QY 1 MetLysLeuAlaAlaMetIleLysValMetCysProSerAspSerGluLeuSerIlePro 20
DB 187 ATGAACCTGGCGCGATGATCAAGAAGATGTGCCGAGCGACTCGGAGCTAGTATCCCG 246
QY 21 AlaLysAsnCysTyrArgMetValIleLeuGlySerLysValGlyLysThrAlaIle 40
DB 247 GCCAAGAACTGCTATCGCATGTCTCTCGCTCGTCCAGGTGGCAAGACGGCCATC 306
QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
DB 307 GTGTGCGCGCTTCTCCACCGCGCGTTCGAGGACGCTTACACGCTACCATCGAGGACTTC 366
QY 61 HisArgLysPheTyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSer 80
DB 367 CACCGCAAGTTCTACTCCATCCCGCGGAGGTTCACAGCTCCACATCTCCGACAGCTCC 426
QY 81 GlyAsnHisProPheProAlaMetArgLysLeuSerIleLeuThrGlyAspValPheIle 100
DB 427 GGCAACCAACCGGTTCCCGCGCATCGCGCGCTCTCCATCTCCACAGGACGTTTTCATC 486
QY 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLysGlnGln 120
DB 487 CTGTGTTCAGTCTGGGAACACCGGAGTCTCTCCAGGAGGTGCGCGGCTCGAGCAGCAG 546
QY 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeu 140
DB 547 ATCTCGACACCAAGTCTTCCTCCAGACAAACCAAGAGAACGTGACGTCGCCCTG 606
QY 141 ValIleCysGlyAsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIle 160
DB 607 GTCATCTGCGGCAACAGGGGTGACCGGAGTCTTACCGGAGGTGAGCAGCGCGAGATC 666

QY 161 GluGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysIlys 180
DB 667 GAGCAGCTGGTGGCGAGCAGACCCAGCGCTGGCGCTACTTCGAGATCTCGCCCAAGAAG 726
QY 181 AsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGlu 200
DB 727 AACAGCAGCTCGACACAGATGTTCGCGCGCTCTTCGTCATGTCAGTCCAGCGAG 786
QY 201 MetSerProAspLeuHisArgLysValSerValGlnTyrCysAspValLeuHisLysIlys 220
DB 787 ATGAGCCAGACCTCCACCGCAAGGTCTCGGTGCAGTACTCGGACGTCTGCACAAGAA 846
QY 221 AlaLeuArgAsnLysLysLeuLeuArgAlaGlySerGly-GlyGly-GlyGlyAspProG 240
DB 847 GCGCTGCGGAAACAGAAACTGCTGCGGCGGCAACGCGCGCGCGCGCGCGCGCGCGG 906
QY 240 LysAspAlaPheGlyIleValAla-----ProPheAlaArg---ArgProSerValHis 256
DB 907 GCGAGCGCCCTTTGGCCATTCGTGGCAACCCCTTTTCGCGCGCGCGCGCGCGCGGAC 965
RESULT 2
BM543472 962 bp mRNA linear EST 20-FEB-2002
LOCUS AGENCOURT 6492614 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5726554
DEFINITION 5', mRNA sequence.
ACCESSION BM543472
VERSION BM543472.1 GI:18773895
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 962)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12719 row: d column: 11
High quality sequence start: 18
High quality sequence stop: 692.
FEATURES
Location/Qualifiers
source
1..962
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5726554"
/clone_lib="NIH MGC_124"
/tissue_type="hippocampus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: EcoRV (destroyed); Site 2: NotI; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."
BASE COUNT 185 a 363 c 272 g 141 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 6.21e-136 Length: 962
Score: 1165.00 Matches: 234
Percent Similarity: 92.55% Conservative: 2
Best Local Similarity: 91.76% Mismatches: 9
Query Match: 80.34% Indels: 10


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Db      681 GAGCAGCTGGTGGGACGACCCCGAGCGCTGCGCTACTTCGAGATCTCGGCCAAGAG 740
Qy      181 AenSerSerLeuAspGlnMetPheAraLeuPheAlaMetAlaLysLeu-ProSerGl 200
Db      741 AA-AGCAGCCTGGACAGATGTTCCGCGCTCTTCGCGCATGGGCGAGCTCCCGGCGGA 799
Qy      200 uMetSerProAspLeuHisAraGlyValSerValGlnTyrCysAspValLeuHis-LysL 220
Db      800 GATGAGCCGAGACCTTGGACCGCAAGGTCTCGGTGAGTACTGCGACGTCGTCACAAAAA 859
Qy      220 yAlaLeuAraGlnLys-LysLeuLeuAraGlnAraGlySerGlyGlyGlyGlyAspPro 239
Db      860 AGGGCTTGGGAAACAGAAAGTGTTCGGGGCCCGGCAACCGCGCGGGCGCGGCCCA 919
Qy      240 GlyAspAla-----PheGlyLeValAlaProPhe---AlaAraGArgProSerValHis 256
Db      920 ACCGGGGCGCAACCCCTTTGGCATCTGGGACCCCTTTCCCGCGCGGGCCCAAGGTACAC 979
Qy      257 -SerAspLeuMetTyrIleAraGlyLysAlaSer---AlaGlySerGlnAlaLysAspLy 275
Db      980 AGGGAACCTTATGGAATCCCCCAAAAGCCAAAGCCCGCCGAGCCAGGCGCAAGAGAAA 1039
Qy      275 s 275
Db      1040 A 1040

RESULT 4
AL533318 LTI_FL015_Brn1 Homo sapiens cDNA clone CS0DN003YU19 5
LOCUS prime, mRNA sequence.
DEFINITION AL533318.1 GI:12796811
ACCESSION AL533318
VERSION AL533318.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 965)
AUTHORS Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
source
1..965
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DN003YU19"
/clone_lib="LTI_FL015_Brn1"
/sex="male"
/tissue_type="Adult brain"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was constructed by Life Technologies.
Contact : Feng Liang Life Technologies, a division of
Invitrogen 9800 Medical Center Drive Rockville, Maryland
20850, USA Fax : (1) 301 610 8371 Email :
filiang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 189 a 352 c 273 g 144 t 7 others
ORIGIN

Alignment Scores:
Pred. No.: 2.21e-130 Length: 965
Score: 1121.00 Matches: 237
Percent Similarity: 95.22% Conservative: 2
Best Local Similarity: 94.42% Mismatches: 11

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Query Match: 77.31% Indels: 5
DB: 9 Gaps: 1
US-09-709-103-1f1 (1-282) x AL533318 (1-965)
Qy      1 MetLysLeuAlaAlaMetIleLysLysMetCysProSerAspSerGluLeuSerIlePro 20
Db      191 ATGAAACTGGCGCGGATGATCAAGAAGATGTGCCGAGGCACTCGAGCTGAGTATCCCG 250
Qy      21 AlaLysAsnCyfTyArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIle 40
Db      251 GCCAAGAACTGCTATCGCATGTCTCTCTCGCTCGTCCAGGTGGCAAGACGCCCATC 310
Qy      41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
Db      311 GTGTCCGCTTCTTCCACCGCGCGCTTCGAGGACGCTACACGCTTACCATCCATCGAGACTTC 370
Qy      61 HisArgLysPheTyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSer 80
Db      371 CACCGCAAGTTCTACTCCATCCGCGGAGGTCTACAGCTCGACATCTCTGACACGTC 430
Qy      81 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIle 100
Db      431 GGCAACACCCCGTTCCCGCCCATGCG-CGCTCTCTCATCTCTCACAGGAGACGTTTTCATC 489
Qy      101 LeuValPheSerIleuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGln 120
Db      490 CTGGTGTTCAGTCTGGACAAACCGCGACTCTTTCGAGGAGGTGCAGCGCTCAGGCGAG 549
Qy      121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeu 140
Db      550 ATCTTCGACACCAAGTCTTTCCTCAAGAACAAACCAAGGAGAACGTGGACGTGCCCTG 609
Qy      141 ValIleCysGlyAsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIle 160
Db      610 GTCATCTGCGGCAACAAGGTGACCGGACTTCTACCGGAGGTGCAGCGCTCAGGCGAG 669
Qy      161 GluGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLys 180
Db      670 GAGCAGCTGTGGGCGGACGACCCCGCGGCTGCGCTACTTTCGAGATCTCGGCCAAGAAG 729
Qy      181 AsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGlu 200
Db      730 AAMAGCAGCTGACACAGATGTTCCGCGCTCTTCGCCATGCGCCAAAGTCCGCCAGCGAG 789
Qy      201 MetSerProAspLeuHisArgLysValSerValGlnTyrCysAspValLeuHisLysLys 220
Db      790 ATGAGCCAGACCTGCACCGCAAGTC-TCGGTGCAGTACTGCGACGTCTGCAMAARAAR 848
Qy      221 AlaLeuArgAsnLysLysLeuLeuArgAlaGlySerGlyGlyGlyAspProGly 240
Db      849 GCGCTGCGGAACAA-AACTGTGCGGCGGCGAGCGS--GGCGGCGGCGGCGGCGCGG 905
Qy      241 AspAlaPheGlyLeValAlaPheAlaArg 251
Db      906 ---AGCTTTGATCTGTGCACCTTGCAGCGG 935

RESULT 5
AL533318 LOCUS
DEFINITION
SEQUENCE
ACCESSION AW028127
VERSION AW028127.1
KEYWORDS GI:5886883
SOURCE EST.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 742)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

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742 bp mRNA linear EST 27-OCT-1999
 wv26c07.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2530668 3'-
 similar to TR:O5626 O35626 RAS, DEXAMETHASONE-INDUCED 1 ;, mRNA

sequence.
 AW028127
 AW028127.1 GI:5886883
 EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 742)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL COMMENT

Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrrp/image/image.html
 Seq primer: -400P from Glibco
 High quality sequence stop: 445.
 Location/Qualifiers

FEATURES

source

1..742
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_1db="IMAGE:2530668"
 /clone_1db="NCI CGAP_Kid11"
 /lab_host="DH10B"
 /note="Organ: Kidney; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1323376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 149 a 260 c 208 g 122 t 3 others
 ORIGIN

Alignment Scores:

Pred. No.: 1,97e-130 Length: 742
 Score: 1120.00 Matches: 220
 Percent Similarity: 95.74% Conservative: 5
 Best Local Similarity: 93.62% Mismatches: 10
 Query Match: 77.24% Indels: 0
 DB: Gaps: 0

US-09-709-103-1F1 (1-282) x AM028127 (1-742)

OY 1 MetLysLeuAlaAlaMetCilLeuSlyMetCysProSerAspSerGluLeuSerIlePro 20
 DB 35 ATGAACACTGCGCCGATGATCAAGAGATGCGCGAGGACTCGAGCTGAGTATCCG 94
 OY 21 AlAluSAsnCySTyArGwEValIleuGlySerSerIySValGlyLysThrAlaIle 40
 DB 95 GCCAAGAACTGCTATCGATGTCATGCTCGCTCGTCCAAAGTGGGCAAGCGGCCATC 154
 OY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaIyTrThrProThrIleGluAspPhe 60
 DB 155 GGTGCGCGCTTCTCACTCGCGCTTCGAGGACGCTTACACCCCTTACCATCAGAGACTTC 214
 OY 61 HisArgLysPheTySerSerIleArgIyGluValIyTrGlnLeuAspIleLeuAspThrSer 80
 DB 215 CACCGCAAGTTTACTTCATCCGCGCGAGGCTTACACAGCTGACATCTCGACACGCTC 274
 OY 81 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIle 100
 DB 275 GCGCAACACCCGCTTCCCGCCCATGGCGGCGCTTCATCTCTCAGAGAGAGCTTTTATC 334
 OY 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGln 120
 DB 335 CTGGGTTCAGTCTGAGCAACCGCATCTCTTCGAGGAGGTGACAGCGGCTCAGCAGCAG 394
 OY 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAspValAspValProleu 140
 DB 395 ATCTCTGACACCAAGTCTTGCTTCAAGAACCAACCAAGAGAGAGTGTGAGTGGCTCTG 454
 OY 141 ValIleCysGlyAsnLysGlyAspArgAspPheTyArgGluValAspGlnArgGluIle 160

DB 455 GTCACTGCGCGCAACAAAGGCTGACCCGACTTCTTACCGGAGGTGACCAAGCGCGAGATC 514
 OY 161 GluGlnLeuValGlyAspAspProGlnArgCysAlaTyPheGluIleSerAluSlyLys 180
 DB 515 GAGCAGCTGTGTGGCGAGCGACCCCGAGCGCTGGCTTCTTCAAGTCTGCGCAAGAG 574
 OY 181 AsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAluSlyLeuProSerGlu 200
 DB 575 AACGAGCAGCTTGAGACCAAGATGTTCCGCGGCTTTCGCATGCGCAAGTGGCCACGAG 634
 OY 201 MetSerProAspLeuHisArgLysValSerValGlnTyCysAspValLeuHisLysLys 220
 DB 635 ATGAGCCCAACACTGACCGCAGGATCTGNGTGCAGTACTGAGACGCTGCGCACAGAG 694

RESULT 6

BOJ719566

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 958)
 NIH-MGC http://mgs.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM13596 row: f column: 19
 High quality sequence stop: 514.
 Location/Qualifiers

FEATURES

source

1..958
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_1db="IMAGE:6193170"
 /clone_1db="Lupski_sympathetic_trunk"
 /sex="male"
 /tissue_type="sympathetic trunk"
 /dev stage="adult, 16 yr"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6 (Life Technologies); Site 1: NotI; Site 2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors:
 5'-TCGACATCTTAGATCGAGCGCGGCGCTT(15)-3'. Size selected > 1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life Technologies."

BASE COUNT

185 a 339 c 275 g 159 t

ORIGIN

Alignment Scores:

Pred. No.: 1.44e-129 Length: 958
 Score: 1114.50 Matches: 226
 Percent Similarity: 94.61% Conservative: 2

Best Local Similarity: 93.78% Mismatches: 10
 Query Match: 76.86% Indels: 3
 DB: 14 Gaps: 1

US-09-709-103-1F1 (1-282) x BQ719566 (1-958)

QY 15 SerGluLeuSerIleProAlaLysAsnCysTyrArgMetValIleLeuGlySerSerLys 34
 DB 1 TCGGAGCTGAGTATCCCGGCAAGACTGCTATCGCATGTCCTCGGCTGCTCCAG 60

QY 35 ValGlyLysThrAlaIleValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThr 54
 DB 61 GTGGCAGACGCGCATGCTGTCGCTTCTCACCGCGCTTCGAGGAGCGCTACAG 120

QY 55 ProThrIleGluAspPheHisArgLysPheTyrSerIleArgGlyGluValTyrGlnLeu 74
 DB 121 CCTACCATCGAGGACTTCCACCGAAGTTCTACCTCCATCGCGCGGAGGTCTACCA 180

QY 75 AspileLeuAspThrSerGlyAsnHisProPheProAlaMetArgArgLeuSerIleLeu 94
 DB 181 GACATCTCGACAGCTCGGCAACACCCGTTCCCGCCATGCGCGCTCTCCATCCTC 240

QY 95 ThrGlyAspValPheIleLeuValPheSerLeuAspAsnArgAspSerPheGluVal 114
 DB 241 ACAGGAGACGTTTTCATCTGCTGTTGTCAGTCTGGACACCGCGACTCTTCGAGGAG 300

QY 115 GlnArgLeuArgGlnGlnIleLeuAspThrLysSerCysLeuLysAsnLysThrLysGlu 134
 DB 301 CAGCGGCTCAGGACGAGATCTCGACACCAAGTCTTGCTTCAAGAAACAAACGAG 360

QY 135 AsnValAspValProLeuValIleCysGlyAsnLysGlyAspArgAspPheTyrArgGlu 154
 DB 361 AACGTGGACGTGCCCCCTGCTGTCATCTCGCGCAACAGGAGTACCGCGACTTCTAC 420

QY 155 ValAspGlnArgGluIleGlnLeuValGlyAspProGlnArgCysAlaTyrPhe 174
 DB 421 GTGGACACGCGGAGATCGACAGCTGGTGGCGACGACCCCGCGCTGCGCTACTTC 480

QY 175 GluLeSerAlaLysLysAsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMet 194
 DB 481 GAGATCTCGGCAAGAAACAGCAGCTCGACCAAGATGTTCCGCGCGCTCTTCGCCATG 540

QY 195 AlaLysLeuProSerGluMetSerProAspLeuHisArgLysValSerValGlnTyrCys 214
 DB 541 GCCAAGTGCCTCAGAGATGAGCCGACCTGCCCGCAAGGTCCTCGGTCGAGTAATGC 600

QY 215 AspValLeuHisLysLysAlaLeuArgAsnLysLysLeuLeuArg-AlaGlySerGly-G 234
 DB 601 GACGTGCTGCACAGAGCGCTCGGNAACAAAAGCTGTCGCGGGCGGCAACGGAAG 660

QY 234 lYgLYGlyAspPro---GlyAspAlaPheGlyIleValAlaProPheAlaArgArg 252
 DB 661 GCGCGGCGCTCGACCCCGGGGAAGCTTTTGGGATCGGGGGCCCCCTTTTCGGGGGCG 719

RESULT 7
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 LOCUS AGENCOURT 6708101 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5753301
 DEFINITION 5', mRNA sequence.
 ACCESSION BM921737
 VERSION BM921737.1 GI:19372116
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1053)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: L1AM12788 Row: n Column: 22
 High quality sequence stop: 600.
 Location/Qualifiers
 1. .1053
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5753301"
 /clone_lib="NIH_MGC_115"
 /lab_host="DH10B"
 /note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH MGC Library."
 BASE COUNT 215 a 390 c 297 g 150 t 1 others
 ORIGIN

Alignment Scores:
 Pred. No.: 9,75e-128 Length: 1053
 Score: 1100.50 Matches: 228
 Percent Similarity: 88.26% Conservative: 5
 Best Local Similarity: 86.36% Mismatches: 22
 Query Match: 75.90% Indels: 9
 DB: 14 Gaps: 3

US-09-709-103-1F1 (1-282) x BM921737 (1-1053)

QY 1 MetLysLeuAlaAlaMetIleLysLysMetCysProSerAspSerGluLeuSerIlePro 20
 DB 200 ATGAACCTGGCGCGATGATCAAGAAGATGTCCCGAGCGACTCGAGCTGAGTATCCG 259

QY 21 AlaLysAsnCysTyrArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIle 40
 DB 260 GCAAGAACTGCTATCGCATGTCATCTCGCTCGTCAAGTGGGCAAGACGCCATC 319

QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
 DB 320 GTGTGGGCTTCTCTCACCGCGCTTCGAGGAGCGCTACACGCTTACCATCGAGGACTTC 379

QY 61 HisArgLysPheTyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSer 80
 DB 380 CACCGCAAGTTCTACTCCATCGCGCGAGGTCTACCAAGCTCGACATCTCGACACGTCC 439

QY 81 GlyAsnHisProPheProAlaMetArgLeuSerIleLeuThrGlyAspValPheIle 100
 DB 440 GGCAACACCCGCTTCCCGCATGCGGCGCTCTCCATCTCACAGGAGAGCTTTTCATC 499

QY 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGln 120
 DB 500 CTGGTGTTCAGTCTCGACAAACCGCGACTCTTCGAGGAGGTGCGAGCGCTCAGGCGAG 559

QY 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeu 140
 DB 560 ATCTCTCGACACCAAGTCTTGCTTCAAGAACAAACCAAGAGAGAACTGGAGCTGCGCCCTG 619

QY 141 ValIleCysGlyAsnLysGlyAspArgPheTyrArgGluValAspGlnArgGluIle 160
 DB 620 GTATCTCGGCAACAAAGGTGACCGGACTTCTACCGGAGGTGACCGCGAGATC 679

QY 161 GluGlnLeuValGlyAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLys 180
 DB 680 GAGGAGCTGTGGCGGACGACCCCGCGCTGCGCTTCTGAGATCTTCGCCCAAAAG 739

QY 181 AsnSerSer-LeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerG1 200
 DB 740 AAGAGCAGCCCTGACCAAGATGTTCCGGCGGCTCCCGCATGCCAACCTGCCAGCGCA 799
 QY 200 UMetSerProAspLeuHisArgLys--ValSerValGlnTyrCysAspValLeuHisLys 219
 DB 800 GATGAGCCCAAGACCTGACCGCAAGGATCTCGGGGCAAGTACTCCGACCTGCTGACCA 859
 QY 219 slyr---AlaLeuArgAsnLysLysLeuArg-AlaGlySer-----G 233
 DB 860 AAAAGGGGCTGCGGGAACAAAAAACTGCTGCGGGCGGTAAACCCGTTGGCGGCGCGG 919
 QY 233 TGT 253
 DB 920 GAGGAACCGGGGGAACCCCTTGGGGAATTCGGGGGCAACCTTGCTGGGCGCGGCGAC 979
 QY 253 roSerVal 255
 DB 980 CAAGGTA 987
 RESULT 8
 BG085090 649 bp mRNA linear EST 26-JAN-2001
 LOCUS H3108E05-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
 DEFINITION H3108E05 5', mRNA sequence.
 ACCESSION BG085090
 VERSION BG085090.1 GI:12567654
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 649)
 Kargul,G.J., Dudekula,D.B., Qian,Y., Lim,M.K., Jaradat,S.A., Tanaka
 T.S., Carter,M.G. and Ko,M.S.H.
 Verification and initial annotation of NIA mouse 15K cDNA clone set
 Unpublished (2001)
 Other ESTs: H3108E05-3
 Contact: George J. Kargul
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@lgsun.grc.nia.nih.gov
 Visit http://lgsun.grc.nia.nih.gov/cDNA/15K.html for details.
 Plate: H3108 row: E column: 05
 Seq primer: -21M13 Reverse
 High quality sequence stop: 649
 POLYA=No.

FEATURES
 source
 1. 649
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:H3108E05-5"
 /db_xref="taxon:10090"
 /clone="H3108E05"
 /clone_11b="NIA Mouse 15K cDNA Clone Set"
 /sex="Clones arrayed from a variety of cDNA libraries"
 /dev_stage="Clones arrayed from a variety of cDNA libraries"
 /lab_host="DH10B"
 /note="vector: pSPORT1; Site 1: SalI; Site 2: NotI. This clone is among a rearranged set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT)-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000,

Proc. Natl. Acad. Sci. U S A. 97: 9127-9132; (2)
 Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."

BASE COUNT 157 a 182 c 177 g 133 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.85e-123 Length: 649
 Score: 1064.00 Matches: 212
 Percent Similarity: 98.62% Conservative: 2
 Best Local Similarity: 97.70% Mismatches: 1
 Query Match: 73.38% Indels: 2
 DB: 12 Gaps: 0

US-09-709-103-1F1 (1-282) x BG085090 (1-649)

QY 18 SerLeuProAlaLysAsnGlyTyrArgMetValLeuGlySerSerLysValGlyLys 37
 DB 3 AGTATCCGGCCCAAGAACTGCTACAGATGTCATCTCGCTCATCAAGTGGCAAG 62
 QY 38 ThrAlaLeuValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIle 57
 DB 63 ACGGCATTTGT 122
 QY 58 GluAspPheHisArgLysPheTyrSerIleArgGlyGluValTyrGlnLeuAspIleLeu 77
 DB 123 GAGGACTTCCACCAAAAGTTTATTCGATCCGCGGCAAGCTTACAGTGGACATCTG 182
 QY 78 AspThrSerGlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAsp 97
 DB 183 GACACATCGGCATCATCATCTCCGCGCATGGGCGCTCTTATCTCACAGGAGAC 242
 QY 98 ValPheIleLeuValPheSerLeuAspAsnArgPhePheGluGluValGlnArgLeu 117
 DB 243 GTTTTCATTTCTGGT 302
 QY 118 ArgGlnGlnIleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsnValAsp 137
 DB 303 AAACGACGATCTTACAGACCAAGCTGTCTCAAGAAACAAACCAAGAAATGTGGAC 362
 QY 138 ValProLeuValIleCysGlyAsnLysGlyAspArgPheTyrArgGluValAspGln 157
 DB 363 GTGCCGCTGTCATTTTGGGTGATCAAGGGGACCGGACCTTACCGGGAAGTAGACGAG 422
 QY 158 ArgGlnIleGlnGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGluIleSer 177
 DB 423 CCGGAGATTGACACCTGT 482
 QY 178 AlaLysLysAsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeu 197
 DB 483 GCCAAGAAAGACAGAGCTTGACCAAGATGTTCTGTGGCTCTTGCATGCGCAACTG 542
 QY 198 ProSerGluMetSerProAspLeuHisArgLys--ValSerValGlnTyrCys--AspValL 217
 DB 543 CTTACCGAAGTAGGCCCGGACCTTGACCGGCAAGGGTATCTGTGAGATCTGGCGACGATAC 602
 QY 217 euHisLysLysAlaLeuArgAsnLysLysLeuLeuArgAlaGlySer 232
 DB 603 TGCACAAAGAGGCTTGAGGAACAAAGAGCTTTCGCTGCGGGGACG 649
 RESULT 9
 LOCUS BM543630 1023 bp mRNA linear EST 20-FEB-2002
 DEFINITION AGENCOURT_6492527 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5726764
 ACCESSION BM543630
 VERSION BM543630.1 GI:18774186
 KEYWORDS EST.


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SOURCE          human.
ORGANISM        Homo sapiens
REFERENCE       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE          1 (bases 1 to 1023)
JOURNAL        NIH-MGC http://mgc.nci.nih.gov/.
COMMENT        National Institutes of Health, Mammalian Gene Collection (MGC)
               Unpublished (1999)
               Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-remail.nih.gov
               Tissue Procurement: Invitrogen
               cDNA Library Preparation: Life Technologies, Inc.
               cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
               DNA Sequencing by: Agencourt Bioscience Corporation
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               http://image.llnl.gov
               Plate: LLAMi2719 row: m column: 05
               High quality sequence stop: 637.
FEATURES       Location/Qualifiers
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               /organism="Homo sapiens"
               /db_xref="taxon:9606"
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               /clone_lib="NIH MGC_124"
               /tissue_type="hippocampus"
               /lab_host="DH10B"
               /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: EcoRV
               (destroyed); Site_2: NotI; RNA source male hippocampus,
               age 27. Library is oligo-dT primed and directionally
               cloned (EcoRV site is destroyed upon cloning). Average
               insert size 1.4 kb, insert size range 0.9-4 kb. Library is
               normalized and enriched for full-length clones and was
               constructed by C. Gruber (Invitrogen). Research Genetics
               tracking code 012."
BASE COUNT     196 a 378 c 281 g 168 t
ORIGIN
Alignment Scores:
Pred. No.:      7,13e-120      Length:      1023
Score:          1038.00        Matches:    222
Percent Similarity: 83.46%      Conservative: 5
Best Local Similarity: 81.62%    Mismatches: 30
Query Match:     71.59%        Indels:     15
DB:              13            Gaps:       3
US-09-709-103-1F1 (1-282) x BM543630 (1-1023)
QY 1 MetLysLeuAlaAlaMetIleLysLysMetCysProSerAspSerGluLeuSerIlePro 20
Db 149 ATGAACCTGGCCGGCGATGATCAAGAGATGTGCCGAGGACTCGGAGCTGAGTATCCCG 208
QY 21 AlalysAsnCysTyrArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIle 40
Db 209 GCCAAGAACTGCTATCGATGATCATCTCGGCTCGTCCAGAGTGGCAGAGCGGCATC 268
QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
Db 269 GTGTGCGGCTTCCTCAGCGGCGGCTTCAGAGAGCGCTTACACGCTACCATCGAGGACTTC 328
QY 61 HisArgLysPheTyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSer 80
Db 329 CACCGCAAGTTTCTACTCCATCCGGGGGAGGTCTTACCAGTCTGCACATCTCCGACAGTCC 388
QY 81 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIle 100
Db 389 GGCAACCAACCGTTCCCGGCATGCGCGGCTCTCCATCTCCACAGGAGCGTTTTCATC 448
QY 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGln 120
Db 449 CTGGTGTTCAGTCTGGACAAACCGCGACTCTCTCAGGAGGTGAGCGGCTCAGGACGAC 508
QY 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeu 140

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Db 509 ATCTCTGCACACCAAGTCTTGCTCAAGAACAAACCAAGAGAACTGGACGTGCCCCCTG 568
QY 141 ValIleCysGlyAsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIle 160
Db 569 GTCACTGCGGCAACAAGGTGACCGGACTTCTACCGGAGGTGGACGAGCGGAGATC 628
QY 161 GluGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLys 180
Db 629 GAGCAGCTGTGTGGCGGACGACCCCGGCGCTCTTTCGAGATCTCGGCCAAGAAG 688
QY 181 AsnSerSerLeu-AspGlnMetPheArgAlaLeuPheAlaMetAla-LysLeu-ProSer 199
Db 689 AACAGAGCTCTGGGACGAGATGTTCCGCGGCTCTTCCCAGGCCCAAGTGCCTCCCGC 748
QY 200 GluMetSerProAspLeuHisArgLys---ValSerValGlnTyrCys---AspValLeu 217
Db 749 GAGATGAGCCAGACCTGCACCGCCCAAGGTCTCGGGTGCAGGTACTGGCGACGGCTGG 808
QY 218 HisLysLysAlaLeuArgAsnLysLysLeuLeuArgAlaGlySerGlyGlyGlyGly 237
Db 809 CACAAGAAAGGCGCTGGCGGAAACACAGAAACTGGCTGTGCGGGCGCGCAATCCGCGGG 868
QY 238 -----AspProGlyAspAlaPheGlyIleValala 247
Db 869 CCTCTCTAGTCATAAACCTTGACCGAAGGACCTTGGGCGGCGCTAGGGCCACCATTTT 928
QY 248 PropheAlaArgArgProSerValHisSer 257
Db 929 CCGGACAGTGGCGGCTCTTGTGTATCC 958
RESULT 10
BQ067637
LOCUS
DEFINITION   BQ067637 1032 bp mRNA linear EST 02-APR-2002
5' mRNA sequence.
ACCESSION   BQ067637
VERSION     BQ067637.1 GI:19896683
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1032)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-remail.nih.gov
           Tissue Procurement: Life Technologies, Inc.
           cDNA Library Preparation: Life Technologies, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAMi2793 row: n column: 15
           High quality sequence stop: 602.
FEATURES   Location/Qualifiers
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           /db_xref="taxon:9606"
           /clone="IMAGE:5755214"
           /clone_lib="NIH MGC_115"
           /lab_host="DH10B"
           /note="Organ: pooled brain, lung, testis; Vector:
           pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
           source anonymous pool of 6 male brains, age range 23-27; 1
           male lung, age 27; and 1 male testis, age 69. Library is
           oligo-dT primed and directionally cloned (EcoRV site is
           destroyed upon cloning). Average insert size 1.8 kb,
           insert size range 1-3 kb. Library is normalized and
           enriched for full-length clones and was constructed by C.

```


Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC library."
BASE COUNT 210 a 375 c 298 g 148 t 1 others
ORIGIN

Alignment Scores:

Pred. No.: 3,09e-119 Length: 1032
Score: 1033.00 Matches: 225
Percent Similarity: 88.37% Conservative: 3
Best Local Similarity: 87.21% Mismatches: 15
Query Match: 71.24% Indels: 15
Gaps: 3

US-09-709-103-1f1 (1-282) x BQ067637 (1-1032)

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QY 1 MetLysLeuAlaAlaMetLysLysMetCysProSerAspSerGluLeuSer1lePro 20
Db 201 ATGAACCTGGCGCGCATATCAAGAGATGTGCCGACGACTCGAGCTAGTATCCCG 260
QY 21 AlaLysAsnCysTyrArgMetVal1leuGlySerSerLysValGlyLysThrAla1le 40
Db 261 GCCAAGAACTGTCATGTCATGTCCTCGGCTGTCCTCAAGTGGCAAGACGGCCATC 320
QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThr1leGluAspPhe 60
Db 321 GTGTGCGCTTCTTACCGCGGCTTCAAGAGAGCGCTTACACGCTTACATCGAGACTTC 380
QY 61 HisArgLysPheTyrSer1leArgGlyGluValTyrGlnLeuAsp1leLeuAspThrSer 80
Db 381 CACCGCAAGTTCTATCTCATCCGCGGCGAGGCTTACAGCTCGACATCTCGACACCTCC 440
QY 81 GlyAsnHisProPheProAlaMetArgArgLeuSer1leLeuThrGlyAspValPhe1le 100
Db 441 GGCAACCACTCCGCTTCCCGCATGCGCGCTTCTTCACTTCAAGAGAGCGTTTTCATC 500
QY 101 LeuVal1PheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGln 120
Db 501 CTGGGTTCAGCTGTGAGAACCGCGACTCTTCAAGAGAGTGCAGCGGCTTCAAGCAGCAG 560
QY 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeu 140
Db 561 ATCTCTGACACCAAGTCTTGGCTTCAAGAACCAAGGAGGAGGAGTGGAGTGGCTCCCTG 620
QY 141 ValIleCysGlyAsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGlu1le 160
Db 621 GTCACTCTCGGCAACAGAGTGCAGCGACTTCTTACCGCGAGTGGACCAACCGGAGATC 680
QY 161 GluGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGlu1leSerAlaLysLys 180
Db 681 GAGCAGCTGTGGGGGAGAGACCCCGGCTGCTTCAAGATCTCGGATCTCGGCAAGAG 740
QY 181 AsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSer 199
Db 741 AACGACCACTGAGAACCAAGATGTTCCGCGCTTCTTCCCAAGGCAAGTGGCCAGCC 800
QY 200 GluMetSerProAspLeuHisArgLysValSerValGln---TyrCysAspValLeuH 218
Db 801 GAGATGAGCCCAAGACCTGAGACCGCGCAAGGTCTGCTGCAATTACATGCAACGGGGCTGC 860
QY 218 IeLysLys---AlaLeuArgAsnLysLysLeuLeu-----A 229
Db 861 ACAAACAAAGGGCGCTGCGGAGAACAAACCTTGTGCGGCGCGGCAACCGCGGCGC 920
QY 229 rgaLagLysSerGlyGlyGlyAspProGlyAspAlaPhe 243
Db 921 GGGCGGCGCGGCAACACCGGGGAGAACCCCTTTGGGCAATT 964

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RESULT 11
BF613135

LOCUS BF613135 726 bp mRNA linear EST 14-DEC-2000
DEFINITION de30e03.v1 Wellcome CRC pR3 dorsal 11p Xenopus laevis cDNA clone
IMAGE:347357 5' similar to IR:035626 O35626 RAS.
DEXAMETHASONE-INDUCED 1, mRNA sequence.

ACCESSION BF613135
VERSION BF613135.1 GI:11784463
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis

REFERENCE
AUTHORS 1 (bases 1 to 726)
Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person, B., Gibbons, M., Harvey, N., Rittner, E., Jackson, Y., McCann, R., Waterston, R. and Wilson, R.
Washu Xenopus EST project, 1999

TITLE
JOURNAL
COMMENT
Other ESTs: de30e03.x1
Contact: Sandy Clifton, Ph.D.
Washu Xenopus EST project, 1999

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu

Library constructed by A.M. Zorn (Wellcome/CRC Institute). DNA
Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/BLNU at: info@image.llnl.gov
Seq primer: -40RP from Gibco
High quality sequence stop: 519.

FEATURES

source

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/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="IMAGE:347357"
/clone_lib="Wellcome CRC pR3 dorsal 11p"
/tissue_type="dorsal 11p"
/lab_host="DH10B (phage-resistant)"
/note="Vector: pBSRN3; Site 1: NotI; Site 2: EcoRI; cDNAs
were oligo-dT primed and directionally cloned. Staging
according to Niwkoop and Faber. Library was constructed
by A.M. Zorn (Wellcome/CRC Institute)."

BASE COUNT 197 a 196 c 181 g 152 t
ORIGIN

Alignment Scores:

Pred. No.: 3,07e-114 Length: 726
Score: 991.50 Matches: 187
Percent Similarity: 92.89% Conservative: 22
Best Local Similarity: 83.11% Mismatches: 15
Query Match: 68.38% Indels: 1
Gaps: 1

US-09-709-103-1f1 (1-282) x BF613135 (1-726)

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QY 3 LeuAlaAlaMetLysLysMetCysProSerAspSerGluLeuSer1leProAlaLys 22
Db 55 CTACCGCAATGATCAAGAAATGTGCCCAAGACGAGACCACTCAACATCCACCCAAAG 114
QY 23 AsnCysTyrArgMetVal1leuGlySerSerLysValGlyLysThrAla1leValSer 42
Db 115 AACTGTACCGCATGTGTCCTGCGGCTTCTTCAAGTGGCAAGACCTCCATCTGTGCT 174
QY 43 ArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThr1leGluAspPheHisArg 62
Db 175 CGCTTCTTAACGCGCATTCAGACGACATACAGCGGACCATGAGAGACTTCCACGA 234
QY 63 LysPheTyrSer1leArgGlyGluValTyrGlnLeuAsp1leLeuAspThrSerGlyAsn 82
Db 235 AAGTTTACAGCATTCGGGAGAGAGTCTACAGCTGAGATCTTGCAGACCTCGGCGAAC 294
QY 83 HisProPheProAlaMetArgArgLeuSer1leLeuThrGlyAspValPhe1leLeuVal 102
Db 295 CACCCCTTCCCGCATGAGAGACTTCCATCTTACCGGAGATGTCTTCACTTGGTGC 354

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Qy 103 PheSerLeuAspSerPheGluValGlnArgLeuArgGlnGlnLeu 122
Db 355 TTCACCTGGACACAGGACTCCTTTGAGGAGGTGCAAGGCTGAAGCAGAGATTATG 414
Qy 123 AspThrLysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeuValIle 142
Db 415 GAGACCAAGTCCCTGCTCAAGAACAAACCAAGAGACGTTGATGTTCCCATCGTTATC 474
Qy 143 CysGlyAsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluLeuGluGln 162
Db 475 TCGCGGAATTAAGTAGACAGGACTTCTACAGGGAAGTCAAGCTCATGAGATTGAGCAG 534
Qy 163 LeuValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLysAsnSer 182
Db 535 CTGGTTGAGAGGAC---AGTAAATGCTTACTTTGAGGTGCGGCCAAGAAAGAACTC 591
Qy 183 SerLeuAspGlnMetPheAlaLeuPheAlaMetAlaLysLeuProSerGluMetSer 202
Db 592 AGCTGGATGAGATGTTTAAAGCTCTCTTCCCATGGACAAAGTTGCCAGCGAGATGAGC 651
Qy 203 ProAspLeuHisArgLysValSerValGlnTyrCysAspValLeuHisLysLysAlaLeu 222
Db 652 TCAGACCTGCACCGCAAGGTGCTGTCCAGTACTGTGAGATCTTACACAAAGAGTCCCTG 711
Qy 223 ArgAsnLysLysLeu 227
Db 712 AAAGAAAGAAAGTA 726

RESULT 12
BG711792 655 bp mRNA linear EST 08-MAY-2001
LOCUS
DEFINITION
pglin.pk009.i15 Normalized Liver Library Gallus gallus cDNA clone
pglin.pk009.i15 5' similar to gb|AA43090.1|AF239157_1 (AF239157)
DEXRSL [Rattus norvegicus]G, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE
1 (bases 1 to 655)
Burnside,J., Morgan,R.W. and Cogburn,L.A.
Chicken ESTs from a normalized liver library
Unpublished (2001)
Contact: Joan Burnside
Molecular Endocrinology
University of Delaware
40 Townsend Hall, Newark, DE 19717, USA
Tel: 302 831-1345
Fax: 302-831-3411
Email: joan@udel.edu, www.chickest.udel.edu.

FEATURES
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BASE COUNT 145 a 206 c 184 g 104 t 16 others
ORIGIN

Alignment Scores:
Pred. No.: 9.68e-114 Length: 655
Score: 987.00 Matches: 192
Percent Similarity: 97.12% Conservative: 10
Best Local Similarity: 92.31% Mismatches: 5
Query Match: 68.07% Indels: 1

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DB: 12 Gaps: 0
US-09-709-103-1f1 (1-282) x BG711792 (1-655)

Qy 1 MetLysLeuAlaMetIleLysLysMetCysProSerAspSerGluLeuSerIlePro 20
Db 14 ATGAACCTGGCAGCGATGATCAAGAAGATGTGCCAGCAGGCTGAGCTGAGCATCCCC 73
Qy 21 AlalysAsnCysTyrArgMetValIleGlySerSerLysValGlyLysThrAlaIle 40
Db 74 GCCAAGAACTCTACCGCATGGTTCATCTGGGCTCTCCCAAGTGGGCAAGACGGCCATC 133
Qy 41 ValSerArgPheLeuThrGlyValArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
Db 134 GTCTCGCGCTTCTCACCGCGGCTTCGAGGAGCAGTACACGCCCCACCATCGAGACTTC 193
Qy 61 HisArgLysPheTyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSer 80
Db 194 CACCGCAAGTTTACAGCATCCGCGGTGAGGTCTACCAGGTCGACATCTCTGGACACGCTG 253
Qy 81 GlyAsnHisProPheProAlaMetArgLeuSerIleLeuThrGlyAspValPheIle 100
Db 254 GGCACACCACTTCCCGCGCATCGCGGCTGTCCATCTCTCACAGGTGACGTTTTCATC 313
Qy 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGln 120
Db 314 CTCGTGTTTCAGCCTGGACACCGGAGCTCTCTTCGAGGAGGTGCGAGCGCTGAAGCAGCAG 373
Qy 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeu 140
Db 374 ATCTCTGGAGACCAAGTCGTGCTGAAGAACAAACCAAGGAGAACATCGAGGTCCGCTG 433
Qy 141 ValIleCysGlyAsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIle 160
Db 434 GTCATCTCGCGCAACCAAGCGGACCGGACTTTTACCGGGAGGTGCGAGCCCCGAGAGATC 493
Qy 161 GluGlnLeuValGlyAspAspProGlnArgCysAla-TyrPheGluIleSerAlaLysLy 180
Db 494 GAGCAGCTGTGGCGGAGAGACCCCAAGAAATCGCANNACTTCGAGATCTCGGCCNAGAA 553
Qy 180 sAsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlalysLeuProSerGl 200
Db 554 GAACAGCAGCTGGATCAGATGTTCCAGCGCTCTTCCCATGGCNAACACTGCCAGCGGA 613
Qy 200 uMetSerProAspLeuHisArg 207
Db 614 GATGAGCCCCGACCTGCACCCG 635

RESULT 13
BG711792 758 bp mRNA linear EST 05-SEP-2001
LOCUS
DEFINITION
603190722P1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5262101 5',
mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 758)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

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http://image.llnl.gov
Plate: LLAM1650 row: 1 column: 06
High quality sequence stop: 738.
Location/Qualifiers

FEATURES

source

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/lab_host="DH10B"
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); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.5 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carnucci, in preparation). Library
constructed by M. Brownstein (NIMH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT      155 a      252 c      249 g      102 t
ORIGIN
```

Alignment Scores:

```
Pred. No.:      6e-106      Length:      758
Score:          926.00      Matches:      182
Percent Similarity: 98.92%      Conservative: 1
Best Local Similarity: 98.38%      Mismatches: 1
Query Match:    63.86%      Indels:      1
DB:             13          Gaps:        0
```

US-09-709-103-1f1 (1-282) x B1553776 (1-758)

```
QY 98 ValPheileLeValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeu 117
Db 6 GTTTCATCTCTGTGTTGCTGCTGCAACCCGCACTCTTTCAGAGAGGTGAGCGGCTC 65
QY 118 ArgGlnGlnIleLeuAspThrLysSerCysLeuLysAsnLysThrLys-GluAsnValAs 137
Db 66 AGCGACGACATCTCGACCAACCAAGCTTGTCTCAAGAACAAACCAAGGAGAACTGGA 125
QY 137 PValProLeuValIleCysGlyAsnLysGlyAspArgAspPheTyrArgGluValAspG 157
Db 126 CGTGGCCCTGTCATCTGGGCAACAGGGTGTACCGCACTTCTACCGCGAGGTGACCA 185
QY 157 nArgGluIleGlnGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGluIleSe 177
Db 186 GCGCGAGATCGAGCGCTGTGGGCAACCCCAAGCGCTGCGCTTCTGAGATCTC 245
QY 177 rAlaLysLysAsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLe 197
Db 246 GGCACAAAGAAAGACAGACAGCTGGACCAAGATGTTCCGGCGGCTCTTCGCAATGGCCAACT 305
QY 197 nProSerGluMetSerProAspLeuHisArgLysValSerValGlnTyrCysAspValle 217
Db 306 GCCCAGCGAGAGAACCCAGACCTGACCGCAAGGTCTCGGTGCACTGCGACGTGCT 365
QY 217 whiLysLysAlaLeuArgAsnLysLysLeuLeuArgAlaGlySerGlyGlyGlyGlyG 237
Db 366 GCAAAAGAAAGCGCTGCGAAGAGTGTGGGCGGCGGCAAGCGGCGGCGGCGGCGG 425
QY 237 yAspProGlyAspAlaPheGlyLysValAlaProPheAlaArgArgProSerValHisSe 257
Db 426 CGACCCGGGCGAGCGCTTGGCATGTGGCAACCTTCGGCGGCGGCGGCGGCGGCAAG 485
QY 257 rAspLeuMetTyrIleArgGluLysAlaSerAlaGlySerGlnAlaLysAspLysGluAr 277
Db 486 CGACCTCATGTATCATCCGAGAAAGCGACGCGCGGCAAGCGGCAAGGAGCAAGAGAGCG 545
QY 277 gCyValIleSer 281
Db 546 CTGCTCATCAGC 558
```

RESULT 14
BM921656 1137 bp MRNA linear EST 12-MAR-2002
LOCUS BM921656
DEFINITION AGENCOURT_6708111 NIH_MGC_115 Homo sapiens CDNA clone IMAGE:5753182
5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12788 row: 1 column: 23
High quality sequence stop: 542.

FEATURES

source

```
1..1137
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5753182"
/clone_1ib="NIH MGC_115"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 Kb,
insert size range 1-3 Kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH MGC Library."
```

BASE COUNT 223 a 427 c 315 g 172 t
ORIGIN

Alignment Scores:

```
Pred. No.:      9.93e-105      Length:      1137
Score:          918.50      Matches:      212
Percent Similarity: 75.25%      Conservative: 10
Best Local Similarity: 71.86%      Mismatches: 45
Query Match:    63.34%      Indels:      29
DB:             14          Gaps:        3
```

US-09-709-103-1f1 (1-282) x BM921656 (1-1137)

```
QY 1 MelLysLeuAlaAlaMetIleLysLysMetCysProSerAspSerGluLeuSerIlePro 20
Db 221 ATGAATGCGCCCGCATGTATCAAGAGATGTGCGCCAGACCTCGAGCTGATATCCCG 280
QY 21 AlLysAsnCysTyrArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIle 40
Db 281 GCCAAGACCTGATATGTCATGTCATCTCGGCTCTTCACAGGTGGCAAGCGGCACTC 340
QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
Db 341 GTGTGGGCTTCTTCCACCGGCGCTTCGAGGAGCGCTTACCGCTTACATCGAGGACTTC 400
QY 61 HisArgLysPheTyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSer 80
Db 401 CACCGCAAGTTTACTTCATCCGCGGCGGAGGTCTTACCACTCGACATCTCTCGACAGTCC 460
```



```

Qy 81 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPhe11e 100
Db 461 GGCAACACCCGTTCCCGCGCATGCGCGCTCTCCATCCTCACAGGAGACGTTTTTCATC 520

Qy 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGln 120
Db 521 CTGGTGTTCAGTCTGGACAAACCGGAGCTCTCTTCAGGAGGTGCGCGCTCAGCGACAG 580

Qy 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeu 140
Db 581 ATCTCTGACACCAAGTCTTGCTTCAAGAACAAACCAAGAGAGATGTGGAGTGGCCCTG 640

Qy 141 ValIleCysGlyAsnLysGlyAspArgAspPheTyrArgGluVal-AspGlnArgGlu11 160
Db 641 GTCATCTCGGCAACACAGAGTGACCGGAGTCTTACCGCGAGGTGGGCAACACCGCGAGAT 700

Qy 160 eGluGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLys11 180
Db 701 CGAGCAGCTGGTGGCGG-ACACCCAGCGGTGGCGCTCTTCAGATCTCGGCCAAGAA 759

Qy 180 sAsnSer-SerLeuAsp-GlnMetPheArgAlaLeuPheAlaMetAlaLys-LeuProSe 199
Db 760 AAACAGATCTCTGACCCCAATGTCGCGGGCTCTTCCCTGGCCCAACCTGGCCAG 819

Qy 199 r-----GluMetSerProAspLeuHisArgLysValSerValGlnTyrCy 214
Db 820 CGGAGAACGAGTCCCGGAACCTTGGACCCCAAGTCTCCGCGGGAATAAAGTGGCGAAC 879

Qy 214 sAspValLeuHisLysLysAlaLeuArgAsnLysLysLeuLeuArg-AlaGlySerGlyG 234
Db 880 GGCTTGGCCCCATAAAGGGCGCTGCCGAAACAAAGAAACTGGCTTGGCGGACCGGCC 939

Qy 234 lYgLYgLYgLYgPro----- 239
Db 940 ACCGGTGGTGGCGGCTGTCTCCACCGCGGGGGAAGCTCTCTTGTGGCGAACCC 999

Qy 240 --GlyAsp-----AlaPheGlyLeValAlaProPheAlaArgProSerValH 256
Db 1000 GGGGGGACACCTTGTTCGCGCGGGCGTGGCCACCAATGGTTACAAACCGGCCCAACCCCTC 1059

Qy 256 isSerAspLeuMetTyrIleArgGluLysAlaSer 267
Db 1060 CCCGGTTACACTCTCTCCGCCAAAGAGGTCC 1094

RESULT 15
BI596688 814 bp mRNA linear EST 07-SEP-2001
LOCUS 603243262F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5285894 5',
DEFINITION mRNA sequence.
ACCESSION BI596688
VERSION BI596688.1 GI:15489627
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 814)
NIH-MGC http://mhc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11722 row: k column: 15
High quality sequence stop: 803.
Location/Qualifiers
FEATURES

```

```

source 1. .814
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5285894"
/clone_lib="NIH_MGC_96"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcagag
); Oligo-dr primed using primer 5'-TTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.3 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT 160 a 310 c 225 g 119 t
ORIGIN
Alignment Scores:
Pred. No.: 9.15e-105 Length: 814
Score: 917.00 Matches: 192
Percent Similarity: 96.48% Conservative: 0
Best Local Similarity: 96.48% Mismatches: 5
Query Match: 63.24% Indels: 4
Db: 13 Gaps: 0
US-09-709-103-1F1 (1-282) x BI596688 (1-814)
Qy 1 MetLysLeuAlaAlaMetIleLysLysMetCysProSerAspSerGluLeuSerIlePro 20
Db 220 ATGAAACTGGCGCGCATGATCAAGAGATGTGCCGAGGACTCGGAGTCGATATCCCG 279
Qy 21 AlaLysAsnCysTyrArgMetValIleLeuGlySerSerLysValGlyLysThrAla11e 40
Db 280 GCCAAGAACTGATATCGCATGTGTCATCTCGCTCGTCCAAGGTGGGCAAGCGGCCATC 339
Qy 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
Db 340 GTGTGCGCGCTTCTCACCAGCGCGCTTCGAGGAGCGCTACACGCTTACCATTGAGACTTC 399
Qy 61 HisArgLysPheTyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSer 80
Db 400 CACCGCAAGTTCTACTCCATCCGCGCGGAGGTCTACACGCTCGACATCTTCGACACGTC 459
Qy 81 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPhe11e 100
Db 460 GGCAACACCCGTTCCCGCGCATGCGCGCTCTCCATCCTCACAGGAGACGTTTTTCATC 519
Qy 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGln 120
Db 520 CTGGTGTTCAGTCTGGACAAACCGGAGTCTTTCGAGGAGGTGCGCGCTCAGGCGAG 579
Qy 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeu 140
Db 580 ATCTCTGACACCAAGTCTTGCTTCAAGAACAAACCAAGGAGAACTGGAGTGGCCCTG 639
Qy 141 ValIleCysGlyAsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGlu11e 160
Db 640 GTCATCTCGGCAACAAAGGCTGACCGGAGTCTTACCGCGAGGTGGGACCGCGAGATC 699
Qy 161 GluGlnLeuValGlyAspAsp-ProGlnArgCysAlaTyrPheGlu-IleSerAlaLys11 180
Db 700 GAGCAGCTGGTGGGCGGAGACCCCGCGCTTTCGAGATCTTCGAGATCTTCGCGCAAGA 759
Qy 180 YsAsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeu 197
Db 760 AGAACAGAGCCG-GACACAGATGTC-CGCGCGCTCTTCGCCCATGGCAAGCTG 810

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Search completed: December 30, 2002, 16:16:36
Job time : 2198 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 28, 2002, 01:02:12 ; Search time 2188 Seconds

(without alignments)
2079.951 Million cell updates/sec

Title: US-09-709-103-2
Sequence: 1449

Scoring table: 1 MKLAAMIKKPCPSDSELSIP.....IREKASGQAKDKKCVIS 281

Scoring table:
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+p2n.spool/US09709103/runat.20122002.162406.818/app_query.fasta_1.455
-O/cpnt2.1/USPRO.spool/US09709103/rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-DB=EST -QPM=fastap -SUFFIX=p2n.rst -MATRIX=blomsum62 -TRANS=human4.cdi -LIST=45
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human4.cdi -LIST=45
-DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pcio -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US09709103 @cgn.1.1.1716 @runat.20122002.162406.818 -NCP=6 -ICPU=3
-NO.XLPXY -NO.MAP -LARGEQUERY -NEG.SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-NARN.TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: em_estdb:*
2: em_estdb:*
3: em_estdb:*
4: em_estdb:*
5: em_estdb:*
6: em_estdb:*
7: em_estdb:*
8: em_estdb:*
9: gb_est1:*
10: gb_est2:*
11: gb_est3:*
12: gb_est4:*
13: gb_est5:*
14: gb_est6:*
15: em_estfun:*
16: em_estfun:*
17: gb_gss:*
18: em_gss:*
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26: em_gss:*
27: em_gss:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1210.5	83.5	1035	14	BM919341
2	1165	80.4	962	12	BM543472
3	1144	79.0	1203	14	BM920514
4	1121	77.4	965	9	AL533318
5	1120	77.3	742	10	AM028127
6	1114.5	76.9	958	14	BM719566
7	1100.5	75.9	1053	12	BM921737
8	1064	73.4	649	12	BM085090
9	1038	71.6	1023	13	BM543630
10	1033	71.3	1032	14	BM067637
11	991.5	68.4	726	12	BF613135
12	987	68.1	655	12	BF711792
13	926	63.9	758	13	BF553776
14	918.5	63.4	1137	14	BM921656
15	917	63.3	814	13	BF596688
16	896.5	61.9	1160	14	BM805574
17	892	61.6	644	13	BM969048
18	890.5	61.5	831	13	BF596637
19	885.5	61.1	710	13	BF526038
20	884	61.0	1006	14	BF073742
21	869	60.0	506	13	BM311047
22	867	59.8	1300	11	AK015898
23	862	59.5	947	14	BF0954076
24	859	59.3	648	10	BM636889
25	859	59.3	689	10	BM636899
26	854	58.9	904	14	BM0947936
27	850	58.7	617	13	BF393669
28	832.5	57.5	640	13	BF490945
29	825	56.9	699	12	BF706012
30	812	56.0	700	13	BF709229
31	812	56.0	700	13	BF596509
32	809	55.8	589	13	BM426066
33	807.5	55.7	888	13	BF540883
34	785.5	54.2	1332	13	BM460899
35	767	52.9	674	13	BF601563
36	748	51.6	675	13	BF545172
37	745	51.4	666	13	BF549939
38	741	51.1	571	13	BF682922
39	732.5	50.6	456	12	BF555582
40	730	50.4	509	10	AM915326
41	703.5	48.6	505	13	BF391213
42	685	47.3	542	9	AA790463
43	674.5	46.5	1438	14	BM807669
44	660.5	45.6	435	10	AM990252
45	655.5	45.2	461	13	BF489219

ALIGNMENTS

RESULT 1
LOCUS BM919341
DEFINITION BM919341
ACCESSION BM919341
VERSION BM919341
KEYWORDS
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1035)
AUTHORS NIH-MGC
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12776 row: 1 column: 10
High quality sequence stop: 658.

FEATURES

source
1. 1035
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="5748585"
/clone_id="NIH_MGC_120"
/lab_host="DH10B"
/note="Organ: pooled pancreas and spleen; Vector: pCMV-Sport6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC library."
BASE COUNT 209 a 386 c 293 g 146 t 1 others
ORIGIN

Alignment Scores:

Pred. No.: 1,27e-141 Length: 1035
Score: 1210.50 Matches: 244
Percent Similarity: 95.028 Conservative: 4
Best Local Similarity: 93.498 Mismatches: 8
Query Match: 83.548 Indels: 5
14 Gaps: 2

US-09-709-103-2 (1-281) x BM919341 (1-1035)

QY 1 MetIysLeuAlaMetIleLysMetCysProSerAspSerGluLeuSerIlePro 20
Db 187 ATGAAACTGGCCGGATGATCAAGAAAGTGTGCCGCGACACCTGAGCTGATATCCG 246
QY 21 AlaIysAsnGlyTyrArgMetValIleLeuGlySerSerIleValGlyThrAlaIle 40
Db 247 GCCAAGACTGCTATCCATGCTATCTCTGCTGCTCCCAAGGTGGCAAGAGCCCATC 306
QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
Db 307 GTGTCGGCGCTTCCACCGCGCGCTTCGAGAGCGCTACACGCTACCATCGAGCACTTC 366
QY 61 HisArgIysPheTyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSer 80
Db 367 CACCGCAAGTCTTCACTCCATCCGCGGAGGTCTACCATCGACATCTCGACAGCTCC 426
QY 81 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIle 100
Db 427 GGCACACCAACCGTCCCGGCGCATCGCGCTCTCCATCTCCACAGAGAGAGGTTTCATC 486
QY 101 LeuValPheSerIleuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGln 120
Db 487 CTGCTGTTCAGCTCGACACACCGCGACTCTTCGAGAGGTGCGAGCGCTCAGGCAACAG 546
QY 121 IleLeuAspThrIysSerCysLeuIleAsnIleThrIysGluAsnValAspValProLeu 140
Db 547 ATCTCTGACACCAAGCTTGTGCTCAAGAAACAAAGGAGACGTGGAGGCGCCCTG 606
QY 141 ValIleCysGlyAsnIysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIle 160
Db 607 GTCATCTGCGGCAACAAAGGTGACCGGACTTCTACCGCGAGGTGAGCAAGCGGAGATATC 666

QY 161 GluGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaIysLys 180
Db 667 GAGACAGTGTGGGGAGACAGACCCCGAGGCTGCGCTACTCTCGAGATCTCGGCCAAGAG 726
QY 181 AsnSerSerIleuAspGlnMetPheArgAlaLeuPheAlaMetAlaIysLysLeuProSerGlu 200
Db 727 AACAGCACCCTGGAGCAAGATGTTCGGCGGCTCTTCGCCATCGGCAAGCTGCCACAGGAG 786
QY 201 MetSerProAspPheHisArgIysValSerValGlnTyrCysAspValIleuHisLysLys 220
Db 787 ATGAGCCAGACCTCGACACCGCAAGCTCTCGGTGCACTGCGACGTCTGCAACAGAA 846
QY 221 AlaLeuArgAsnLysLysLeuLeuArgAlaGlySerGly-GlyGly-AspProG 240
Db 847 GCGCTCGGCAACAAAGTCTGCGGCGCGGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCG 906
QY 240 IysAspAlaPheGlyIleValAla-----ProPheAlaArg---ArgProSerValHis 256
Db 907 GCGGACGCGCTTTGGCCATTCGTGGCAACCTTTTGGCGGCGCGCGCGCGCGCGCGCG 965

RESULT 2
BM543472
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 962)
NIH-MGC http://mgi.nci.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
COMMENT
Email: c9apbs-remail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12719 row: d column: 11
High quality sequence start: 18
High quality sequence stop: 692.

FEATURES

source

1. 962
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="5726554"
/clone_id="NIH_MGC_124"
/tissue_type="hippocampus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-Sport6; Site_1: EcoRV (destroyed); Site_2: NotI; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."
BASE COUNT 185 a 363 c 272 g 141 t 1 others
ORIGIN

Alignment Scores:

Pred. No.: 6.21e-136 Length: 962
Score: 1165.00 Matches: 234
Percent Similarity: 92.55% Conservative: 2
Best Local Similarity: 91.76% Mismatches: 9
Query Match: 80.40% Indels: 10


```

DB: 13 Gaps: 1
US-09-709-103-2 (1-281) x BM543472 (1-962)
QY 1 MetLysLeuAlaMetIleLysMetCysProSerAspSerGluLeuSerIlePro 20
DB 224 ATGAACTGGCCCGGATGATCAAGAGATGTGCCAGGACACGAGCTGATATCCCG 283
QY 21 AlAluYsancYsTyrArgMetValIleLeuGlySerSerLysValGlyThrAlaIle 40
DB 284 GCCAAGACTGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 343
QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
DB 344 GTGTCGGCTTCTCCACCGCGCTTCCAGAGAGCGCTACACGCTACATCGAGACTTC 403
QY 61 HisArgLysPheTyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSer 80
DB 404 CACCGCAAGTTCTACATCCATCCGCGGAGGTCTACCATCTCCATCTCCATCTCC 463
QY 81 GlysAnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIle 100
DB 464 GGCACACACCCGTTCCCGGCAATGCGCGCTCTCCATCTCCATGAGAGACGTTTCATC 523
QY 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGln 120
DB 524 CTGGTGTTCAGTCTGACACACCGCGACTCTTCGAGAGAGGTGACGCGCTCAGGCA 583
QY 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGlnAsnValAspValProLeu 140
DB 584 ATCTCTCACACCAAGTCTGCTCTCAAGACAAACCAAGAGAACGTGGACGTCGCTG 643
QY 141 ValIleCysGlyAsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIle 160
DB 644 GTATCTGCGGCAACAAAGGAGTACCGGACTTCTACCGCGAGTGGACGAGCGAGATC 703
QY 161 GluGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLys 180
DB 704 GAGCAGCTGTGGGCGAGACGACCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 763
QY 181 AsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLysProSerGlu 200
DB 764 AACGACACCTGAGCAGATGTTCTCCGCGCTCTCCGCAATGCGCGCAAGCTGCCAG 823
QY 201 MetSerProAspLeuHisArgLysValSerValGlnTyrCysAspValLeuHisLysLys 220
DB 824 ATGAGCCAGACTGACCGCAGAGTCTCGGTGCTGCTGCTGCTGCTGCTGCTGCTG 883
QY 221 AlaLeuArg-AsnLysLysLeuLeuArg-AlaGlySerGlyGlyGlyLysAspProG 240
DB 884 GCGTGTGGGAAACAACTGCTGCGGCGCGGCGGCAACCGCGGCGCGGCGGCCCA 943
QY 240 LysAspAlaPheGlyIleValAlaProPheAlaArgArgPro 253
DB 944 ACCCG-----GGGCGACGCGCT 960

RESULT 3
LOCUS BM920514 1103 bp mRNA linear EST 12-MAR-2002
DEFINITION AGENCOURT 6709473 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5750507
5', mRNA sequence.
ACCESSION BM920514
VERSION BM920514.1 GI:19370893
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1103)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

```

Email: cgaabs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Consortium
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LLM12781 row: 3 column: 12
 High quality sequence stop: 676.
 Location/Qualifiers

FEATURES

source

1..1103

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5750507"

/clone_11b="NIH_MGC_122"

/lab_host="DH10B"

/note="Organ: pooled lung and spleen; vector: pCMV-Sport6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lungs, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH-MGC Library."

BASE COUNT 230 a 402 c 314 g 156 t 1 others

ORIGIN

Alignment Scores:

Pred. No.:

3,42e-133

Length:

1103

Score:

1144.00

Matches:

246

Percent Similarity:

88.69%

Conservative:

5

Best Local Similarity:

86.93%

Mismatches:

24

Query Match:

78.95%

Indels:

9

Gaps:

3

```

US-09-709-103-2 (1-281) x BM920514 (1-1103)
QY 1 MetLysLeuAlaMetIleLysMetCysProSerAspSerGluLeuSerIlePro 20
DB 201 ATGAACTGGCCCGGATGATCAAGAGATGTGCCAGGAGCTGAGTATCCCG 260
QY 21 AlAluYsancYsTyrArgMetValIleLeuGlySerSerLysValGlyThrAlaIle 40
DB 261 GCCAAGACTGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 320
QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
DB 321 GTGTCGGCTTCTCCACCGCGCTTCCAGAGAGCGCTACACGCTACATCGAGACTTC 380
QY 61 HisArgLysPheTyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSer 80
DB 381 CACCGCAAGTTCTACATCCATCCGCGGAGGTCTACACGCTCGACATCTCGACAGTCC 440
QY 81 GlysAnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIle 100
DB 441 GGCACACACCCGTTCCCGGCAATGCGCGCTCTCCATCTCCATGAGAGACGTTTCATC 500
QY 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGln 120
DB 501 CTGGTGTTCAGTCTGACACACCGCTGACTCTTCGAGAGAGTGGACGGGCTCAGGAGAG 560
QY 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGlnAsnValAspValProLeu 140
DB 561 ATCTCTCACACCAAGTCTGCTCTCAAGACAAACCAAGAGAACGTCGAGCGCTGCTG 620
QY 141 ValIleCysGlyAsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIle 160
DB 621 GTATCTGCGGCAACAAAGGAGTACCGGACTTCTACCGCAGGTGGACCGCGGAGATC 680
QY 161 GluGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLys 180

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Db 661 GAGCAGCTGGTGGGAGACCCAGCGCTGCGCTACTTCGAGATCTGCCAAG 740
Qy 181 AsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeu-ProSerGI 200
Db 741 AA-AGCAGCTGGACACAGATGTTCCGGCGCTCTTCGCGATGGCGCCGCGGA 799
Qy 200 uMetSerProAspLeuHisArgLysValSerValGlnTyrCysAspValLeuHis-LysL 220
Db 800 GATGAGCCCGACCTGCACCCGCAAGGTCGTCTGTCAGTACGACCTGCTGCACAA 859
Qy 220 yAlaLeuArgAsnLys-LysLeuLeuArgAlaLysSerLysLysLysLysPro 239
Db 860 AGGCGTTCGGACAAAGAAAGCTCTTCGCGCGCCGACACCGCGCGCGCGCGCA 919
Qy 240 GLysAlaPhe-----PheGlyIleValAlaProPhe---AlaArgArgProSerValHis 256
Db 920 ACCGGGGGGAACCCCTTTGGATGCTGGAGCCCTTTCCCGCGCGCGCGCGCGCAAGGTAC 979
Qy 257 -SerAspLeuMetTyrIleArgGlyLysAlaSer---AlaGlySerGlnAlaLysAspLys 275
Db 980 AGGGAACCTTATGGAATCCCGCCCAAAAGCAACGCCCGCGCGCGCGCAAGGAAA 1039
Qy 275 s 275
Db 1040 A 1040

```

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RESULT 4
LOCUS AL533318 LTL_FL015_Brn1 Homo sapiens cDNA clone CS0DN003Y019 5
DEFINITION AL533318 LTL_FL015_Brn1 Homo sapiens cDNA clone CS0DN003Y019 5
VERSION AL533318.1 GI:12796811
SOURCE EST.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 965)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr.

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FEATURES
source
1..965
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DN003Y019"
/clone_lib="LTL_FL015_Brn1"
/sex="male"
/tissue_type="Adult brain"

```

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/Note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was constructed by Life Technologies.
Contact: Feng Liang Life Technologies, a division of
Invitrogen 9800 Medical Center Drive Rockville, Maryland
20850, USA Fax: (1) 301 610 8371 Email:
liang@lifestech.com URL:
http://fulllength.invitrogen.com"

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BASE COUNT 189 a 352 c 273 g 144 t 7 others
ORIGIN

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Alignment Scores:
Pred. No.: 2, 21e-130 Length: 965
Score: 1121.00 Matches: 237
Percent Similarity: 95.22% Conservative: 2
Best Local Similarity: 94.42% Mismatches: 11

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Query Match: 77.36% Indels: 5
DB: 9 Gaps: 1
US-09-709-103-2 (1-281) x AL533318 (1-965)
Qy 1 MetLysLeuAlaAlaMetIleLysLysMetCysProSerAspSerGluLeuSerIlePro 20
Db 191 ATAAACTGGCCCGCATGATCAAGAAAGATGTCGCGAGCTCGAGCTGATCCCG 250
Qy 21 AlaLysAsnCysTyrArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIle 40
Db 251 GCCAAGAACTGATATGATGATGATCTCGGCTGTCCAAAGTGGGCAAGAGGCCATC 310
Qy 41 ValSerArgPheLeuThrLysArgPheGlyLysAlaLysValTyrProThrIleGluAspPhe 60
Db 311 GTGTCCGGCTCTCTCCCGCGCGCTTCGAGAGCGCTTACACCCCTCAACATCCAGACATC 370
Qy 61 HisArgLysPheTyrSerIleArgGlyLysValTyrGlnLeuAspIleLeuAspThrSer 80
Db 371 CACCGCAATGTTCTACATCCATCCGCGCGAGGTCTTACAGCTGACATCTGACACGTCC 430
Qy 81 GlyAsnHisProPheProAlaMetArgLysSerIleLeuThrGlyAspValPheIle 100
Db 431 GGCAACACCGCTTCCCGCGCATGCG -CGCTCTCATCTCAGACAGAGAGCTTTTCATC 489
Qy 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGln 120
Db 490 CTGGTCTTCACTGCTGACACACCGCATCTTCGAGAGGTGACAGCGCTCAGCGCACAG 549
Qy 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeu 140
Db 550 ATCTCTGACACCAAGCTTCTGCTCAAGAAACCAAGAAAGAGTGGAGCTGCCCTG 609
Qy 141 ValIleCysGlyAsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIle 160
Db 610 GTCATCTGGCGAACAAGGTGACCGCATCTTACCCCGAGGTGACACAGCGAGATC 669
Qy 161 GluGlnLeuValAlaAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLys 180
Db 670 GAGCAGCTGGTGGGAGAGAGACCCCGCGCTGCTTCTGAGATCTCGGCCAAGAG 729
Qy 181 AsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGlu 200
Db 730 AAMACGACCTGGACCAATGTTCCGCGCTTCCGCGCATGGCCAGCTCCAGAGAG 789
Qy 201 uMetSerProAspLeuHisArgLysValSerValGlnTyrCysAspValLeuHisLysLys 220
Db 790 ATGACCCCAAGACCTGCACCGCAAGTC -TCGGTGCAGTACTCGACGTGTCAMAAARAAR 848
Qy 221 AlaLeuArgAsnLysLysLeuLeuArgAlaLysSerGlyGlyLysLysLysProGly 240
Db 849 GCGCTGCGGAACA -AARCTGCTGGCGGCGGCGACGGS -GGCGCGCGCGGCGGCGCGG 905
Qy 241 AspAlaPheGlyIleValAlaProPheAlaArg 251
Db 906 ---ACCTTTGCAATCTGTCACCTTGGCGCGG 935

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RESULT 5
LOCUS AM028127 742 bp mRNA linear EST 27-OCT-1999
DEFINITION w26c07.x1 NCI-CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2530668 3'
sequence.
similar to TR:035626 035626 RAS, DEXAMETHASONE-INDUCED 1, mRNA
sequence.
ACCESSION AM028127
VERSION AM028127.1 GI:5886883
SOURCE EST.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 742)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

```


JOURNAL
COMMENT

Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: c9apbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmett-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 445.
Location/Qualifiers

FEATURES
source

1..742
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2530668"
/clone_lib="NCI-CGAP_Kid11"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker. Site.1: Not I; Site.2: Eco RI;
Plasmid DNA from the normalized library NCI-CGAP_Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(clones 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo."

BASE COUNT 149 a 260 c 208 g 122 t 3 others
ORIGIN

Alignment Scores:
Pred. No.: 1,976-130 Length: 742
Score: 1120.00 Matches: 220
Percent Similarity: 95.74% Conservative: 5
Best Local Similarity: 93.62% Mismatches: 10
Query Match: 77.29% Indels: 0
DB: 10 Gaps: 0

US-09-709-103-2 (1-281) x AM028127 (1-742)

OY 1 MetLysLeuAlaMetLysLysMetCysProSerAspSerGluLeuSerIlePro 20
DB 35 ATGAAGCTGGCCGGGATGATCAAGAGATGTCGCCAGCGAGCTCGAGTATCCCG 94
OY 21 AlAlasAncysTyrArGMetValIleLeuGlySerSerLysValGlyLysThrAla 40
DB 95 GCCAAGAACTGCTATGCCATGTCATCTCGCTCCCAAGTGGCGAAGAGCGGCATTC 154
OY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
DB 155 GTGTGGCTTCCTCCACCTGCGCTTGAGAGAGCGCTTACACGCTTACATCGAGGACTTC 214
OY 61 HisArgLysPheTyrSerIleArgGlyGluValTyrGluLeuAspIleLeuAspThrSer 80
DB 215 CACCCCAAGTCTACTCCATCCGCGGCGAGTACACAGCTCGACATCCCTCGACAGCTTC 274
OY 81 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIle 100
DB 275 GGCACACACCCCTTCCTCCGCGCATGCGGCGCTTCCATCTCCACAGAGAGCGTTTTCATC 334
OY 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGln 120
DB 335 CTGGTGTTCAGTCTGAGACACCGGAGCTCTTCGAGGAGGTGCGCGCTCAGGACAG 394
OY 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeu 140
DB 395 ATCTCGACACCAAGTCTTGGCTCAAGACCAACAGGAGGAGGAGAGCTGAGCTGCCCTG 454
OY 141 ValIleCysGlyAsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIle 160

DB 455 GTCAATCGCGCAACAAAGGTGACCGGACTTCTACCGGAGGTGACCGGAGATC 514
OY 161 GluGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLys 180
DB 515 GAGCAGCTGGGGGCGAGCAGCCCCAGCGGTGGCTTACTTGAGATCTCNCACAGAG 574
OY 161 AsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerIle 200
DB 575 AACACAGACCTGGACACAGATCTTCCGCGCTTCGCCATGGCCAAAGCTCCAGCGAG 634
OY 201 MetSerProAspLeuHisArgLysValSerValGlnTyrCysAspValLeuHisLysLys 220
DB 635 ATGAGCCCGACACTTCACCGCAGAGTCTCNGTGAGACTGACCTGCTGCACAGAG 694
OY 221 AlaLeuArgAsnLysLysLeuLeuArgAlaGlySerGlyGly 235
DB 695 GCGCTGCGAAGACAGAACGCTGTGCGTCCGACAGCAGCGCTGGT 739

RESULT 6
LOCUS B0719566 958 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8305191 lupsk1_sympathetic_trunk Homo sapiens CDNA clone
IMAGE:6193170 5', mRNA sequence.
ACCESSION B0719566
VERSION B0719566.1 GI:21858463
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 958)
AUTHORS NIH-MGC
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
EMAIL: c9apbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM13596 row: f column: 19
High quality sequence stop: 514.
Location/Qualifiers

FEATURES
source

1..958
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6193170"
/clone_lib="lupsk1_sympathetic_trunk"
/sex="male"
/tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site.1:
NotI; Site.2: SalI; CDNA made by oligo-dT priming.
directionally cloned using the following adaptors:
5'-TCGACCAAGCGGTCGCG-3' and
5'-GACTAGTCTAGATCGCAGGCGCGGCGCT(15)-3'. Size selected
1 kb for average insert length 1.9 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine); available through Life
Technologies."

BASE COUNT 185 a 339 c 275 g 159 t
ORIGIN
Alignment Scores:
Pred. No.: 1,446-129 Length: 958
Score: 1114.50 Matches: 226
Percent Similarity: 94.61% Conservative: 2

Best Local Similarity: 93.788 Mismatches: 10
 Query Match: 76.928 Indels: 3
 DB: 14 Gaps: 1

US-09-709-103-2 (1-281) x BQ719566 (1-958)

QY 15 SerGluLeuSerIleProAlaIleValSerGlyAspGlySerIleValIleLeuGlySerSerLys 34
 Db 1 TCGAGAGTGAAGTATCCCGGCAAGAACTGATTCGATGATGATCCTCGGCTGCTCCAG 60
 QY 35 ValGlyIleThrAlaIleValSerArgPheLeuThrGlyArgPheGluAlaIleThr 54
 Db 61 GTGGGCAAGACGGCCATCTGCTGGCTTCCACAGGCCCTTCGAGAGCGCTACAGC 120
 QY 55 ProThrIleGluAspPheHisArgLysPheIleValIleValIleValIleValIleVal 74
 Db 121 CCGACATCGAGACTTCCACCGCAAGTTCATCCATCCCGCGGAGGCTCTACAGCTC 180
 QY 75 AspIleLeuAspPheSerGlyAsnHisProPheProAlaMetArgArgLeuSerIleLeu 94
 Db 181 GACATCTCGACACGTCGGCAACACCGCTTCCCGCCATCGGCGCTCTCCATCTC 240
 QY 95 ThrGlyAspValPheIleLeuValPheSerLeuAspAsnArgAspSerPheGluVal 114
 Db 241 ACAGAGAGACTTTTCATCTGCTGTCAGTCTGACACACCGCAGCTCTTCGAGAGGTC 300
 QY 115 GluArgLeuArgGluGluIleLeuAspPheIleValSerGlyAsnHisProGlu 134
 Db 301 CAGCGGCTCAGGACAGATCTCGACACCAAGTCTTCCCTCAAGAAACCAAGAG 360
 QY 135 AsnValAspValProLeuValIleValGlyAsnHisProGluAspArgPheIleVal 154
 Db 361 AACGTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 QY 155 ValAspGluArgGluIleGluGluIleValIleValIleValIleValIleValIleVal 174
 Db 421 GTGAGCAGCGCGGACATCGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 QY 175 GluIleSerAlaIleValSerAsnHisProLeuAspGluMetPheArgAlaLeuPheAlaMet 194
 Db 481 GAGATCTCGGCGGCAAGAAACAGACAGCTGACAGATGCTTCCGCGCTCTTCCGATG 540
 QY 195 AlaIleValProSerGluMetSerProAspPheIleValIleValIleValIleValIleVal 214
 Db 541 GCCAAGCTGCCAGAGATGAGCCAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 QY 215 AspValLeuHisIleValSerAlaLeuArgAsnLysLysLeuLeuArg-AlaGlySerGly-G 234
 Db 601 GAGCTGCTGACAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 QY 234 LysGlyIleValAspPro--GlyAspAlaPheGlyIleValAlaProPheAlaArgArg 252
 Db 661 GCCGCGGCGCTGACCCCGGGGGAAGCCTTTTGGGATCGGGGCGCTTTCGCGCGC 719

RESULT 7
 BM921737 1053 bp mRNA linear EST 12-MAR-2002
 LOCUS BM921737 5' mRNA sequence.
 DEFINITION AGENCOURT_6708101 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5753301
 ACCESSION BM921737
 VERSION BM921737.1 GI:19372116
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM12788 row: n column: 22
 High quality sequence stop: 600.

FEATURES

source

Location/Qualifiers

1..1053

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5753301"

/lab_host="DH10B"

/note="Organ: pooled brain, lung, testis; Vector: pCMV-Sport6; Site: 1; Not: Site 2; EcoRV (destroyed); RNA

male lung, age 27; and 1 male testis, age 69. Library is

oligo-dT primed and directionally cloned (Rcovr site is

destroyed upon cloning). Average insert size 1.8 kb,

insert size range 1-3 kb. Library is normalized and

enriched for full-length clones and was constructed by C.

Gruber (Invitrogen). Research Genetics tracking code

021. Note: this is a NIH MGC Library."

BASE COUNT 215 a 390 c 297 g 150 t 1 others

ORIGIN

Alignment Scores:

Pred. No.: 9,75e-128 Length: 1053

Score: 1100.50 Matches: 228

Percent Similarity: 88.26% Conservative: 5

Best Local Similarity: 85.36% Mismatches: 22

Query Match: 75.95% Indels: 9

DB: 14 Gaps: 3

US-09-709-103-2 (1-281) x BM921737 (1-1053)

QY 1 MetLysLeuAlaIleMetIleLysMetCysProSerAspSerGluLeuSerIlePro 20

Db 200 ATGAACAGTGGCGGCGGATGATCAGAAAGATGTGCCAGAGCTCGAGAGCTGATCCCG 259

QY 21 AlaLysAsnGlyTrpArgMetValIleLeuGlySerSerLysValGlyIleThrAlaIle 40

Db 260 GCCAAGAACTGCTATCGCATGTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 319

QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaIleValIleValIleValIleVal 40

Db 320 GTGTCGGCTTCTCTACCGCGCCGCTTTCGAGAGCGCTACACCGCTTACCATGAGACTTC 379

QY 61 HisArgLysPheGlySerIleArgGlyGluValIleValIleValIleValIleValIleVal 80

Db 380 CACCGCAAGTTCATCTCCATCCGCGGCGAGGCTTCACAGCTCGACATCTCGACACGCTCC 439

QY 81 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIle 100

Db 440 GGCAACACCGCTTCCCGCGCATGCGCGCTTCTCATCTCAGACAGAGCGTTTCATC 499

QY 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValIleValIleValIleVal 120

Db 500 CTGGTTCAGTCTGACACCGGCGACCTCTTCAGAGAGCTCGACGCGCTCAGCGAGAG 559

QY 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeu 140

Db 560 ATCTCTGACACCAAGTCTTCTGCTCAAGAAACCAAGAGAGAGAGCGTTCCTG 619

QY 141 ValIleCysGlyAsnLysGlyAspArgAspPheTrpArgLysValAspGluArgGluIle 160

Db 620 GTCATCTGCGGCAACAGGAGGCTTCTACCGCAGGTGAGCCAGCGCAGATC 679

QY 161 GluGluLeuValGlyAspAspProGluArgCysAlaIleValIleValIleValIleVal 180

Db 680 GAGCAGCTGTGGCGAGACACCCCGGCGCTTCTGAGATCTCGCGCCCAAAAG 739

SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS 1 (bases 1 to 1023)
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.llnl.gov
Plate: LLM12719 row: m column: 05
High quality sequence stop: 637.

FEATURES
source
1..1023
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:575214"
/clone_lib="NIH_MGC_124"
/tissue_type="hippocampus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: EcoRV (destroyed); Site_2: NotI; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research genetics tracking code 012."

BASE COUNT 196 a 378 c 281 g 168 t
ORIGIN

Alignment Scores:

Pred. No.: 7.13e-120 Length: 1023
Score: 1038.00 Matches: 222
Percent Similarity: 83.46% Conserved: 5
Best Local Similarity: 81.62% Mismatches: 30
Query Match: 71.64% Indels: 15
DB: 13 Gaps: 3

US-09-709-103-2 (1-281) x BM543630 (1-1023)

QY 1 MetTysLeuAlaAlaMetIleIleYlyMetCysProSerAspSerGluLeuSerIlePro 20
DB 149 ATGAAGCTGCGCCGATGATCAAGAAAGATGTGCCCGAGCGACATCGAGCTGATCCCG 208
QY 21 AlAlaYsancysTyrArGmetValIleIleGlySerSerIlyValGlyLysThrAlaIle 40
DB 209 GCCAAGAACTGCTATCGATCGATCTCGGCTCGTCCCAAGGTGGGCAAGAGGGCCATC 268
QY 41 ValSerArgPheLeuThrArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
DB 269 GTGTCGGCTTCCCTCACCGGCGCTTCGAGAGCGCTTACACCGCTTACATCGAGGACTTC 328
QY 61 HisArgLysPheTyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSer 80
DB 329 CACCGCAAGTTTACATCCATCCCGCGAGGTCTACCACTGCACATCTCCGACACGTCC 388
QY 81 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIle 100
DB 389 GGCAGACACCCGTTCCCGCATGCGGCGCTCTCCATCTCCTCACAGAGAGCTTTTATC 448
QY 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValAlaGlnArgLeuArgGln 120
DB 449 CTGGCTTTCAGTGTGACAAACCGGAGCTCTTCGAGAGGTGACACGGCTCAGGACGACG 508
QY 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeu 140

DB 509 ATCTCCAGACCAAGTCTGCTCAAGAACAAACACAGAGAGACTGGACTGCCCTG 568
QY 141 ValTleCysGlyAsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIle 160
DB 569 GTATCTGCGGCAACAAAGGTGACCGGACTTCTTACCGGAGGTGGACCGAGATC 628
QY 161 GluGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGlnIleSerAlaLys 180
DB 629 GAGAGCTGTGGGCGACGACCCCGCGCTGGCTTCTGATCTCGGCTCAGAG 688
QY 181 AsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAla-LysLeu-ProSer 199
DB 689 AACAGACCTTGGAGACCAAGTGTCTCGCGCTTCTCCATGCCCAAGTGCCTCCG 748
QY 200 GluMetSerProAspLeuHisArgLys--ValSerValGlnTyrCys--AspValLeu 217
DB 749 GAGATGAGCCCAAGCTGACCGCCAGGTCTCGGCTGAGGTACTGGCGAGCGGCTGG 808
QY 218 HisLysLeuAlaLeuArgAsnLysLysLeuLeuArgAlaGlySerGlyGlyGly 237
DB 809 CACAGAAAGCGCGCTGCGGAAACAGAAACTGCTGCGGCGCGGCGCATCGCGGG 868
QY 238 -----AspProGlyAspAlaPheGlyIleValAla 247
DB 869 CCCTCTCTAGTCATTAACCTTGACCGAAGGACCTTGGGCGAGCTTGGGCCACCATTTT 928
QY 248 ProPheAlaArgArgProSerValHisSer 257
DB 929 CCGGAGACTGCGGCTCTTGTGTGATCC 958

RESULT 10
B0067637
LOCUS B0067637 1032 bp mRNA linear EST 02-APR-2002
DEFINITION AGENCOURT_6759053 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5755214
ACCESSION B0067637
VERSION B0067637.1 GI:19896683
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS 1 (bases 1 to 1032)
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.llnl.gov
Plate: LLM12793 row: n column: 15
High quality sequence stop: 602.

FEATURES

source
1..1032
Location/Qualifiers

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5755214"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C.

Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH/MGC library "

BASE COUNT 210 a 375 c 298 g 148 t 1 others

ALIGNMENT SCORES:

Pred. No.: 3,09e-119 Length: 1032
Score: 1033.00 Matches: 225
Percent Similarity: 88.37% Conservative: 3
Best Local Similarity: 87.21% Mismatches: 15
Query Match: 71.29% Indels: 15
Gaps: 3

US-09-709-103-2 (1-281) x B0607637 (1-1032)

OY 1 MetIysLeuAlaMetIleLysMetCysProSerAspSerGluLeuSerIlePro 20
DB ATGAAACTGGCCCGATGATCAAGAAAGATGGCCGACGACCTGAGCTGATATCCCG 260
OY 21 AlaIysAsnCysTyrArgMetValIleLeuGlySerSerIysValGlyIleThraIle 40
DB GCCAAGACTGCTATGTCATGTCATCTCTGCTCTCCAGGTGGCAAGCGGCATC 320
OY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
DB GTGTCGGGCTTCTCCACCGCGCTTCGAGAGCGCTACACGCTACCATCGAGCATTC 380
OY 61 HisArgLysPheTyrSerIleArgGlyValTyrGlnLeuAspIleLeuAspThrSer 80
DB CACCGGCAAGTTCATCCATCCCGCGGAGGTCTACCATCTCCATCCGACGCTCC 440
OY 81 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIle 100
DB GGCAACACACCGCTTCCCGGCTATGCGCGCTCTCATCTCCACAGAGACGTTTCATC 500
OY 101 LeuValPheSerLeuAspAsnArgAspSerPheGluValGlnArgLeuArgGlnGln 120
DB CTGCTGTTCACTGTCGACCAACCGGACCTCTGAGAGGTGCAGCGGCTCAGCAGCAG 560
OY 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGlnAsnValAspValProLeu 140
DB ATCTCTGACACCAAGTCTCTCCATCAAGCAACCAAGCAAGCAAGTGGGCGTCCCTG 620
OY 141 ValIleCysGlyAsnLysGlyAspArgAspPheTyrArgIleValAspGlnArgGluIle 160
DB GTATCTGCGGCAACAAAGGATGACCGGACTTACCGGAGGTGACGACGCGAGATC 680
OY 161 GluGlnLeuValGlyAspAspProGlnArgCysAlaTyrThrGluIleSerAlaLysLys 180
DB GAGCAGCTGTGGGCGACGACCGCCGACGCTGCGCTACCTTCGATCTGGGCGCAAGAG 740
OY 181 AsnSerSerLeu-AspGlnMetPheArgAlaLeuPheAla-MetAlaLysLeuProSer 199
DB AAGCAACCTCGNACCAAGATGTTCCCGCGCTCTTGGCCCATGCGCAACCTGCGCCAGC 800
OY 200 GluMetSer-ProAspLeuHisArg-LysValSerValGln---TyrCysAspValLeu 218
DB GAGATGAGCCCGACGACCTGCGCAAGGCTCTGCTGACGTTACATGCAACGGGCGTGC 860
OY 218 LysLysLys---AlaLeuArgAsnLysLysLeuLeu-----A 229
DB ACAAAAAAGGCGCTGCGGCAACAAAAAAGCTTCTGCGGCGCGCGGCAACCGCGCGGC 920
OY 229 rgAlaGlySerGlyGlyGlyLysAspProGlyAspAlaPhe 243
DB GGGCGCGCGCGCGCAACCGCGGCGGCAACCGCTTGGCGCATTT 964
RESULT 11 726 bp mRNA linear EST 14-DEC-2000
B0613135
LOCUS de10e03.y1 Wellcome CRC PRN3 dorsal 135526 RAS,
DEFINITION IMAGE:3473357 5' similar to TR:035626 O15526 RAS,
DEANETHASONE-INDUCED 1 ;, mRNA sequence.

ACCESSION B0613135
VERSION B0613135.1 GI:11784463
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis

REFERENCE
AUTHORS 1 (bases 1 to 726)
Clifton,S., Johnson,S.L., Blumberg,B., Song,T., Hillier,L., Page,D.,
'B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
Waterston,R. and Wilson,R.
Washu Xenopus EST Project, 1999
Unpublished (1999)
Other ESTs: de30e03.x1
Contact: Sandy Clifton, Ph.D.
Washu Xenopus EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu

TITLE
JOURNAL
COMMENT Library constructed by A.M. Zorn (Wellcome/CRC Institute). DNA
Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Seq primer: -40RP from Glibco
High quality sequence stop: 519.

FEATURES

source

1..726
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="IMAGE:3473357"
/clone_id="Wellcome CRC PRN3 dorsal 11p"
/tissue_type="dorsal lip"
/lab_host="DH10B (phage-resistant)"
/note="Vector: pBSK3; Site:1: NotI; Site:2: EcoRI; cDNAs
were oligo-dT primed and directionally cloned. Staging
according to Nieuwkoop and Faber. Library was constructed
by A.M. Zorn (Wellcome/CRC Institute)."

Location/Qualifiers

BASE COUNT 197 a 196 c 181 g 152 t

ALIGNMENT SCORES:

Pred. No.: 3.07e-114 Length: 726
Score: 991.50 Matches: 187
Percent Similarity: 92.89% Conservative: 22
Best Local Similarity: 83.11% Mismatches: 15
Query Match: 68.43% Indels: 1
Gaps: 1

US-09-709-103-2 (1-281) x B0613135 (1-726)

OY 3 LeuAlaMetIleLysMetCysProSerAspSerGluLeuSerIleProAlaLys 22
DB CTTACCGCATGTATCAAGAAATGTCCCGAGGAGACGAACTCAACTCCACCCAAAG 114
OY 23 AsnCysTyrArgMetValIleLeuGlySerSerIysValGlyIleThraIleValSer 42
DB AACTGTTACCGCATGTGTCATCCGCGCTCTCCCAAGGTGGGCAAGCACTCGATGTC 174
OY 43 ArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPheHisArg 62
DB CGCTTTCTTGAACGCGGATTCGAGGACATACACCGCGCATTCGAGAGCTTCCACCGA 234
OY 63 LysPheTyrSerIleArgGlyGlyValTyrGlnLeuAspIleLeuAspThrSerGlyAsn 82
DB AAGTCTACAGCATTCGGGAGAGGCTCTACCACTGATATCTCGACACCTCGGCAAC 294
OY 83 HisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuVal 102
DB CACCGCTTCCCGGCGCATGAGAAAGACTCTCCATCTTACCGAGAGATGTCTTCATCTGTC 354

QY 103 PheserleusaspasnaargaspserPhegluGlulValGlnargleuargGlnGlnIleleu 122
 DB 355 TTGAGCCTGGACACAGGAGCTCTTTGAGAGAGTGCAGGAGTGAAGCAGCATATG 414
 QY 123 AsphirlysserCysleuLysAsnLysThrLysGlnAsnValaspValProleuValIle 142
 DB 415 GAGACCAAGTCCTCTTCAGACAGACAAACAGAGAGATGTTCCCATCGTTATC 474
 QY 143 CysglYAsnLysglYAspArgaspPheTyrArgLysValaspLysLysLysLysLysLys 162
 DB 475 TGGCGGAATTAAGTACAGAGAGCTTCTACAGGAGTGCAGGAGTGCAGGAGTGCAGG 534
 QY 163 LeuValGlyaspPaspProGlnarGlysalatYrPhegluLysSerAlaLysLysAsnSer 182
 DB 535 CTGGTGGAGAGGAC--AGTAAATGCTCTTACTTGGAGGTGCGGCAAGAGAAACTC 591
 QY 183 SerleuaspLysmetPheargAlaLeuPheAlaMetAlaLysLeuProserGlnumtSer 202
 DB 592 AGCCTGATGAGATGTTTAAAGCTCTCTTACCATGACAGATGCGCCAGCGAGATGAGC 651
 QY 203 ProaspLeuHisArgLysValSerValGlnTyrCysaspValLeuHisLysLysAlaLeu 222
 DB 652 TCAGACTGCAGCCGACAGAGTGTCTGCAGTACTGTGAGATTTTACACAAAGAGTCCCTG 711
 QY 223 ArgAsnLysLysLeu 227
 DB 712 AAGAAAGAAAGTA 726

RESULT 12
 BG711792 655 bp mRNA linear EST 08-MAY-2001
 LOCUS BG711792
 DEFINITION pgl1n.pk009.115 Normalized Liver Library Gallus gallus cDNA clone
 pgl1n.pk009.115 5' similar to gb|AAFA3090.1|AF239157.1 (AF239157)
 DEKRA1 (Rattus norvegicus)g, mRNA sequence.
 BG711792
 ACCESSION BG711792.1 GI:14005742
 VERSION EST.
 KEYWORDS
 SOURCE chicken.
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 REFERENCE 1 (bases 1 to 655)
 AUTHORS Burnsides J., Morgan R.W. and Coopburn L.A.
 TITLE Chicken ESTs from a normalized liver library
 JOURNAL Unpublished (2001)
 COMMENT Contact: Joan Burnsides
 Molecular Endocrinology
 University of Delaware
 40 Townsend Hall, Newark, DE 19717, USA
 Tel: 302 831-1345
 Fax: 302 831-3411
 Email: joan@udel.edu, www.chickest.udel.edu.

FEATURES
 source
 1. .655
 /organism="Gallus gallus"
 /db_xref="taxon:9031"
 /clone="pgl1n.pk009.115"
 /clone_lib="Normalized Liver Library"
 /sex="Male and Female"
 /tissue="Liver"
 /lab_host="E.coli EMDH10B"
 /note="Vector: pCMVSPORT 6"

BASE COUNT 145 a 206 c 184 g 104 t 16 others
 ORIGIN

Alignment Scores:
 Pred. No.: 9.68e-114 Length: 655
 Score: 987.00 Matches: 192
 Percent Similarity: 97.12% Conservative: 10
 Best Local Similarity: 92.31% Mismatches: 5
 Query Match: 68.12% Indels: 1

DB: 12 Gaps: 0
 US-09-709-103-2 (1-281) x BG711792 (1-655)

QY 1 MetLysLeuAlaAlaMetLysLysMetCysProSerAspSerGlnLeuSerIlePro 20
 DB 14 ATGAAACTGGCAGCATGATCAAGAAAGATGTGTCCAGAGAGCGTACGATGCC 73
 QY 21 AlalyAsnCysTyrArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIle 40
 DB 74 GCCAGAACTGCTACCGCATGTCTCATCTGCTCTCCAAAGGTGGCAGAGCGCCATC 133
 QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrTrpProThrIleGluAspPhe 60
 DB 134 GTCTGGCGCTTCTCTACCGCGCTTCCAGAGAGAGTACAGCCCATGAGAGACTTC 193
 QY 61 HisArgLysPheTyrSerIleArgGlyLysValTyrGlnLeuAspIleLeuAspThrSer 80
 DB 194 CACCCCAAGTCTTACAGCATCCGCGTGAGGTCTACAGTCTGACATCTGACACAGTGC 253
 QY 81 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIle 100
 DB 254 GGCAACCACTCTTCCCGCATGCGCGCTGTCTCATCTTCCACAGAGTGAAGTTCATC 313
 QY 101 LeuValPheSerLeuAspAsnArgAspSerPhegluGluValGlnarGleuArgGln 120
 DB 314 CTCTGTTCAGCTGTGACACACGGGACTCTTCCAGAGAGTGCAGCGCTTGAACACAG 373
 QY 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsnValaspValProleu 140
 DB 374 ATCTGTGAGACCAAGTCTCTCTCTCAAGAAACCAAGAGAGACATCGAGTCCCTG 433
 QY 141 ValIleCysGlyAsnLysGlyAspArgaspPheTyrArgLysValaspLysLysLysLys 160
 DB 434 GTCACTCTCGGCAACAGAGCGGAGCTTTTACCGGAGGTGGAGCCCGCAGAGATC 493
 QY 161 GluGlnLeuValGlyaspPaspProGlnarGlysalA-TyrPhegluLysSerAlaLys 180
 DB 494 GAGCAGCTGTGTGGCGCAGACCAAGAAATGCCNNACTGCAGATCTCGGCCAAGAA 533
 QY 180 sAsnSerleuaspLysmetPheargAlaLeuPheAlaMetAlaLysLeuProserGln 200
 DB 554 GACACGAGCCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 613
 QY 200 umetSerProaspLeuHisArg 207
 DB 614 GATGAGCCCGGACCTGCACCGC 635

RESULT 13
 BI553776 758 bp mRNA linear EST 05-SEP-2001
 LOCUS BI553776
 DEFINITION 603190722F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5262101 5',
 mRNA sequence.
 BI553776
 ACCESSION BI553776.1 GI:15441088
 VERSION EST.
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 758)
 AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Miklos Palcovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 28, 2002, 02:48:57 ; Search time 36.7548 Seconds
(without alignments)
7058.899 Million cell updates/sec

Title: US-09-709-103-1

Perfect score: 846
Sequence: 1 atgaactgcccgcgatgat.....agcgcgcgcatacagctag 846

Scoring table: IDENTITY_NUC
Gapop 10.0 ; Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_patents.NA:*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCBUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	846	100.0	1841 4 US-09-053-374A-1	Sequence 1, Appl1
2	678	80.1	1689 4 US-09-053-374A-4	Sequence 4, Appl1
3	625	73.9	3986 4 US-09-053-374A-3	Sequence 3, Appl1
4	531	62.8	3079 4 US-09-053-374A-6	Sequence 6, Appl1
5	89.6	10.6	450 4 US-08-884-866A-10	Sequence 10, Appl1
6	89.6	10.6	480 4 US-08-884-866A-9	Sequence 9, Appl1
7	89.6	10.6	570 4 US-08-884-866A-11	Sequence 11, Appl1
8	89.4	10.6	570 4 US-08-884-866A-2	Sequence 2, Appl1
9	79.2	9.4	4480 4 US-09-167-322-12	Sequence 12, Appl1
10	67	7.9	240 4 US-08-884-866A-14	Sequence 14, Appl1
11	67	7.9	240 4 US-08-884-866A-20	Sequence 20, Appl1
12	65.6	7.8	240 4 US-08-884-866A-8	Sequence 8, Appl1
13	65.4	7.7	240 4 US-08-884-866A-12	Sequence 12, Appl1
14	65.4	7.7	240 4 US-08-884-866A-18	Sequence 18, Appl1
15	65.4	7.7	240 4 US-08-884-866A-19	Sequence 19, Appl1
16	65.4	7.7	240 4 US-08-884-866A-23	Sequence 23, Appl1
17	65.4	7.7	240 4 US-08-884-866A-24	Sequence 24, Appl1
18	64	7.6	1248 4 US-09-105-537-7	Sequence 7, Appl1
19	64	7.6	13613 4 US-09-105-537-3	Sequence 3, Appl1
20	63.8	7.5	240 4 US-08-884-866A-13	Sequence 13, Appl1
21	63.8	7.5	240 4 US-08-884-866A-21	Sequence 21, Appl1
22	63.8	7.5	240 4 US-08-884-866A-22	Sequence 22, Appl1
23	63.8	7.5	6453 1 US-08-306-691B-14	Sequence 14, Appl1
24	63.8	7.5	6453 3 US-09-209-668-10	Sequence 10, Appl1
25	63.8	7.5	6453 3 US-09-356-952-8	Sequence 8, Appl1
26	59.2	7.0	1506 4 US-09-158-767-7	Sequence 7, Appl1
27	59.2	7.0	1506 4 US-09-158-767-8	Sequence 8, Appl1

28	59.2	7.0	1506 4 US-09-158-767-9	Sequence 9, Appl1
29	59.2	7.0	2261 4 US-09-158-767-1	Sequence 1, Appl1
30	57.6	6.8	3177 1 US-08-042-747A-4	Sequence 4, Appl1
31	57.4	6.8	1394 4 US-08-935-450-3	Sequence 3, Appl1
32	55	6.5	2277 1 US-08-676-967-5	Sequence 5, Appl1
33	55	6.5	2277 1 US-08-676-974-5	Sequence 5, Appl1
34	55	6.5	2277 2 US-09-098-487-5	Sequence 5, Appl1
35	55	6.5	2504 1 US-08-073-384C-3	Sequence 3, Appl1
36	55	6.5	2504 1 US-08-254-359A-3	Sequence 3, Appl1
37	55	6.5	2504 1 US-08-483-043-3	Sequence 3, Appl1
38	55	6.5	2504 1 US-08-481-238-3	Sequence 3, Appl1
39	55	6.5	2504 2 US-08-471-066B-3	Sequence 3, Appl1
40	55	6.5	2504 2 US-08-484-956-3	Sequence 3, Appl1
41	55	6.5	2504 2 US-08-757-653-3	Sequence 3, Appl1
42	55	6.5	2504 2 US-08-599-491-3	Sequence 3, Appl1
43	55	6.5	2504 2 US-08-756-386-3	Sequence 3, Appl1
44	55	6.5	2504 2 US-08-823-516-3	Sequence 3, Appl1
45	55	6.5	2504 3 US-08-682-853A-3	Sequence 3, Appl1

ALIGNMENTS

```
RESULT 1
US-09-053-374A-1
; Sequence 1, Application US/09053374A
; Patent No. 6462177
; GENERAL INFORMATION:
; APPLICANT: YEN, KWANG-MU
; TITLE OF INVENTION: MAMMALIAN BLOOD LOSS-INDUCED GENE, KD312
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: US
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/053,374A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-514
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1841 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 255..1097
; US-09-053-374A-1

Query Match 100.0%; Score 846; DB 4; Length 1841;
Best Local Similarity 100.0%; Pred. No. 1.5e-156;
Matches 846; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGTGGCGCGATGATCAAGAGATGTCGCGAGCTCGAGCTGATGATCCG 60
DB 255 ATGAAGTGGCGCGATGATCAAGAGATGTCGCGAGCTCGAGCTGATGATCCG 314
QY 61 GCCAAGTGGTATGCGATGTCATCCCTGCTGCAAGTGGCAAGCGCCATC 120
```


Db 315 GCCAAGACTGATATGATGATATCTGAGCTCGTCCAAAGGTGGGCAAGAGGCAATC 374
QY 121 GTGTGGGCTTCTCTCAACGGGGGCTTGGAGAGCGCTTACAGCGCTTACATGAGACTTC 180
Db 375 GTGTGGGCTTCTCTCAACGGGGGCTTGGAGAGCGCTTACAGCGCTTACATGAGACTTC 434
QY 181 CACCGCAAGTTCTATCTCATCTCCGGGCGAGGTTACAGCTGACATCTCTGACAGCTCC 240
Db 435 CACCGCAAGTTCTATCTCATCTCCGGGCGAGGTTACAGCTGACATCTCTGACAGCTCC 494
QY 241 GGCAGACACCGCTTCCCGGCGAGGCGCTTCTCATCTCTGACAGGAGCTTTTCATC 300
Db 495 GGCAGACACCGCTTCCCGGCGAGGCGCTTCTCATCTCTGACAGGAGCTTTTCATC 554
QY 301 CTGGTTTCACTGTGAGCAACCGGAGCTCTTGGAGAGGTGACAGGCTCAGCAGCAG 360
Db 555 CTGGTTTCACTGTGAGCAACCGGAGCTCTTGGAGAGGTGACAGGCTCAGCAGCAG 614
QY 361 ATCTGACACCAAGTTGCTCTCAAGAACAAAACCAAGAGAACTGGAGCTGCCCTTG 420
Db 615 ATCTGACACCAAGTTGCTCTCAAGAACAAAACCAAGAGAACTGGAGCTGCCCTTG 674
QY 421 GTCTATGCGGCAACAAGGTGACCGGAGCTTCTACCGGCGAGGTGACCGGCGAGATC 480
Db 675 GTCTATGCGGCAACAAGGTGACCGGAGCTTCTACCGGCGAGGTGACCGGCGAGATC 734
QY 481 GAGAGAGTGGTGGGCGAGACCGCCAGCGCTGCGCTACTTCTGAGATCTTGGCCAGAG 540
Db 735 GAGAGAGTGGTGGGCGAGACCGCCAGCGCTGCGCTACTTCTGAGATCTTGGCCAGAG 794
QY 541 AACAGACGCTGAGACCAAGATGTTCCGGCGCTCTTGGCATGAGCCAAAGCTGGCCAGCAG 600
Db 795 AACAGACGCTGAGACCAAGATGTTCCGGCGCTCTTGGCATGAGCCAAAGCTGGCCAGCAG 854
QY 601 ATGAGCCCAAGCTGAGACCGCCAGCGAGTGTGAGTACGCGAGCGAGTGTGAGCAAGAG 660
Db 855 ATGAGCCCAAGCTGAGACCGCCAGCGAGTGTGAGTACGCGAGCGAGTGTGAGCAAGAG 914
QY 661 GCGCTGCGGCAACAAGAGCTGTCGGGCGCGGAGCGCGGCGGCGGCGAGCCCGGGC 720
Db 915 GCGCTGCGGCAACAAGAGCTGTCGGGCGCGGAGCGCGGCGGCGGCGGCGAGCCCGGGC 974
QY 721 GAGCGCTTGGCATGTCGCGACCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 780
Db 975 GAGCGCTTGGCATGTCGCGACCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1034
QY 781 TACATCCGCGAAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840
Db 1035 TACATCCGCGAAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1094
QY 841 AGCTAG 846
Db 1095 AGCTAG 1100

RESULT 2
US-09-053-374A-4
; Sequence 4, Application US/09053374A
; Patent No. 6462177
; GENERAL INFORMATION:
; APPLICANT: YEN, KWANG-MU
; TITLE OF INVENTION: MAMMALIAN BLOOD LOSS-INDUCED GENE, KD312
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: US
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/053,374A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-514
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1689 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: Linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 132..971
US-09-053-374A-4

Query Match 80.1%; Score 678; DB 4; Length 1689;

Best Local Similarity 88.4%; Pred. No. 7.2e-124;

Matches 748; Conservative 0; Mismatches 95; Indels 3; Gaps 1;

QY 1 ATGAAACTGGGCGGATGATCAAGAGATGTCGCCGAGCTCGGAGCTGAGTATCCCG 60
Db 132 ATGAAACTGGGCGGATGATCAAGAGATGTCGCCGAGCTCGGAGCTGAGTATCCCG 191
QY 61 GCCAAGAACTGCTATGCGATGTCGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 192 GCCAAGAACTGCTATGCGATGTCGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 251
QY 121 GTGTGCGGCTTCTCTCAACGGGGGCTTGGAGAGCGCTTACAGCGCTTACATGAGACTTC 180
Db 252 GTGTGCGGCTTCTCTCAACGGGGGCTTGGAGAGCGCTTACAGCGCTTACATGAGACTTC 311
QY 181 CACCGCAAGTTCTATCTCATCTCCGGGCGAGGTTCTACAGCTGACATCTCTGACAGCTCC 240
Db 312 CACCGCAAGTTCTATCTCATCTCCGGGCGAGGTTCTACAGCTGACATCTCTGACAGCTCC 371
QY 241 GGCAGACACCGCTTCCCGGCGCATGGGCGGCTCTCTCATCTCTCAAGAGAGCTGTCATC 300
Db 372 GGCAGACACCGCTTCCCGGCGCATGGGCGGCTCTCTCATCTCTCAAGAGAGCTGTCATC 431
QY 301 CTGGTTTCACTGTGAGCAACCGGAGCTCTTGGAGAGGTGACAGGCTCAGGCGCAG 360
Db 432 CTGGTTTCACTGTGAGCAACCGGAGCTCTTGGAGAGGTGACAGGCTCAGGCGCAG 491
QY 361 ATCTGACACCAAGTTGCTCTCAAGAACAAAACCAAGAGAACTGGAGCTGCCCGCTG 420
Db 492 ATCTGACACCAAGTTGCTCTCAAGAACAAAACCAAGAGAACTGGAGCTGCCCGCTG 551
QY 421 GTCTATGCGGCAACAAGGTGACCGGAGCTTCTACCGGAGGTGACCGGCGGAGATC 480
Db 552 GTCTATGCGGCAACAAGGTGACCGGAGCTTCTACCGGAGGTGACCGGCGGAGATC 611
QY 481 GAGCAGCTGTGGGCGAGACCGCCAGCGCTGCGCTTCTGAGATCTCTGCGGCAAGAG 540
Db 612 GAGCAGCTGTGGGCGAGATCCTCAGCGCTTGTGCTTCTGAGATCTCTGCGGCAAGAG 671
QY 541 AACAGACGCTGAGACCAAGATGTTCCGGGCGGCTTGGGAGGAGGAGGAGGAGGAGGAG 600
Db 672 AACAGACGCTGAGACCAAGATGTTCCGGGCGGCTTGGGAGGAGGAGGAGGAGGAGGAG 731
QY 601 ATGAGCCCAAGCTGAGACCGGAGGTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 732 ATGAGCCCAAGCTGAGACCGGAGGTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 791
QY 661 GCGCTGCGGCAACAAGAGCTTCTGCGGCGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGG 720
Db 792 GCTCTGAGAAACAAGAGCTTCTGCGGCGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGG 848

QY	721	GACGGCTTTGGCATCGTGGACACCTTCGGGGGCGCGCCAGCGTACACAGCGACCTCATG	780
Db	849	GATGCTTTTGGCATCTTGGCCCGCTTTGTCTGCGAGACCTTACCGCGCATTAACGCACTTCATG	908
QY	781	TACATCCGCGAGAAAGCCACGCGCGCGGACGCCAGGCGCAAGGACAAAGAGGCGCTCGTCATC	840
Db	909	TACATCTCTGTGAAAAACCAAGTGTACAGCAGCCAGGCTAAAGGACAAAGAGCGCTGTGTATC	968
QY	841	AGCTAG	846
Db	969	AGTTAG	974

```

1  RESULT 3
2  US-09-053-374A-3
3  Sequence 3, Application US/09053374A
4  Patent No. 6462177
5  GENERAL INFORMATION:
6  APPLICANT: YEN, KWANG-MU
7  TITLE OF INVENTION: MAMMALIAN BLOOD LOSS-INDUCED GENE, KD312
8  NUMBER OF SEQUENCES: 9
9  CORRESPONDENCE ADDRESS:
10 ADDRESS: AMGEN INC.
11 STREET: ONE AMGEN CENTER DRIVE
12 CITY: THOUSAND OAKS
13 STATE: CA
14 COUNTRY: US
15 ZIP: 91320
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: PatentIn Release #1.0, Version #1.30
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/09/053,374A
23 FILING DATE:
24 CLASSIFICATION: 435
25 ATTORNEY/AGENT INFORMATION:
26 NAME: COOK, ROBERT R.
27 REGISTRATION NUMBER: 31,602
28 REFERENCE/DOCKET NUMBER: A-514
29 INFORMATION FOR SEQ ID NO: 3:
30 SEQUENCE CHARACTERISTICS:
31 LENGTH: 3986 base pairs
32 TYPE: nucleic acid
33 STRANDEDNESS: single
34 TOPOLOGY: linear
35 MOLECULE TYPE: DNA (genomic)
36 US-09-053-374A-3

```

Query Match	73.98;	Score 625;	DB 4;	Length 3986;
Best Local Similarity	80.08;	Pred. No. 1.6e-113;		
Matches 846;	Conservative 0;	Mismatches 0;	Indels 211;	Gaps 1

QY	1	ATGAAATGCGCCGAGATGATCAGAAGAGATGTGGCCGAGGACTCGGAGCTGGATGTTCCG	60
Db	774	ATGAAATGCGCCGAGATGATCAGAAGAGATGTGGCCGAGGACTCGGAGCTGGATGTTCCG	833
QY			
Db			
QY	61	GCCAAAGACGTATGCGATGTCATCTTCGCTGTCTCAAGGTGGCAAGCGGCATC	120
Db	834	GCCAAAGACGTATGCGATGTCATCTTCGCTGTCTCAAGGTGGCAAGCGGCATC	893
QY			
Db			
QY	121	GTGTGCGCTTCCTACCGGGCGCTTCGAGGAGCGCTACACGCTTACCATTCGAGGACTTC	180
Db	894	GTGTGCGCTTCCTACCGGGCGCTTCGAGGAGCGCTTACACGCTTACCATTCGAGGACTTC	953
QY			
Db			
QY	181	CACCGCAAGTTCACTCATTCGCGCGCGAGAGTCTACACTGGAATCTCGACAGCTCC	240
Db	954	CACCGCAAGTTCACTCATTCGCGCGCGAGAGTCTACCACTCGACATCTCGACAGCTCC	1013
QY	241	GGCAACACCCGTTCCCGCGCATGCGGCGCTTCATCTCTAC-----	284

Db	1014	GGCAACACCCGCTTCCCGCATGCGGCGCTCTTCATCTCTCAAGGTAGCCGGGGGCC	1073
QY	285	-----	284
Db	1074	GGGAGGTTGGCGGAGGAGGAGGGGGGAACCTTCGGGCAGGGGGCCCCCGAGCCGGT	1133
QY	285	-----	284
Db	1134	CCGGCTGCTGCGCGCCAGTAGTATGCGCTTGCCCTTAGAGAGGCTTAGCGGCCCGCGG	1195
QY	285	-----	284
Db	1194	GCTCTAAGTCAGCCGACCTGTGTCCTGGGGGGCACCCCTCACTTCTCTTTCGT	1255
QY	285	-----AGAGACGTTTTTCATCTGTGTGTTTCAGTCTGTGACACCCGAGTC	329
Db	1254	CTGTGTCCCCCTTATAGAGACGTTTTTCATCCCTGGTGTTCAGTCTGTGACACCCGAGTC	1313
QY	330	CTTCGAGAGGTGCGAGGGGCTTCAGGACAGCATCTCTCGACACCAAGTCTGTGCTCAAGA	389
Db	1314	CTTCGAGAGAGTGCAGGGGCTTCAGGACAGCATCTCTCGACACCAAGTCTGTGCTCAAGA	1373
QY	390	CAAAACCAAGGAGACGTGGACGTGCCCTGTGTCATCTCGGCAACCAAGGTTGACCCGA	449
Db	1374	CAAAACCAAGGAGACGTGGACGTGCCCTGTGTCATCTCGGCAACCAAGGTTGACCCGA	1433
QY	450	CTTCTACCCGCGAGGTGGACACGCGCCGACATCCAGACAGCTGTGTGGCGACACCCCAAGC	509
Db	1434	CTTCTACCCGCGAGGTGGACACGCGCCGACATCCAGACAGCTGTGTGGCGAGACCCCAAGC	1493
QY	510	CTGCGCTACTCTCGAGATCTCGGCGCAAGAAAGAACACACACCTGTGGACCAATGTCGGGC	569
Db	1494	CTGCGCTACTCTCGAGATCTCGGCGCAAGAAAGAACACACACCTGTGGACCAATGTCGGGC	1553
QY	570	GCTCTTCGCGCATGGCCAAAGCTGCGCCAGCGAGATGAGCCCAAGCTTCACCCGCAAGTCTC	629
Db	1554	GCTCTTCGCGCATGGCCAAAGCTGCGCCAGCGAGATGAGCCCAAGCTTCACCCGCAAGTCTC	1613
QY	630	GGTGCATACTCTCGAGACTGTCTGCACAAAGAGCGGCTGTGGCAACAAGAGTCTGTCCGGGC	689
Db	1614	GGTGCATACTCTCGAGACTGTCTGCACAAAGAGCGGCTGTGGCAACAAGAGTCTGTCCGGGC	1673
QY	690	CGGAGAGGGGGGGGGCGGCGGACACCCGGGGCGAGGCTTTGGCATGCTGAGACCTTGTGC	749
Db	1674	CGGAGAGGGGGGGGGCGGCGGCGGCGGACACCCGGGGCGAGGCTTTGGCATGCTGAGACCTTGTGC	1733
QY	750	GGCGCGGCGCCAGCGTACACGCGACCTCATGTATCATCCGCGAAGAGGCCAGCGCGCGAG	809
Db	1734	GGCGCGGCGCCAGCGTACACGCGACCTCATGTATCATCCGCGAAGAGGCCAGCGCGCGAG	1793
QY	810	CCAGGCCAAGAGACAGGAGCGGCTGCTCATACAGCTAG	846
Db	1794	CCAGGCCAAGAGACAGGAGCGGCTGCTCATACAGCTAG	1830

1 RESULT 4
 2 US-09-053-374A-6
 3 Sequence 6, Application US/09053374A
 4 Patent No. 6462177
 5
 6 GENERAL INFORMATION:
 7
 8 APPLICANT: YEN, KWANG-MO
 9 TITLE OF INVENTION: MAMMALIAN BLOOD LOSS-INDUCED GENE, KD312
 10 NUMBER OF SEQUENCES: 9
 11 CORRESPONDENCE ADDRESS:
 12 ADDRESSEE: AMGEN INC.
 13 STREET: ONE AMGEN CENTER DRIVE
 14 CITY: THOUSAND OAKS
 15 STATE: CA
 16 COUNTRY: US
 17 ZIP: 91320
 18
 19 COMPUTER READABLE FORM:
 20 MEDIUM TYPE: Floppy disk
 21 COMPUTER: IBM PC compatible


```

? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent Invention #1.0, Version #1.30
?
? CURRENT APPLICATION DATA:
?
? APPLICATION NUMBER: US/09/053,374A
?
? FILING DATE:
?
? CLASSIFICATION: 435
?
? ATTORNEY/AGENT INFORMATION:
?
? NAME: COOK, ROBERT R.
? REGISTRATION NUMBER: 31,602
? REFERENCE/DOCKET NUMBER: A-514
? INFORMATION FOR SEQ ID NO: 6:
?
? SEQUENCE CHARACTERISTICS:
?
? LENGTH: 3079 base pairs
?
? type: nucleic acid
?
? STRANDEDNESS: single
?
? TOPOLOGY: linear
?
? MOLECULE TYPE: DNA (genomic)
?
?
? US-09-053-374A-6

```

Query Match	62.88;	Score 531;	DB 4;	Length 3079;
Best Local Similarity	76.18;	Pred. NO. 3.1e-95;		
Matches 748; Conservative	0;	Mismatches 95;	Indels 140;	Gaps 2

QY	1	ATGAACTGGCCCGCATGATATCAAGAAGATGTCCGAGCGATCGAGACTGTATGCCG	60
Db	303	ATGAACTGGCCGCGATGATCAAGAAAGATGTGCCAAGGACTGTGAAGTATCCG	362
QY	61	GCCACAGACTGCTATGCGATGTCATCTCCGCGCTGCCAAGTGGGCAAGCGCCATC	120
Db	363	GCCAAAGAACTGTACAGAGATGGTCATCTCCGCGCTCACTCAAAAGTGGGCAAGCGCCATC	422
QY	121	GTGCGGCGCTCTCCACCGGCGGCTTCGAGGAAGCGCTACAGCTTACCATCGAAGATTC	180
Db	423	GTGTCCGCGCTCTCCACGCGGCGCTTCGAGAGACGCTTACACCCCTTACCATTTGAAGACTTC	482
QY	181	CACCGCAAGTTCCTACTCCATCCGCGCGAGAGTCTACCAAGCTGACATCCTCGACACGTCC	240
Db	483	CACCGAAAGTTTACTCGATCCGCGCGAGAAAGTCTACCAAGTTGGAATATCTGACACACTCT	542
QY	241	GGCACACACCCGCTCCCGGCATGCGGGCGGCTCTCATCCCTAC-----	284
Db	543	GGCATCATCCGTTCCCGCATGCGGGCGCTCTCATCTCACAGGTGATGGGGGACC	602
QY	285	-----	284
Db	603	GACAGGACCGCTGGGAGGGAATCTCGGGGAGAGCGGATGGGGCGGTGTGTGCTTGGG	662
QY	285	-----	284
Db	663	GCTGTGCTCTCTGCTCGCTGCTTGGGAGGTGCCCTTACCTTTCACCTGTTCCCTTG	722
QY	285	-AGGAGACGTTTTCATCTCGGTGTTCATAGTCTGGACAACCGGACATCTTCGAGAGGTGC	343
Db	723	TAGAGACGTTTTCATCTCGGTGTTCATAGTCTTACACAACCGGACATCTTCGAGAGGTGC	782
QY	344	AGCGGCTCAGGACGAGATCTCTGACACCAAGTCTTGCCTCAAGAACAAACCAAGGAGA	403
Db	783	AAAGGCTCAACAGACGAGATCTTGAACACCAAGTCTTGCCTCAAGAACAAACCAAGGAGA	842
QY	404	ACGTGACGCTGCCCCCTGTGTCATCTGGGGAACAAGGTTACCGGACATTTCACCGGAGG	463
Db	843	ATGTGGACGTGCGCTGTGTCATTTGGGGTAAACAAAGGAGACCGGACATTTCACCGGAGG	902
QY	464	TGGACACGCGCGAGATCGAGCAGCTGTGGGGGACAGCCCCAGGCGTGGCGCTACTTCGG	523
Db	903	TGGAGCAGCGCGGAGATTGAGCAGCTGTGGGGGATGATACCCCTTACGCGTTGTGCTACTTCG	962
QY	524	AGATCTCGGCGCAAGAAACAGACGCGCTGGACAGATGTTCGCGCGGCTCTTCGCGCATGG	583
Db	963	AGATCTCGGCGCAAGAAATAGACGCGCTGGACAGATGTTCGCGCGGCTCTTCGCGCATGG	1022
QY	584	CCAAAGCTGCCAGAGATGAGCCCAAGACTGACACCGCAAGTCTGCGTGCAGTACTCGG	643

[illegible]

RESULT 5
US-08-884-866A-10
; Sequence 10, Application US/08884866A

```

1  APPLICANT: Chien, Shu
2  APPLICANT: SHAY, John Y-J
3  TITLE OF INVENTION: GENE THERAPY IN CORONARY ANGIOPLASTY AND
4  TITLE OF INVENTION: BYPASS
5  FILE REFERENCE: UCSD1100-1
6  CURRENT APPLICATION NUMBER: US/08/884,866A
7  CURRENT FILING DATE: 1997-06-30
8  PRIOR APPLICATION NUMBER: 60/030,358
9  PRIOR FILING DATE: 1996-11-08
10 NUMBER OF SEQ ID NOS: 25
11 SOFTWARE: FastSeq for Windows Version 4.0
12 SEQ ID NO 10
13 LENGTH: 450
14 TYPE: DNA
15 ORGANISM: Rattus norvegicus
16 FEATURE:
17 NAME/KEY: misc_feature
18 LOCATION: (49)...(51)
19 OTHER INFORMATION: mm = Any nucleic acid triplet, except for UCA
20 OTHER INFORMATION: UCC, UCG, UCU, AGC, or AGU
21 US-08-884-866A-10

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Query Match	10.68;	Score 89.6;	DB 4;	Length 450;
Best Local Similarity	56.4%;	Pred. No. 1.9e-09;		
Matches 164;	Conservative	0;	Mismatches 127;	Indels 0;
				Gaps 0;

QY	73	TATGCGATGGCATCTTCGCGTCTCCAAAGTGGGCAAGACGGCCAAATCGGTGCGCTTC	132
Db	10	TATTAAGCTGTGTGTGTGTGTGGCGCGCGGTGTGTGGGCAAAANNNGCGCTGACCATTCACGTC	69
QY	133	CTCACCGGCGCGCTTCGAGAGACGCCCTACAGCGCTACCATGTGAGGACCTTCACGCGAAGTTC	192
Db	70	ATCCAGAACCATTTTGTGGGAGAAATACGAGCCGCCCTATTAAGGATTCCTACCGGAAGACAG	129
QY	193	TACTCCATCCGCGCGGAGGTGTACACGCTGACATCCCTGCAACGTCGCGGCAACCCACCGG	252
Db	130	GTGGCTCATTTATGTGGGGAGACGCTGCTTTGTGACATCTTGATATCCGCGGCGCTGGAGAG	189
QY	253	TTCCCGCGCCATGCGGGCGCGCTCTCCATCCCTACAGGAGACGTTTTTCATCTCGGTGCTCAGT	312
Db	190	TACAGCGCCATGCGGGAGACAACTCAATCGCAGCGGGAGGGCGTTCTGTGTGTGTTGCC	249
QY	313	CTGAGCAAAACCGCGACCTCTTCGTGAGAGAGTGCAGGGGCTCAGGCAAGCAGATC	363
Db	250	ATCAACAACACCAAGCTTTTGTGAGACATCCACCAGTACAGGGAGGCGAGATC	300

RESULT 6
US-08-884-866A-9
; Sequence 9, Application US/08884866A


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;; GENERAL INFORMATION:
;; APPLICANT: Chien, Shu
;; TITLE OF INVENTION: GENE THERAPY IN CORONARY ANGIOPLASTY AND
;; FILE REFERENCE: BYPASS
;; CURRENT APPLICATION NUMBER: US/08/884,866A
;; CURRENT FILING DATE: 1997-06-30
;; PRIOR APPLICATION NUMBER: 60/030,358
;; PRIOR FILING DATE: 1996-11-08
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 9
;; LENGTH: 480
;; TYPE: DNA
;; ORGANISM: Rattus norvegicus
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (49)...(51)
;; OTHER INFORMATION: nnn = Any nucleic acid triplet, except for UCA,
;; OTHER INFORMATION: UCC, UCG, UCU, AGC, or AGU
US-08-884-866A-9
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```
Query Match          10.6%; Score 89.6; DB 4; Length 480;
Best Local Similarity 56.4%; Pred. No. 2e-09;
Matches 164; Conservative 0; Mismatches 127; Indels 0; Gaps 0;
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```
OY 73 TATCGATGTCATCTCGCTGCTCCAAAGTGGGCAAGACGGCCATCTGTCGGCTTC 132
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 10 TATAAGCTGTGTGTGGTGGCGCGGCTGTGGGCAANNNGGCTGACATCCAGCTG 69
OY 133 CTCACCGCGCGCTTCGAGAGAGCCTTCACAGCCTTACATGAGAGCTTCACCGCAATTC 192
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 70 ATCCAGAACCAATTTGTGTGAGCAATACGACCCCACTATGAGAGATTCCTACCGGAGAG 129
OY 193 TACTCCATCCGCGGAGGCTTACACAGCTCGACATCTCGACACGCGCGCAACCAACCG 252
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 130 GTGTCATTTGATGGGAGAGAGCTGCTGTGGACATCTGATACCGCGCGCTGAGAGAG 189
OY 253 TTCCCGGCGATGGCGGCTCTTCATCTTCACAGAGAGAGCTTTTCATCTGTTCACT 312
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 190 TACAGCGCATGGGAGGAGCAATGACGACCGGAGGAGGCTTCTGTTGTTGCC 249
OY 313 CTGGAACACCGGAGCTCTTCAGAGAGGAGGAGGAGGCTGAGCAGCAGATC 363
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 250 ATCAACACCAACCAAGCTTTTGGAGCATCCACAGTACAGGAGAGATC 300
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RESULT 7

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;; Sequence 11, Application US/08884866A
;; GENERAL INFORMATION:
;; APPLICANT: Chien, Shu
;; TITLE OF INVENTION: GENE THERAPY IN CORONARY ANGIOPLASTY AND
;; FILE REFERENCE: BYPASS
;; CURRENT APPLICATION NUMBER: US/08/884,866A
;; CURRENT FILING DATE: 1997-06-30
;; PRIOR APPLICATION NUMBER: 60/030,358
;; PRIOR FILING DATE: 1996-11-08
;; NUMBER OF SEQ ID NOS: 25
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 11
;; LENGTH: 570
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (49)...(51)
;; OTHER INFORMATION: nnn = Any nucleic acid triplet, except for UCA,
;; OTHER INFORMATION: UCC, UCG, UCU, AGC, or AGU
;; OTHER INFORMATION: Variation of SEQ ID NO.: 2
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US-08-884-866A-11

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Query Match          10.6%; Score 89.6; DB 4; Length 570;
Best Local Similarity 56.4%; Pred. No. 2e-09;
Matches 164; Conservative 0; Mismatches 127; Indels 0; Gaps 0;
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```
OY 73 TATCGATGTCATCTCGCTGCTCCAAAGTGGGCAAGACGGCCATCTGTCGGCTTC 132
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 10 TATAAGCTGTGTGTGGTGGCGCGGCTGTGGGCAANNNGGCTGACATCCAGCTG 69
OY 133 CTCACCGCGCGCTTCGAGAGAGCCTTCACAGCCTTACATGAGAGCTTCACCGCAATTC 192
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 70 ATCCAGAACCAATTTGTGTGAGCAATACGACCCCACTATGAGAGATTCCTACCGGAGAG 129
OY 193 TACTCCATCCGCGGAGGCTTACACAGCTCGACATCTTCAGACAGTCCGCGCAACCAACCG 252
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 130 GTGTCATTTGATGGGAGAGAGCTGCTGTGGACATTCCTGATACCGCGCGCTGAGAGAG 189
OY 253 TTCCCGGCGATGGCGGCTCTTCATCTTCACAGAGAGCTTTTCATCTGTTCACT 312
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 190 TACAGCGCATGGGAGGAGCAATGACGACCGGAGGAGGCTTCTGTTGTTGCC 249
OY 313 CTGGAACACCGGAGCTCTTCAGAGAGGAGGAGGAGGCTGAGCAGCAGATC 363
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 250 ATCAACACCAACCAAGCTTTTGGAGCATCCACAGTACAGGAGAGATC 300
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RESULT 8

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;; Sequence 2, Application US/08884866A
;; GENERAL INFORMATION:
;; APPLICANT: Chien, Shu
;; TITLE OF INVENTION: GENE THERAPY IN CORONARY ANGIOPLASTY AND
;; FILE REFERENCE: BYPASS
;; CURRENT APPLICATION NUMBER: US/08/884,866A
;; CURRENT FILING DATE: 1997-06-30
;; PRIOR APPLICATION NUMBER: 60/030,358
;; NUMBER OF SEQ ID NOS: 25
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 2
;; LENGTH: 570
;; TYPE: DNA
;; ORGANISM: Rattus norvegicus
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (1)...(570)
US-08-884-866A-2
```

```
Query Match          10.6%; Score 89.4; DB 4; Length 570;
Best Local Similarity 56.7%; Pred. No. 2e-09;
Matches 165; Conservative 0; Mismatches 126; Indels 0; Gaps 0;
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OY 73 TATCGATGTCATCTCGCTGCTCCAAAGTGGGCAAGACGGCCATCTGTCGGCTTC 132
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 10 TATAAGCTGTGTGTGGTGGCGCGGCTGTGGGCAAAATGCGTACCATCCAGCTG 69
OY 133 CTCACCGCGCGCTTCGAGAGAGCCTTCACAGCCTTACATGAGAGCTTCACCGCAATTC 192
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 70 ATCCAGAACCAATTTGTGTGAGCAATACGACCCCACTATGAGAGATTCCTACCGGAGAG 129
OY 193 TACTCCATCCGCGGAGGCTTACACAGCTCGACATCTTCAGACAGTCCGCGCAACCAACCG 252
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 130 GTGTCATTTGATGGGAGAGAGCTGCTGTGGACATCTGATACCGCGCGCTGAGAGAG 189
OY 253 TTCCCGGCGATGGCGGCTCTTCATCTTCACAGAGAGCTTTTCATCTGTTCACT 312
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 190 TACAGCGCATGGGAGGAGCAATGACGACCGGAGGAGGCTTCTGTTGTTGCC 249
OY 313 CTGGAACACCGGAGCTCTTCAGAGAGGAGGAGGAGGCTGAGCAGCAGATC 363
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Db 10 TATAGCTGTGTGTGTGTGGCCCGCGCGGTGTGGGCAAAAGCGCTGACCATTCACGCTG 69
 QY 133 CTCACCGGCCGCTTGGAGAGCGCTTAACAGCGCTTACCATGAGAGACTTCCACGCAAGTTC 197
 Db 70 ATCCAGAACCATTTGTGTGGAGGAAATAGACCCCGCATATGAGAGATTCTACCGGAAGAG 122
 QY 193 TATCCATCCGGGGGAGAGTGTACCACGCTGCAATCTCTGACACGTCGGGACACCCACCG 257
 Db 130 GTGTGATTGATGGGAGAGACGTCGCTGTGTGGAACTATCTGGATTAACGCGCGCTGGAGAG 189
 QY 253 TTCCCGGCACATCGGCGGCTCTCCATCATCTCAAGAGAGAGTTTCAAT 299
 Db 190 TACAGCGGCATGTGGGAGACCAATCAATCGGACCGGGGAGGCGCTTCT 236

```

RESULT 12
US-08-884-866A-8
; Sequence 8, Application US/08884866A
; GENERAL INFORMATION:
; APPLICANT: Chien, Shu
; TITLE OF INVENTION: GENE THERAPY IN CORONARY ANGIOPLASTY AND
; FILE OF INVENTION: BYPASS
; FILE REFERENCE: UCSD100-1
; CURRENT APPLICATION NUMBER: US/08/884,866A
; CURRENT FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/030,358
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 240
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (49)..(51)
; OTHER INFORMATION: mm = Any nucleic acid triplet, except for UCA,
; US-08-884-866A-8
; OTHER INFORMATION: UCC, UCG, UCU, AGC, or AGU

```

RESULT 13
US-08-884-866A-12
Sequence 12, Application US/08884866A
GENERAL INFORMATION:
APPLICANT: SHYY, John Y-J
APPLICANT: Chien, Shu
TITLE OF INVENTION: GENE THERAPY IN CORONARY ANGIOPLASTY AND
TITLE OF INVENTION: Bypass
FILE REFERENCE: UCD1100-1
CURRENT APPLICATION NUMBER: US/08/884,866A
CURRENT FILING DATE: 1997-06-30

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Query Match	7.7%;	Score 65.4;	DB 4;	Length 240;
Best Local Similarity	55.5%;	Pred. No. 9.3e-05;		
Matches 126;	Conservative 0;	Mismatches 101;	Indels 0;	Gaps 0;

QY 133 CTACACGGCCGCTTTGGAGAGAGCCCTTAACACGCTTACATGTGAGAGACTTCCACCGCAAGTTC 1922

Db 70 ATCCAGACACCATTTGTTGTGAGAGAAATACGACCCCATATGAGAGATTCCTACCGGAGCAG 1299

QY 193 TACTCCATCCGCGGCGAGGCTTACCACTCGACATCTCTGAGACGCTCCGGCAGACACCCG 252

Db 130 GTGCTGATTTGATGGGGAACGCTGCTTGTGGAAATCTCTGGAAATCCGCGCGGCTGGAGAG 189

QY 253 TTCCCGCCCATCGGCGGCGCTCTCCATCCTACAGAGAGGTTTTCAT 299

Db 190 TACAGCGCCATCGGGACCACTCAATCGGACCGGGGAGAGGCTTCTT 236

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RESULT 14
US-08-884-866A-18
; Sequence 18, Application US/0884866A
; GENERAL INFORMATION:
; APPLICANT: Chien, Shu
; APPLICANT: Shyy, John Y.-J.
; TITLE OF INVENTION: GENE THERAPY IN CORONARY ANGIOPLASTY AND
; TITLE OF INVENTION: BYPASS
; FILE REFERENCE: US2001100-1
; CURRENT APPLICATION NUMBER: US/08/884,866A
; CURRENT FILING DATE: 1997-06-30
; PRIOR APPLICATION NUMBER: 60/030,358
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ. ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 240
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variation of SEQ ID NO.:2
US-08-884-866A-18

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Query Match	7.78;	Score 65.4;	DB 4;	Length 240;
Best Local Similarity	55.58;	Pred. No. 9.3e-05;		
Matches 126; Conservative	0;	Mismatches 101;	Indels 0;	Gaps 0;

[illegible]

Db 190 TACAGCGCCATGCGGGACCAAGTCATATGCGCACCGGGAGGGCTTCT 236

RESULT 15
US-08-884-866A-19

US-08-884-866A-19
Sequence 19, Application US/08884866A

US-08-884-866A-19
; Sequence 19, Application US/08884866A
: GENERAL INFORMATION:

; Sequence 19, Application
; GENERAL INFORMATION:
; ADDITIONAL: Chief S

;; GENERAL INFORMATION:
; APPLICANT: Chien, Shu
; IDENTIFICATION: Chien, Shu v-t

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;
; APPLICANT: Chien, Shu
; APPLICANT: Shyy, John Y-J
;
; INTERNATIONAL TRADE UNIVERSITY IN COBOROV ANTIPODASTEV AND
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APPLICANT: Shyy, John Y-J
TITLE OF INVENTION: GENE THERAPY IN CORONARY ANGIOPLASTY AND

TITLE OF INVENTION: GENE TH
; ;
TITLE OF INVENTION: BYPASS

FILE REFERENCE: UCSD1100-1

FILE OF INVENTION: 2-10-68
FILE REFERENCE: UCSD1100-1
CURRENT APPLICATION NUMBER: US/00

FILE REFERENCE: OCCB100 1
CURRENT APPLICATION NUMBER: US/00
CURRENT FILING DATE: 1997-06-30

;; CURRENT APPLICATION NUMBER: 03/00/00
;; CURRENT FILING DATE: 1997-06-30
PRIOR APPLICATION NUMBER: 60/030,358

;; CURRENT FILING DATE: 1997-08
;; PRIOR APPLICATION NUMBER: 60/
;; PRIOR FILING DATE: 1996-11-08

; PRIOR APPLICATION NUMBER:
 ; PRIOR FILING DATE: 1996-1
 ;

PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 25

NUMBER OF SE
SOFTWARE: Fa

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; SOFTWARE: Fa
; SEQ ID NO 19

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SEQ ID NO 19
LENGTH: 240

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; SEQ ID NO 1
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; LENGTH: 240
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; TYPE: DNA

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; LENGTH: 240
; TYPE: DNA
; ORGANISM: Artificial Sequence

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;;
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
FEATURE:

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; ORGANISM: Artificial sequence
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; FEATURE:
; OWNED INFORMATION: Variation of SEQ ID NO.:2

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; FEATURE:  
; OTHER INFORMATION: Variation of SEQ ID NO.:2  
; ;  
; 00-004-668-10
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OTHER INFORMATION: Variation of SEQ ID NO.:2
US-08-884-866A-19

US-08-884-866A-19

7.7%; Score 65.4; DB 4; Length 240;

Query Match	7.78;	Score 65.4;	DB 4;	Length 240;
Best Local Similarity	55.58;	Pred. NO. 9.3e-05;		

very match		
query match		
Best Local Similarity	55.58;	Pred. No. 9.3e-05;
Matches 126; Conservative	0;	Mismatches 101; Indels 0; Gaps

Matches	126;	Conservative	0;	Mismatches	101;	Indels	0;	Gaps	0;
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Matches	126;	conservative	0;	mismatches	207;	inserts	0;	de-
73	TATCGCATGTCATTCCTCGGCTCGTCCAAAGGTGGCCAGACGCCCATCGTGTGCGCCTTC	132						

73 TATCGCATGTCATTCCTCGGCTCGTCCAGTAGTGGCAGAGAGGCCATCGTGTGCGGCTTC 132

73 TATCGCATGTCATCTCGGCTCGTCCAGAGTGGGCAAGACGGCCATCGTGG

Db 10 TATAAGCTGCTGCTGGGCGCGCGGTGTGGGCAAGCAGCGCTGACC

Search completed: December 28, 2002, 05:52:50
Job time : 45.7548 secs

Job time : 45.7548 secs

67 GCTCACCCTGGTGCCA

Db 168 GCTCACCCCGGTGCGACCCGAGCACCCTCAGCCGCTCTCTGCGCTTCTCTGCGCCCG 227
 QY 127 GCGCCGCGCTGCGCGGCGCTCTGCGCCCAATGAACCTGCGCGGATGATCAAGAGATGTC 186
 Db 228 GCGCCGCGCTGCGCGGCGCTCTGCGCCCAATGAACCTGCGCGGATGATCAAGAGATGTC 287
 QY 187 CCGAGCGAGCTGCGGAGCTGATGATCCCGGCGCAAGAACTGCTATCGCATGCTGCTGCGC 246
 Db 288 CCGAGCGAGCTGCGGAGCTGATGATCCCGGCGCAAGAACTGCTATCGCATGCTGCTGCGC 347
 QY 247 TCGTCCAAGGTGGGCAAGACGCGCATGCTGTCGCGCTTCTCAGCGCGCGCTGAGAGAC 306
 Db 348 TCGTCCAAGGTGGGCAAGACGCGCATGCTGTCGCGCTTCTCAGCGCGCGCTGAGAGAC 407
 QY 307 GCTTACAGCGCTTACCATGAGAGAGCTTCCACCGCAAGTCTCTACTCCATCCGCGGAGTTC 366
 Db 408 GCTTACAGCGCTTACCATGAGAGAGCTTCCACCGCAAGTCTCTACTCCATCCGCGGAGTTC 467
 QY 367 TACAGCTGAGCATCTCTGACACAGTCCGCGCAACACCGCTTCCCGCGCATGCGCGGCTC 426
 Db 468 TACAGCTGAGCATCTCTGACACAGTCCGCGCAACACCGCTTCCCGCGCATGCGCGGCTC 527
 QY 427 TCCATCTCTACAGAGAGCTTTTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 486
 Db 528 TCCATCTCTACAGAGAGCTTTTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 587
 QY 487 GAGGAGGTGACAGCGCTGACGAGAGATCTCGACACCAAGTCTTGGCTCAGAGACAA 546
 Db 588 GAGGAGGTGACAGCGCTGACGAGAGATCTCGACACCAAGTCTTGGCTCAGAGACAA 647
 QY 547 ACCAAGAGAGAGTGGAGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 606
 Db 648 ACCAAGAGAGAGTGGAGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 707
 QY 607 TACCGGAGAGTGGAGAGAGAGATCGAGAGTGGTGGGAGAGAGAGAGAGAGAGAGAGAG 666
 Db 708 TACCGGAGAGTGGAGAGAGAGAGATCGAGAGTGGTGGGAGAGAGAGAGAGAGAGAGAG 767
 QY 667 GCTTACTTGCAGATCTGCGCGCAAGAGAGACAGCAGCTTGGACAGATGTTCCGCGGCTC 726
 Db 768 GCTTACTTGCAGATCTGCGCGCAAGAGAGACAGCAGCTTGGACAGATGTTCCGCGGCTC 827
 QY 727 TTTGCGCATGCGCAAGCTGCGCGCAAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 786
 Db 828 TTTGCGCATGCGCAAGCTGCGCGCAAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 887
 QY 787 CAGTACTGAGAGTGTCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 846
 Db 888 CAGTACTGAGAGTGTCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 947
 QY 847 AGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 906
 Db 948 AGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1007
 QY 907 CCGCGCGAGGTACACAG 966
 Db 1008 CCGCGCGAGGTACACAG 1067
 QY 967 GCCAAG 1026
 Db 1068 GCCAAG 1127
 QY 1027 TAAG 1086
 Db 1128 TAAG 1187
 QY 1087 CCGCGGAG 1146
 Db 1188 CCGCGGAG 1247
 QY 1147 AACCGAG 1206
 Db 1248 AACCGAG 1307

QY 1207 TTCCCGACCCCGGTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 1266
 Db 1308 TTCCCGACCCCGGTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 1366
 QY 1267 CAGCGGAGAGTGTATTTATCTTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1326
 Db 1367 CAGCGGAGAGTGTATTTATCTTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1426
 QY 1327 TGTGAAGTATTCAGAGCTTGTGCTAGAGCTTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAG 1386
 Db 1427 TGTGAAGTATTCAGAGCTTGTGCTAGAGCTTGTGCTGAGAGAGAGAGAGAGAGAGAGAG 1486
 QY 1387 GACCCAGGAGAGATTTATCTTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1446
 Db 1487 GACCCAGGAGAGATTTATCTTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1546
 QY 1447 TGCCTTCCCGAACTAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1506
 Db 1547 TGCCTTCCCGAACTAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1606
 QY 1507 ATGTGAGTGAAGTGAACAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1566
 Db 1607 ATGTGAGTGAAGTGAACAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1666
 QY 1567 GTGTCAACATGAGACAG 1626
 Db 1667 GTGTCAACATGAGACAG 1726
 QY 1627 CTTTAAAGTATTTGCTTATTTGTTTAAATATTAATTAATTAATTAATTAATTAATTA 1686
 Db 1727 CTTTAAAGTATTTGCTTATTTGTTTAAATATTAATTAATTAATTAATTAATTAATTA 1786
 QY 1687 AAAAAAAAAA 1698
 Db 1787 AAAAAAAAAA 1798

RESULT 2
 US-09-053-374A-3
 : Sequence 3, Application US/09053374A
 : Patent No. 6462177
 : GENERAL INFORMATION:
 : APPLICANT: YEN, KWANG-MU
 : TITLE OF INVENTION: MAMMALIAN BLOOD LOSS-INDUCED GENE, KD312
 : NUMBER OF SEQUENCES: 9
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: AMGEN INC.
 : STREET: ONE AMGEN CENTER DRIVE
 : CITY: THOUSAND OAKS
 : STATE: CA
 : COUNTRY: US
 : ZIP: 91320
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/053,374A
 : FILING DATE:
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:
 : NAME: COOK, ROBERT R.
 : REGISTRATION NUMBER: 31,602
 : REFERENCE/DOCKET NUMBER: A-514
 : INFORMATION FOR SEQ ID NO: 3:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 3986 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: DNA (genomic)


```

CITY: THOUSAND OAKS
STATE: CA
COUNTRY: US
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/053,374A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-514
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1689 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 132..971
US-09-053-374A-4

Query Match 42.2% Score 760 4; DB 4; Length 1689;
Best Local Similarity 72.3%; Pred. No. 2,7e-126;
Matches 1222; Conservative 0; Mismatches 366; Indels 102; Gaps 14;

```

```

OY 642 GTGGGCGAGAGACCCCGAGCGCTGCGCTACTTGTGAGATCTCGGCCAAGAAGAACAG 701
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 620 GTGGGCGAGATACCTTACGCTGTGCTTGTGAGATCTCGGCCAAGAAGATACAG 679
OY 702 CCGGACGAGATGTTCGCGCGGCTCTTCGCCATGGCCAGCTGCGCCAGAGATGAGCCC 761
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 680 CCGGACGAGATGTTCGCGCGGCTCTTCGCCATGGCCAGCTGCGCCAGAGATGAGCCC 739
OY 762 AGACCTGCAGCGCAAGGTCTCGGTGACAGTACGTGACGTCTGCACAAAGCGCGTGC 821
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 740 TGACTTGCAGCGCAAGGTGTGTGTGACGTACTGTGACGTCTGCACAAAGCGCTGAG 799
OY 822 GAACAAGAGCTGCTGCGGCGGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTT 881
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 800 GAACAAGAGCTTGTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTT 856
OY 882 TGCGATGTGGCACCTTCCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 941
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 857 TGCGATGTGGCGCGCTTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 916
OY 942 CGAAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1001
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 917 TGAGAAAACCAAGTGTGACAGCGAGGCTAAGGACAAAGAGCGCGCTGTGTATCAGTAA 976
OY 1002 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1057
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 977 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1036
OY 1058 AGCGCGCG-----GTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1107
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1037 TTTCCCGAGGCTTACCTGTGACCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1096
OY 1108 TCCCGGCGATCC--GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1166
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1097 TCCCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1156
OY 1167 CTGCTCGGAGAGAAAGAGAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1226
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1157 CTGCTGTGAGAGAGAA--GAACAGCTAAGACTGTGGCGCTT----- 1195
OY 1227 ATTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1286
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1196 -----CGCTCGATTTGTGGATGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 1242
OY 1287 TTCTCAAGACTTAAGAGTGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1346
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1243 TTTTTCGAGAGCTTTGAGAGTG-----TGTGAAGGCGCTTCGCGCTCT 1286
OY 1347 GCTAGGCTTAAGAAACGCTATGCGCGCTTGAGGCTGAGAGCCAGCGGCGATTATCTT 1406
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1287 G--AGACTTCAGTAACTGTGCGCGCTTGTGCGCGCGCGCGCGCGCGCGCGCGCGCT 1344
OY 1407 GTCTGTGATTCGCGGTTGTGTGACAGCGCGGTAG-----AGCTTCGCGCTCCCGAA 1458
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1345 GTCTGTGATTT--GCTGTGCGATGACCGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGAA 1403
OY 1459 ACTAAGCGGCGGCGCGTGTGCTAATCATAGCCAGTGAAGTCTGTTTACATGTGAGTAAA 1518
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1404 ACTTGTGCTGAGAGTGTGGGTTCAATCATAGCGCAACTGTTTACATGTGTGTGTGT 1463
OY 1519 CTGCAAGAGAAACACAAAGAACTTGCACTTTAAGCGTGTGCTGCTGCAACATGG 1578
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1464 GTGTATTTTACCCAAAGAGAAACAAACAAACTTGCACTTTAAGCTTTCACATGTCA 1523
OY 1579 ACAGAAACAAACCTTACACGAGTGTATACGTGTGTGTGAGGTCTTTAAAGTTAT 1638
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1524 AGCTGACATGAACAAATCTTACATTTTATTTGTGTGAGT----- 1565
OY 1639 TGTCTATTTGTTTTTATATATACATTAATTAATTAATTAATTAATTAATTAATTAAT 1698
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1566 --CTTATATATTTTATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1623
OY 1699 AAAAAAAAAA 1708

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```

; Sequence 9, Application US/08884866A
; GENERAL INFORMATION:
; APPLICANT: Chien, Shu
; TITLE OF INVENTION: GENE THERAPY IN CORONARY ANGIOPLASTY AND
; FILE REFERENCE: UCDSD100-1
; CURRENT APPLICATION NUMBER: US/08/884,866A
; PRIOR FILING DATE: 1997-06-30
; PRIOR APPLICATION NUMBER: 60/030,358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; NAME/KEY: misc_feature
; LOCATION: (49)...(51)
; OTHER INFORMATION: nnn = Any nucleic acid triplet, except for UCA,
; OTHER INFORMATION: UCC, UCG, UCU, AGC, or AGU
US-08-884-866A-9

Query Match          5.0%; Score 89.6; DB 4; Length 480;
Best Local Similarity 56.4%; Pred. No. 1.1e-07;
Matches 164; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

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RESULT 5
US-08-884-866A-10
; Sequence 10, Application US/08884866A
; GENERAL INFORMATION:
; APPLICANT: Chien, Shu
; TITLE OF INVENTION: GENE THERAPY IN CORONARY ANGIOPLASTY AND
; FILE REFERENCE: UCDSD100-1
; CURRENT APPLICATION NUMBER: US/08/884,866A
; PRIOR FILING DATE: 1997-06-30
; PRIOR APPLICATION NUMBER: 60/030,358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 450
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; NAME/KEY: misc_feature
; LOCATION: (49)...(51)
; OTHER INFORMATION: nnn = Any nucleic acid triplet, except for UCA,
; OTHER INFORMATION: UCC, UCG, UCU, AGC, or AGU
US-08-884-866A-10

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; Sequence 11, Application US/08884866A
; GENERAL INFORMATION:
; APPLICANT: Chien, Shu
; TITLE OF INVENTION: GENE THERAPY IN CORONARY ANGIOPLASTY AND
; FILE REFERENCE: UCDSD100-1
; CURRENT APPLICATION NUMBER: US/08/884,866A
; PRIOR FILING DATE: 1997-06-30
; PRIOR APPLICATION NUMBER: 60/030,358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Artificial Sequence
; NAME/KEY: misc_feature
; LOCATION: (49)...(51)
; OTHER INFORMATION: nnn = Any nucleic acid triplet, except for UCA,
; OTHER INFORMATION: UCC, UCG, UCU, AGC, or AGU
US-08-884-866A-11

Query Match          5.0%; Score 89.6; DB 4; Length 450;
Best Local Similarity 56.4%; Pred. No. 1.1e-07;
Matches 164; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

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```

; Sequence 12, Application US/08884866A
; GENERAL INFORMATION:
; APPLICANT: Chien, Shu
; TITLE OF INVENTION: GENE THERAPY IN CORONARY ANGIOPLASTY AND
; FILE REFERENCE: UCDSD100-1
; CURRENT APPLICATION NUMBER: US/08/884,866A
; PRIOR FILING DATE: 1997-06-30
; PRIOR APPLICATION NUMBER: 60/030,358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Artificial Sequence
; NAME/KEY: misc_feature
; LOCATION: (49)...(51)
; OTHER INFORMATION: nnn = Any nucleic acid triplet, except for UCA,
; OTHER INFORMATION: UCC, UCG, UCU, AGC, or AGU
US-08-884-866A-12

Query Match          5.0%; Score 89.6; DB 4; Length 450;
Best Local Similarity 56.4%; Pred. No. 1.1e-07;
Matches 164; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

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RESULT 6
US-08-884-866A-9

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; Sequence 9, Application US/08884866A
; GENERAL INFORMATION:
; APPLICANT: Chien, Shu
; TITLE OF INVENTION: GENE THERAPY IN CORONARY ANGIOPLASTY AND
; FILE REFERENCE: UCDSD100-1
; CURRENT APPLICATION NUMBER: US/08/884,866A
; PRIOR FILING DATE: 1997-06-30
; PRIOR APPLICATION NUMBER: 60/030,358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; NAME/KEY: misc_feature
; LOCATION: (49)...(51)
; OTHER INFORMATION: nnn = Any nucleic acid triplet, except for UCA,
; OTHER INFORMATION: UCC, UCG, UCU, AGC, or AGU
US-08-884-866A-9

Query Match          5.0%; Score 89.6; DB 4; Length 480;
Best Local Similarity 56.4%; Pred. No. 1.1e-07;
Matches 164; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

```

```

; Sequence 10, Application US/08884866A
; GENERAL INFORMATION:
; APPLICANT: Chien, Shu
; TITLE OF INVENTION: GENE THERAPY IN CORONARY ANGIOPLASTY AND
; FILE REFERENCE: UCDSD100-1
; CURRENT APPLICATION NUMBER: US/08/884,866A
; PRIOR FILING DATE: 1997-06-30
; PRIOR APPLICATION NUMBER: 60/030,358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 450
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; NAME/KEY: misc_feature
; LOCATION: (49)...(51)
; OTHER INFORMATION: nnn = Any nucleic acid triplet, except for UCA,
; OTHER INFORMATION: UCC, UCG, UCU, AGC, or AGU
US-08-884-866A-10

Query Match          5.0%; Score 89.6; DB 4; Length 450;
Best Local Similarity 56.4%; Pred. No. 1.1e-07;
Matches 164; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

```

```

; Sequence 11, Application US/08884866A
; GENERAL INFORMATION:
; APPLICANT: Chien, Shu
; TITLE OF INVENTION: GENE THERAPY IN CORONARY ANGIOPLASTY AND
; FILE REFERENCE: UCDSD100-1
; CURRENT APPLICATION NUMBER: US/08/884,866A
; PRIOR FILING DATE: 1997-06-30
; PRIOR APPLICATION NUMBER: 60/030,358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Artificial Sequence
; NAME/KEY: misc_feature
; LOCATION: (49)...(51)
; OTHER INFORMATION: nnn = Any nucleic acid triplet, except for UCA,
; OTHER INFORMATION: UCC, UCG, UCU, AGC, or AGU
US-08-884-866A-11

Query Match          5.0%; Score 89.6; DB 4; Length 450;
Best Local Similarity 56.4%; Pred. No. 1.1e-07;
Matches 164; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

```



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Db 2442 TGTAAATCTATTTATGTTTATTTTGTAAATTAAGATTCTTTTAACCACTGGCA 2501
QY 1662 ACAATTAATTAATTTAAATGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1721
Db 2502 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2561
QY 1722 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGGC 1754
Db 2562 AAAAAAAAAAAAAAAAAAAAAAAAAAGGGGGGC 2594

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Search completed: December 28, 2002, 05:53:08
 Job time : 96.2452 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: December 28, 2002, 01:13:57 ; Search time 76 Seconds

(without alignments)
1133.897 Million cell updates/sec

Title: US-09-709-103-2
Sequence: 1 MKIAAMIKKMCPSDSLSTP.....IRKASAGQADKRCVCIS 281

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 segs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ptn.model -DEV=xlp
-O=/cgn2_1/USPTO.spool/US09709103/runat.20122002.162406.833/app_query.fasta.1.455
-DB=Issued_Patents_NA -QEMT=fastap -SUFFIX=ptn.rn1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=ptc -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USPR=US09709103 @CEN 1.1.31 @runat.20122002.162406.833 -NCTP=6 -ICP=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMECUT=120
-WARN_TIMECUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*

1: /cgn2_6/ptodata/1/lna/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/lna/5B.COMB.seq:*
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5: /cgn2_6/ptodata/1/lna/PCTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/lna/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1449	100.0	1841	4	US-09-053-374A-1 Sequence 1, Appl1
2	1399.5	96.6	1689	4	US-09-053-374A-4 Sequence 4, Appl1
3	1387	95.7	3986	4	US-09-053-374A-3 Sequence 3, Appl1
4	1343	92.7	3079	4	US-09-053-374A-6 Sequence 6, Appl1
5	300	20.7	615	1	US-08-247-946A-5 Sequence 5, Appl1
6	300	20.7	615	1	PCT-US95-06420-5 Sequence 5, Appl1
7	279	19.3	5775	1	US-08-306-691B-15 Sequence 15, Appl1
8	279	19.3	5775	5	PCT-US93-06251-29 Sequence 29, Appl1
9	277.5	19.2	570	4	US-08-884-866A-2 Sequence 2, Appl1
10	277.5	19.2	570	4	US-08-884-866A-11 Sequence 11, Appl1
11	276	19.0	607	2	US-08-429-964-85 Sequence 85, Appl1
12	275.5	19.0	480	4	US-08-884-866A-9 Sequence 9, Appl1

13	271.5	18.7	4480	4	US-09-167-322-12 Sequence 12, Appl1
14	266.5	18.4	450	4	US-08-884-866A-10 Sequence 10, Appl1
15	266.5	18.4	574	2	US-08-429-964-83 Sequence 83, Appl1
16	265.5	18.3	2436	1	US-08-306-691B-16 Sequence 16, Appl1
17	237	16.4	2309	3	US-09-078-317-3 Sequence 3, Appl1
18	237	16.4	2309	3	US-09-078-317-3 Sequence 3, Appl1
19	234.5	16.2	600	3	US-09-454-818-3 Sequence 1, Appl1
20	234.5	16.2	600	3	US-09-454-818-3 Sequence 1, Appl1
21	219.5	15.1	563	4	US-09-385-982-426 Sequence 426, App
22	204	14.1	3497	4	US-09-503-505A-2 Sequence 2, Appl1
23	186	12.8	6453	1	US-08-306-691B-14 Sequence 14, Appl1
24	186	12.8	6453	3	US-09-209-668-10 Sequence 10, Appl1
25	186	12.8	6453	3	US-09-356-952-8 Sequence 8, Appl1
26	185.5	12.8	2964	2	US-08-846-790A-2 Sequence 2, Appl1
27	185.5	12.8	2964	3	US-08-935-333-2 Sequence 2, Appl1
28	180	12.4	702	3	US-08-842-975-2 Sequence 2, Appl1
29	180	12.4	702	3	US-09-213-397-2 Sequence 2, Appl1
30	180	12.4	702	3	US-09-213-397-2 Sequence 2, Appl1
31	177.5	12.2	1166	5	PCT-US96-12129B-1 Sequence 1, Appl1
32	175.5	12.1	603	4	US-09-325-932A-29 Sequence 29, Appl1
33	175.5	12.1	932	4	US-09-325-932A-28 Sequence 28, Appl1
34	175	12.1	1175	4	US-09-387-341-215 Sequence 215, App
35	173	11.9	1175	2	US-08-773-423-6 Sequence 6, Appl1
36	172	11.9	897	2	US-09-006-535-2 Sequence 2, Appl1
37	172	11.9	1443	1	US-08-076-089-1 Sequence 1, Appl1
38	172	11.9	1443	2	US-08-707-200-1 Sequence 1, Appl1
39	172	11.9	1443	1	US-08-996-565-1 Sequence 1, Appl1
40	172	11.9	1443	5	PCT-US93-05643-1 Sequence 1, Appl1
41	172	11.9	1525	2	US-09-006-535-1 Sequence 1, Appl1
42	167	11.5	897	2	US-09-006-535-7 Sequence 7, Appl1
43	166.5	11.5	5197	4	US-09-293-170-6 Sequence 6, Appl1
44	166	11.5	890	4	US-09-075-454-14 Sequence 14, Appl1
45	165	11.4	240	4	US-08-884-866A-8 Sequence 8, Appl1

ALIGNMENTS

RESULT 1
US-09-053-374A-1
; Sequence 1, Application US/09053374A
; Patent No. 6462177
; GENERAL INFORMATION:
; APPLICANT: YEN, KWANG-MU
; TITLE OF INVENTION: MAMMALIAN BLOOD LOSS-INDUCED GENE, KD312
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: US
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/053,374A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-514
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1841 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:

NAME/KEY: CDS
LOCATION: 255..1097
US-09-053-374A-1

Alignment Scores:

Pred. No.: 5,336-166 Length: 1841
Score: 1449.00 Matches: 281
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-709-103-2 (1-281) x US-09-053-374A-1 (1-1841)

QY 1 MetLysLeuAlaAlaMetLysLysMetCysProSerAspSerGluLeuSerIlePro 20
DB 255 ATGAAACTGGCCGATGATCAAGAGATGCGCGAGCTCGAGGTGAGTATCCG 314
QY 21 AlaLysAsnCysTyrArgMetValIleLeuGlySerSerValGlyLysThrAlaIle 40
DB 315 GCCAAGACTGCTATGCGATGCGATCGCTCGCTCCAGAGTGGCAAGCGCCATC 374
QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
DB 375 GTGTCCGCTTCTCCACCGCGCTTCCAGAGCGCTTCCACAGCTTCCAGAGCTTC 434
QY 61 HisArgLysPheTyrSerIleArgGlyValIleTyrGlnLeuAspIleLeuAspThrSer 80
DB 435 CACCGCAAGTGTACTTCATCCCGCGAGGTACCAGCTGCACTCTCCAGACGTCC 494
QY 81 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIle 100
DB 495 GGCACACACCCTTCCCGCGCATGCGCGCTCTCCATCTCCACAGAGAGCTTTCATC 554
QY 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGln 120
DB 555 CTGGTGTGCTGTGCAACCGCGACTCTTCGAGAGGTGCAAGCGCTCGACGCGAG 614
QY 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGlnAsnValAspValProLeu 140
DB 615 ATCTCTGCACCAAGTCTTCTCCAGAGAACCAAGAGAGAGTGGAGCGTCCGCTG 674
QY 141 ValIleCysGlyAsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIle 160
DB 675 GTCATCTGCGCAAGAGGTGACCGGACTTCTACCGCGAGGTGAGCACGCGCAGATC 734
QY 161 GlnGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLys 180
DB 735 GAGCAGCTGTGGGCGAGCGACCCCGCGCTGCTACTTCCAGATCTGGCCCAAGAG 794
QY 181 AsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGln 200
DB 795 AACGAGCGCTGGACGAGATGTTCCGCGCTTTCGCCATGGCCAAAGTGGCCACGAG 854
QY 201 MetSerProAspLeuHisArgLysValSerValGlnTyrCysAspValLeuHisLysLys 220
DB 855 ATGAGCCCAACCTGCACCGCCAGAGTCTCGGTGCAAGTGCAGCGTGCACAGAGAG 914
QY 221 AlaLeuArgAsnLysLysLeuLeuArgAlaGlySerGlyLysGlyLysGlyLysProGly 240
DB 915 GCGCTGGGAGCAAGAGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 974
QY 241 AspAlaPheGlyIleValAlaProPheAlaArgProSerValHisSerAspLeuMet 260
DB 975 GAGCGCTTGGCATCGTGGCGACCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCTCATG 1034
QY 261 TyrIleArgGlyLysLysAlaSerAlaGlySerGlnAlaLysAspLysGlyLysValIle 280
DB 1035 TACATCGCGAGAGCGCGAGCGCGCGAGCGCAAGAGCAAGAGCGCTGCTGATC 1094
QY 281 Ser 281
DB 1095 AGC 1097

RESULT 2

US-09-053-374A-4

Sequence 4, Application US/09053374A

Patent No. 6462177

GENERAL INFORMATION:

APPLICANT: YEN, KWANG-MU

TITLE OF INVENTION: MAMMALIAN BLOOD LOSS-INDUCED GENE, KD312

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: AMGEN INC.

STREET: ONE AMGEN CENTER DRIVE

CITY: THOUSAND OAKS

STATE: CA

COUNTRY: US

ZIP: 91320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/053,374A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: COOK, ROBERT R.

REGISTRATION NUMBER: 31,602

REFERENCE/DOCKET NUMBER: A-514

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1689 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 132..971

US-09-053-374A-4

Alignment Scores:

Pred. No.: 4,746-160 Length: 1689
Score: 1399.50 Matches: 273
Percent Similarity: 98.22% Conservative: 3
Best Local Similarity: 97.15% Mismatches: 4
Query Match: 96.58% Indels: 1
DB: Gaps: 1

US-09-709-103-2 (1-281) x US-09-053-374A-4 (1-1689)

QY 1 MetLysLeuAlaAlaMetLysLysMetCysProSerAspSerGluLeuSerIlePro 20
DB 132 ATGAAACTGGCCGATGATCAAGAGATGCGCGAGCTCGAGGTGAGTATCCG 191
QY 21 AlaLysAsnCysTyrArgMetValIleLeuGlySerSerValGlyLysThrAlaIle 40
DB 192 GCCAAGACTGCTATGCGATGCGCTCGCTCCAGAGTGGCAAGCGCGCATC 251
QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
DB 252 GTGTCCGCTTCTCCACCGCGCTTCCAGAGCGCTTTCACACCTTGAAGACTTC 311
QY 61 HisArgLysPheTyrSerIleArgGlyValIleTyrGlnLeuAspIleLeuAspThrSer 80
DB 312 CACCGCAAGTGTACTGATCGATCGCGCGAGAGTCTACACAGTTGACATCTGACACATCT 371
QY 81 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIle 100
DB 372 GGCATCATCTCCGTCATGCGCGAGCGCGCTCTCTATCTTACAGAGAGCTTTTCATT 431
QY 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGln 120

Db 432 CTGGTGTTCAGCTTAGACACCGGACCTCTTCAGAGAGGTGCAAAAGGCTCAACAGCAG 491
 QY 121 ILeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeu 140
 Db 492 ATCTAGACACCAAGTCTCTCTCAGAAACCAAGAGATGTGGAGCTGCCGCTG 551
 QY 141 ValIleCysGlyAsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIle 160
 Db 552 GTCAATTGCGGTAAACAAGGGGACCGGACTTCTACCGCGAAGGAGGACGCGGAGATT 611
 QY 161 GluGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLys 180
 Db 612 GAGACAGCTGGTGGCGATGACCCGACGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 671
 QY 181 AsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLysLeuProSerGlu 200
 Db 672 AATGACGACCTGGACACGAGATGTTCCGTGCGCTCTTCCATGGCCCAAGCTGCTAGCGAG 731
 QY 201 MetSerProAspLeuHisAspGlyValSerValGlnTyrCysAspValIleHisLysLys 220
 Db 732 ATGAGCCCTGACTTGCACCCGACAGGTCTGTGTGCACTGTGACGTGTGCAACAAAG 791
 QY 221 AlaLeuArgAsnLysLysLeuLeuArgAlaGlySerGlyGlyGlyGlyAspProGly 240
 Db 792 GCTCTGAGAAACAAGAGCTTCTGCGTGGCGGACG---GGAGGTGGGGGCGACACGGA 848
 QY 241 AspAlaPheGlyIleValAlaProPheAlaArgArgProSerValHisSerAspLeuMet 260
 Db 849 GATGCTTTGGCATCTTGGGCGCTTGTCTGTGCGACCTGACCTGCTATGCGACCTCATG 908
 QY 261 TyrIleArgGluLysAlaSerAlaGlySerGlnAlaLysAspLysGluValIle 280
 Db 909 TACATTGCTGAGAAACCACTGTTCAGCAGCAGGCTTAAGCAAGGAGCGCTGTGTATC 968
 QY 281 Ser 281
 Db 969 AGT 971

RESULT 3

US-09-053-374A-3
 Sequence 3, Application US/09053374A
 Patent No. 6462177
 GENERAL INFORMATION:
 APPLICANT: YEN, KWANG-MU
 TITLE OF INVENTION: MAMMALIAN BLOOD LOSS-INDUCED GENE, KD312
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: AMGEN INC.
 STREET: ONE AMGEN CENTER DRIVE
 CITY: THOUSAND OAKS
 STATE: CA
 COUNTRY: US
 ZIP: 91320
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/053,374A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: COOK, ROBERT R.
 REGISTRATION NUMBER: 31,602
 REFERENCE/DOCKET NUMBER: A-514
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3986 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)

US-09-053-374A-3
 Alignment Scores:
 Pred. No.: 5, 53e-158
 Score: 1387.00
 Percent Similarity: 79.83%
 Best Local Similarity: 79.83%
 Query Match: 95.72%
 DB: 4
 Gaps: 1
 US-09-709-103-2 (1-281) x US-09-053-374A-3 (1-3986)
 QY 1 MetLysLeuAlaIleMetIleLysMetCysProSerAspSerGluLeuSerIlePro 20
 Db 774 ATGAACCTGGCCCGCATGATCAAGAAAGATGTGCCAGGACATCGAGCTGATTCGG 833
 QY 21 AlaLysAsnCysTyrArgMetValIleGluGlySerSerLysValGlyLysThrAlaIle 40
 Db 834 GCCAAGACTGCTATGTCATGTGTCATCTCGGCTGCTCCAAAGGTGGCAAGACGGCATC 893
 QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspHe 60
 Db 894 GTGTCCGCTTCTCTACCGGCGCTTTCAGAGAGGCTTACACGCTTACACCTTACAGAGACTTC 953
 QY 61 HisArgLysPheTyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSer 80
 Db 954 CACCGCAAGTTCATCTCCATCCGCGGAGGTCCTACACCTGACATCTCTGACACGCTTC 1013
 QY 81 GlyAsnHisProPheProAlaMetArgLysSerIleLeuThr----- 95
 Db 1014 GGCACACCCCGTCCCGCCCATGGGCGCTCTCATCTCTCAGGTGAGCCGGGGGCC 1073
 QY 95 ----- 95
 Db 1074 GGGCAGTGGGGAGGAGGAGGGCGGGAACCTCGGCCAGGGCGCCCGCAGCGCGCT 1133
 QY 95 ----- 95
 Db 1134 CCGGCTGCTGGCGCCGAGTAGTGGCTTCCGGCTTAGAGAGCTAAGCGCGCCCGCGCG 1193
 QY 95 ----- 95
 Db 1194 GCCTCAAGTACGCCGACTTGTCCCTGGGGGCGCACCTCACCCTTCTCTTCTGCT 1253
 QY 96 ----- 95
 Db 1254 CTCTGCCCCCTCAGAGAGAGCTTTTCATCTGTGTCTGCTGACCAACCGGACTTC 1313
 QY 110 PheGluGluValGlnArgLeuArgGlnIleLeuAspThrLysSerCysLeuLysAs 130
 Db 1314 CTTTCAGAGAGGTGACAGCGGCTCAGCAGACATCTCGACACCAAGTCTTGCCTCAAGAA 1373
 QY 130 nLysThrLysGluAsnValAspValProLeuValIleCysGlyAsnLysGlyAspArgAs 150
 Db 1374 CAAGAACCAAGGAGAGAGAGGTGAGCTGCCCTGTCTCTGCGGCAACAAGGTGACCGGGA 1433
 QY 150 PheTyrArgGluValAspGlnArgGluIleGluGlnLeuValGlyAspAspProGlnArg 170
 Db 1434 CTTTACCGCGAGGTGAGCAAGCGGAGATGAGAGCTGTGTGGCGACGACCCCGACCG 1493
 QY 170 GcysAlaTyrPheGluIleSerAlaLysLysAsnSerSerLeuAspGlnMetPheArgAl 190
 Db 1494 CTTCGCTTCTGCTGAGATCTGCGCCCAAGAAAGACGAGCTTCCGCGGC 1553
 QY 190 AlaPheAlaMetAlaLysLeuProSerGlnMetSerProAspLeuHisArgLysValSe 210
 Db 1554 GCTCTTCCCATGCGCAAGCTGCGCAGGAGATGAGCCCAACCTGACCGCAAGGCTC 1613
 QY 210 rValGlnTyrCysAspValLeuHisLysLysAlaLeuArgAsnLysLysLeuLeuArgAl 230
 Db 1614 GGTGAGTACTGCGACGTCGTGCAACAAGAGCGCTGTGGGCAACAAGAGCTGCGCGGC 1673
 QY 230 aGlySerLysLysGlyGlyAspProGlyAspAlaPheGlyIleValAlaProPheAl 250

Db	1674	CGCGAGCGGGGGGGGGGGCGCGACCGCCCTTGGCATGCTGGACACCTTCGC	1733
Qy	250	atgatagtproservalhisseraspleumettyrlleatrgglulysalaserflaglyse	270
Db	1734	GGCGGGGGCCGCGCTTACAGCGACGCTCAATGTCATTCGCGGAAAGCCAGCGCGCGAG	1793
Qy	270	rgllalalalsaplysglulargcysvalilleser	281
Db	1794	CCAGGCCAAGACAGAGAGCGGCTGCGTCAATCAC	1827
RESULT 4			
US-09-053-374A-6			
; Sequence 6, Application US/09053374A			
; Patent No. 6462177			
GENERAL INFORMATION:			
APPLICANT: YEN, KWANG-MU			
TITLE OF INVENTION: MAMMALIAN BLOOD LOSS-INDUCED GENE, KD312			
NUMBER OF SEQUENCES: 9			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: AMGEN INC.			
STREET: ONE AMGEN CENTER DRIVE			
CITY: THOUSAND OAKS			
STATE: CA			
COUNTRY: US			
ZIP: 91320			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Patent Release #1.0, Version #1.30			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/09/053,374A			
FILING DATE:			
CLASSIFICATION: 435			
ATTORNEY/AGENT INFORMATION:			
NAME: COOK, ROBERT R.			
REGISTRATION NUMBER: 31,602			
REFERENCE/DOCKET NUMBER: A-514			
INFORMATION FOR SEQ ID NO: 6:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 3079 base pairs			
TYPE: nucleic acid			
STRANDEDNESS: single			
TOPOLOGY: linear			
MOLECULE TYPE: DNA (genomic)			
US-09-053-374A-6			
Alignment Scores:			
Pred. No.: 8,2e-153			
Score: 1343.00			
Percent Similarity: 84.10%			
Best Local Similarity: 83.18%			
Query Match: 92.68%			
DB: 4			
Gaps: 2			
US-09-709-103-2 (1-281) x US-09-053-374A-6 (1-3079)			
Qy	1	Mettlyslenuallalameilllyslslysmetysproseraspserglulenusertllepro	20
Db	303	ATGAAACATCGCGCGCATGATCAAGAAAGATGTGCCCAAGCAGCTTCGTGACGTGAGATTC	362
Qy	21	AtAlasAsnCysTyARMeTValIlleuNlysSerSerlySValGlySThAlaIle	40
Db	363	GCCAAAGACTGCTACAGATGTCTATCTCGGCTCATCCAAAGTGGGCAAGACGGC	422
Qy	41	ValSerArgpHeLeuThrGlyARgPheGlulAspaLarThrProThrIleGluaspHe	60
Db	423	GGTGGCGGCTTCTACAGCGCGGCTTCGAGGACGCTTACACCCCTACCATTTGAAGCTTC	482
Qy	61	HisArgGlypHtySerIleArgGlyGluValTyrgInleuAspIleAspThrSer	80
Db	483	CACCGAAATTTTACTCGATCGCGGCGCAAGTGTACCAATTGGACATACTGGACACATCT	542

OY	81	Glysnhisproheprialmetatargleusertile-----	93
Db	543	GCGATCATCCGTTTCCCCGCATGGGGCGCTCTATTCTTCACAGGTAGTGGGAGACC	602
OY	93	-----	93
Db	603	GACAGGACCGTGGGAGGGAATCTCGGGGAGCGGATGGCGGTGTTGTGCTTGG	662
OY	94	-----leu 94	
Db	663	GCTGTGCTGTGCTGCTGCTCCGTGCTTGGAGCTGCCCTTCACCTTTTCACCTGCTCCCTTG	722
OY	95	ThrglyaspvalPheilleuleValIpheSerleuAspasnArgasPserPheglugluVal	114
Db	723	TA-GGAGACGTTTCACTTCGTGTGTTCACGTTTAGACAACCGGACTCCTTGGAGSAGTG	781
OY	115	GlnargleuarnglnglnlleleuasprhrLysSerCysLeuLyAsnlysthrLysGlu	134
Db	782	CAAAGGCTCAACAGCAGATCTAGCACCAACCAAGTCTGTCAAAACAAAACCAAAAG	841
OY	135	AsnValaspValProleuValIIecysglyAsnlysglyAsparAspPheThrArgIu	154
Db	842	AATGGAGCGTGGCGGTGGTCATTTCGGGTAAACAAAGSGGAGCCGGAGACTTCTACCGCGAA	901
OY	155	ValaspcInarngluillegluginleuValIyAspaSPProglinarGcysAlatyRhe	174
Db	902	GTGGAGCGAGGGGAGATTGAGACAGCTGTGTGGCGGATGACCTCTACGCTTGTCCCTAC	961
OY	175	GluIleSerAlalyLysAsnSerSerleuAspBclMetPheargAlaleuPhealMet	194
Db	962	GAGATCTCGCCCAAGAAGATAGACAGCTGTGACCAAGATCTTCCGGCGCTCTTTGCCATG	1021
OY	195	AlalyseurProsergImetsetProAspleuHIsArgLyValserValIdIntryCs	214
Db	1022	GCCAAGCTGCTTACCGAGATAGCCCTGACTTCACCGCAAGGTGTCTGTGCAGTACTGT	1081
OY	215	AspValleuHIsLysLysAlaleuArGAsnLysLysLeuLeuArlaGlYserGlyGly	234
Db	1082	GACGTGCTGCACAAAAAGCGCTGAGGAACAAGACTTCTGGGTGGGAGC---GGA	1138
OY	235	GlylglyLysAPProglYasPalaPheGlyIlleValAlaProPheAlaArgProser	254
Db	1139	GGTGGGGCGACCAAGGAGATGCTTTGGCATCTTGGCGCCCTTTGCTGCGAGACTTAGC	1198
OY	255	ValHisserAPleuMetTryrIleArgGlyLysAlaserAlaglySerGlnAlaLysASP	274
Db	1199	GTGCACTACGACCTCATGTACTTCGTGAGAAAAACGAGTGTACGACCGCAGGCTTAAGAC	1258
OY	275	LysGIuaRGcysValIIeser 281	
Db	1259	AAGGAGCGCTGTGTCAATCAGT 1279	
RESULT 5			
US-08-247-946A-5			
Sequence 5, Application US/08247946A			
Patent No. 5792638			
GENERAL INFORMATION:			
APPLICANT: AARONSON, S.A.; CHAN, A.;			
APPLICANT: MIKI, T.			
TITLE OF INVENTION: NOVEL HUMAN RAS-RELATED			
TITLE OF INVENTION: ONCOGENES UNMASKED BY EXPRESSION OF CDNA			
NUMBER OF SEQUENCES: 11			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: MORGAN & FINNEGAN			
STREET: 345 PARK AVENUE			
CITY: NEW YORK			
STATE: NEW YORK			
COUNTRY: USA			
ZIP: 10154			
COMPUTER READABLE FORM:			
MEDIUM TYPE: FLOPPY DISK			


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Qy      145 AsnIlysgAsPAdgAsPhetYArGluInValAspGlnArGluITLeGlunGlnLeuVal 164
Db      379 AATAAGACAGATCTCGATCATCAACAAGACAGGTAAACACAGGAAGAAGACACACTTGCA 438
Qy      165 GlyspAsPProGlnAagCyAlAtYrPhelGluIleSerAlaLysLysAsnSerSerLeu 184
Db      439 CGGCAG-----CTTAAGGTAACTACATGGAGGACATCAGCAAGAATTAGATGAATGTA 492
Qy      185 AspGlnMetPheatrgAlaLeuPheAlaMeFAlaLysLeuProSerGIumet----- 201
Db      493 GATCAAGCTTTCATGCAATGCTGTCGGGGTTATTCAGAAATTTCAGAACAGAGAAATGTCT 552
Qy      202 ---SerProaspLeuHIsArgLys 208
Db      553 CCTTCACCACGAACCAACACGGAAA 576

RESULT 6
PCT-US95-06420-5
; Sequence 5, Application PC/TUS9506420
; GENERAL INFORMATION:
; APPLICANT: AARONSON, S.A.; CHAN, A.;
; APPLICANT: MIKI, T.
; TITLE OF INVENTION: NOVEL HUMAN RAS-RELATED
; TITLE OF INVENTION: ONCOGENES UNMASKED BY EXPRESSION OF CDNA
; TITLE OF INVENTION: CLONING
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06420
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/247,946
; FILING DATE: 24-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. ADTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4150PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 615
; TYPE: Nucleic acid
; STRANDEDNESS: Double
; TOPOLOGY: Unknown
; MOLECULE TYPE: cDNA
; HYPOCHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; FEATURE:

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Db 649 GATGATCCCTCTCATACATTAGTTCGAGAAATTCGAAACATTAAGAAAGATGACGACAA 708
 Oy 204 AspleuHisArgLys 208
 Db 709 GATGTAAGAAAAAGAG 723

RESULT 8

PCT-US93-06251-29
 ; Sequence 29, Application PC/TUS9306251

GENERAL INFORMATION:

APPLICANT: Wicksstrom, Eric and Rife, Jason P.

TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing

TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates

NUMBER OF SEQUENCES: 93

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCULLY, SCOTT MORPHY & PRESSER

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: NY

COUNTRY: USA

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/06251

FILING DATE: 19930630

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Digiglio, Frank S.

REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 8586

TELECOMMUNICATION INFORMATION:

TELEPHONE: 516-742-4343

TELEFAX: 516-742-4366

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 5775 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

PCT-US93-06251-29

Alignment Scores:

Pred. No.: 2.37e-23

Score: 279.00

Percent Similarity: 54.59%

Best Local Similarity: 36.22%

Query Match: 19.25%

DB: 5

Gaps: 4

US-09-709-103-2 (1-281) x PCT-US93-06251-29 (1-5775)

Oy 25 TyrArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIleValSerArgPhe 44

Db 202 TATAAAGCTTGGTGGTGGAGCTTGGCGGAGGCAAGAGTGGCTTACGATACAGCTA 261

Oy 45 LeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPheHisArgLysPhe 64

Db 262 ATTCAGAAATCATTTTGTGGAGCAATATGATCCACAAATAGAGATTCCTACAGAAAGCA 321

Oy 65 TyrSerIleArgGlyGluValLysGlnLeuAspIleLeuAspThrSerGlyAsnHisPro 84

Db 322 GTAGTAATGATGAGAAACCTGCTCTTGGATATTCGACACAGCAGGTCACAGAGAG 381

Oy 85 PheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSer 104

Db 382 TACAGTCAATGACGAGACACAGTACATGAGAGACTGGGAGGCGCTTCTTGTGCTATTGCC 441

Oy 105 LeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnIleLeuAspThr 124
 Db 442 ATAAATATACATAATCATTTGAAGATATTCACCATTAATAGAAACAAT----- 492
 Oy 125 LysSerCysLeuLysAsnLysThrGlyGlnAsnValAspValProLeuValIleCysGly 144
 Db 493 -----AAAAGATTAGGAGCTGTGAAGATGTAAGTACTATGCTCTCTAGAGA 537

Oy 145 AsnLysGlyAspArgAspPheLysArgLysValAspGlnArgLysIleGluGlnLeuVal 164

Db 538 ATAAATGATGATTTGCTCTTGAAGATATTCACCATTAATAGAAACAAT----- 594

Oy 165 GlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysAsnSerLys 184

Db 595 AGAAGT-----TATGAATTCCTTTTATGAAACATCAGAAAAGAACAGAGAGGTT 648

Oy 185 AspGlnMetPheArgAlaLeuPhe---AlaMetAlaLysLeuProSerGlnMetSerPro 203

Db 649 GATGATCCCTCTCATACATTAGTTCGAGAAATTCGAAACATTAAGAAAGATGACGACAA 708

Oy 204 AspleuHisArgLys 208

Db 709 GATGTAAGAAAAAGAG 723

RESULT 9

US-08-884-866A-2

; Sequence 2, Application US/0884866A

GENERAL INFORMATION:

APPLICANT: Chien, Shu

APPLICANT: Shyu, John Y-J

TITLE OF INVENTION: GENE THERAPY IN CORONARY ANGIOPLASTY AND

TITLE OF INVENTION: BYPASS

FILE REFERENCE: US/08/884,866A

CURRENT FILING DATE: 1997-06-30

PRIOR APPLICATION NUMBER: 60/030,358

PRIOR FILING DATE: 1996-11-08

NUMBER OF SEQ ID NOS: 25

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO: 2

LENGTH: 570

TYPE: DNA

ORGANISM: Rattus norvegicus

FEATURE:

NAME/KEY: CDS

LOCATION: (1)...(570)

US-08-884-866A-2

Alignment Scores:

Pred. No.: 1.18e-24

Score: 277.50

Percent Similarity: 53.23%

Best Local Similarity: 36.32%

Query Match: 19.15%

DB: 4

Gaps: 6

US-09-709-103-2 (1-281) x US-08-884-866A-2 (1-570)

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Oy 65 TyrSerIleArgGlyGluValLysGlnLeuAspIleLeuAspThrSerGlyAsnHisPro 84

Db 130 GTGTCATTTATGAGGAGAGAGTGGCTGTGGAATCTCGATACCCGCGCTGAGAGAG 189

Oy 85 PheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSer 104

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RESULT 15
US-08-429-964-83
; Sequence 83, Application US/08429964
; Patent No. 5962243
GENERAL INFORMATION:
APPLICANT: BROWN, MICHAEL S.
APPLICANT: GOLDSTEIN, JOSEPH L.
APPLICANT: REISS, YUVAL
APPLICANT: JAMES, GUY L.
TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF FARNESYL
TITLE OF INVENTION: TRANSFERASE INHIBITORS
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: UNITED STATES OF AMERICA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,964
FILING DATE: 27-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/021,625
FILING DATE: 16-FEB-1993
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/822,011
FILING DATE: ABANDONED
CLASSIFICATION: 435
APPLICATION NUMBER: PCT/US/91/02650
FILING DATE: 18-APR-1991
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/615,715
FILING DATE: 20-NOV-1990
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/510,706
FILING DATE: 18-APR-1990 (ABANDONED)
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: USPD-432/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 769-2679
TELEX: 79-0924

QY 25 TYA¹RMET¹VAL¹ILEU¹GLYSER¹LYS¹VAL¹GLYS¹TH¹LEU¹VAL¹SER¹ARG¹HE 44
 |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||::: 45
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[illegible]

Search completed: December 28, 2002, 02:48:53
Job time : 87 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 28, 2002, 02:13:37 ; Search time 2147.44 Seconds

(without alignments)
11465.267 Million cell updates/sec

Title: US-09-709-103-1

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Scoring table:

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	846	100.0	846	AF498923	AF498923 Homo sapi
2	846	100.0	979	AF172846	AF172846 Homo sapi
3	846	100.0	1740	AF069506	AF069506 Homo sapi
4	846	100.0	1758	BC018041	BC018041 Homo sapi
5	838	99.1	1187	AF153192	AF153192 Homo sapi
6	835	98.7	1746	AF177335	AF177335 Homo sapi
7	678	80.1	1612	BC034166	BC034166 Homo sapi
8	678	80.1	1616	AF239157	AF239157 Mus muscu
9	676.4	80.0	1623	AF009246	AF009246 Mus muscu
10	625	73.9	4990	AF222979	AF222979 Homo sapi
11	625	73.9	18334	AC020558	AC020558 Homo sapi
12	623.4	73.7	5141	AF262018	AF262018 Homo sapi
13	609.4	72.0	58882	AC073621	AC073621 Homo sapi
14	607.8	71.8	183598	AC090608	AC090608 Homo sapi
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17	407.4	48.2	2832	AX393244	AX393244 Sequence
18	407.4	48.2	2832	AF279143	AF279143 Homo sapi
19	407.4	48.2	2973	AX393267	AX393267 Sequence
20	407.4	48.2	3058	BC013419	BC013419 Homo sapi
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22	359.6	42.5	3469	AF134409	AF134409 Rattus no
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35	125.8	14.9	1249	AX430295	AX430295 Sequence
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37	113.6	13.4	2145	AB062937	AB062937 Homo sapi
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ALIGNMENTS

RESULT 1
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LOCUS AF498923
DEFINITION Homo sapiens activator of G protein signaling (RASD1) mRNA,
complete cds.
ACCESSION AF498923
VERSION AF498923.1 GI:20379021
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 846)
AUTHORS Publ.H.L., Ikeda,S.R. and Aronstam,R.S.
TITLE Direct Submission

JOURNAL Submitted (05-Apr-2002) cDNA Resource Center, Guthrie Research Institute, One Guthrie Square, Sayre, PA 16840, USA

FEATURES
Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 1.1e-103; Mismatches 0; Indels 0; Gaps 0;
Matches 846; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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LOCUS Homo sapiens ras-related protein (DEXRAS1) mRNA, complete cds.
DEFINITION
AF172846
AF172846.1 GI:6014488
KEYWORDS
SOURCE
ORGANISM
Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 979)
Tu Y. and Wu C.
Cloning, expression and characterization of a novel human
ras-related protein that is regulated by glucocorticoid hormone
Biochim. Biophys. Acta 1489 (2-3), 452-456 (1999)
MEDLINE
20135605
PUBMED
10673050
REFERENCE
2 (bases 1 to 979)
Tu Y. and Wu C.
Direct Submission
Submitted (27-JUL-1999) Department of Cell Biology, University of
Alabama at Birmingham, 1670 University Blvd., Birmingham, AL 35294,
USA

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BASE COUNT 195 a 347 c 284 g 153 t
ORIGIN

Query Match 100.0%; Score 846; DB 9; Length 979;
Best Local Similarity 100.0%; Pred. No. 1.1e-103; Mismatches 0; Indels 0; Gaps 0;
Matches 846; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
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 ACCESSION AF069506
 VERSION AF069506.1 GI:4959037
 KEYWORDS
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 Cismowski, M.J., Takesono, A., Ma, C., Lizano, J.S., Xie, X.,
 Fuenkranz, H., Lanier, S.M., and Duzic, E.
 Genetic screens in yeast to identify mammalian nonreceptor

modulators of G-protein signaling
 Nat. Biotechnol. 17 (9), 878-883 (1999)
 MEDLINE 9940338
 PUBMED 10471929
 REFERENCE 2 (bases 1 to 1740)
 AUTHORS Cismowski, M.J., Fuenkranz, H., Ma, C., Spruyt, M., Xie, X.,
 Lanier, S.M., and Duzic, E.
 TITLE Direct Submission
 JOURNAL Submitted (01-JUN-1998) Receptor Pharmacology/Biochemistry, Cadus
 Pharmaceutical Corporation, 777 Old Saw Mill River Rd., Tarrytown,
 NY 10591, USA

FEATURES
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 Best Local Similarity 100.0%; Pred. No. 9.8e-104;
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Db 626 GAGCAGCTGTGGCGAGACCCAGCGCTGCTACTTCGATCTCGCGCAAGAG 685
QY 541 AACAGCAGCTCGACAGATGTTCCGGCGCTCTTCGCCATGGCCAGCTGCCAGGAG 600
Db 686 AACAGCAGCTCGACAGATGTTCCGGCGCTCTTCGCCATGGCCAGCTGCCAGGAG 745
QY 601 ATGAGCCAGACCTGACAGCCGCAAGGTCGCTGACATGACGACGTCGACAGAG 660
Db 746 ATGAGCCAGACCTGACAGCCGCAAGGTCGCTGACATGACGACGTCGACAGAG 805
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QY 721 GAGCGCTTGGCATCGTGGCGACCTTGGCGCGCGCGCGCGCGCGCGCGCGCG 780
Db 866 GAGCGCTTGGCATCGTGGCGACCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCG 925
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Db 986 AGCTAG 991

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RESULT 4
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ACCESSION BC018041
VERSION BC018041.1 GI:17390075
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1758)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (03-DEC-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcdgexil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
 Series: IRAC Plate: 32 Row: f Column: 11.
 Location/Qualifiers

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DB	1053	AGCTAG 1058	
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ACCESSION	AF153192		
VERSION	AF153192.1	GI:4960166	
KEYWORDS			
SOURCE			
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	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 1187)		
AUTHORS	Kempainen,R.J.		
TITLE	Identification of human pituitary Dextral		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1187)		
AUTHORS	Kempainen,R.J.		
TITLE	Direct Submission		
JOURNAL	Submitted (20-MAY-1999) Anatomy & Physiology, Auburn University,		
	College of Veterinary Medicine, Auburn, AL 36849, USA		
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DB	61	GCCAGAGACTCTATCGATGATGTCATCTCGGCTGTCGCAAGTGGGCAAGCGGCATC	120
QY	121	GTGTGCGCTTCTCACCGCGCGCTTCGAGAGCGGCTACAGCGCTACCATCGAGACTTC	180
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DB	241	GGCAACACACCGTTCCCGCCATGGGGGCGCTCTCTCATCTTCACAGGAGAGAGCTTTTCAC	300

OY		301	CTGGGTTCAGTCTGGAACCGGCATCTCTCCAGAGAGTGACAGCGCTCAGGAGAG	360
Db		301	CTGGGTTCAGTCTGGAACCGGCATCTCTCCAGAGAGTGACAGCGCTCAGGAGAG	360
OY		361	ATTCCTGACACCAGTCTTGCTCAAGAACAACCAAGAGAGAACGTGGAGTGCCTTG	420
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OY		421	GTCATCTGCGGGCAACAAGGTGACCGGCACACTTCTACCGGAGGTGGACAGCGCAATC	480
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DEFINITION		Homo sapiens clone SP1942 unknown mRNA.	Linear	PRI 03-OCT-2000
ACCESSION		AF177335		
VERSION		AF177335.1		GI:10503968
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SOURCE				
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REFERENCE		1 (bases 1 to 1746)		
AUTHORS		Gu,J.R., Wan,D.F., Zhao,X.T., Zhou,X.M., Jiang,H.Q., Zhang,P.P., Qin,W.X., Huang,Y., Qiu,X.K., Qian,L.F., He,L.P., Li,H.N., Yu.Y., Yu.J. and Han,L.H. Novel human cDNA clone with function of inhibiting cancer cell growth		
TITLE		Unpublished 2 (bases 1 to 1746) Gu,J.R., Wan,D.F., Zhao,X.T., Zhou,X.M., Jiang,H.Q., Zhang,P.P., Qin,W.X., Huang,Y., Qiu,X.K., Qian,L.F., He,L.P., Li,H.N., Yu.Y., Yu.J. and Han,L.H. Direct Submission Submitted (06-AUG-1999) National Laboratory For Oncogenes & Related Genes, Shanghai Cancer Institute, 25/Ln 2200 Xie Tu Road, Shanghai 200032, P.R. China Location/Qualifiers 1. 1746 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="SP1942"		
JOURNAL				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
FEATURES				
SOURCE				

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BASE COUNT 388 a 569 c 496 g 293 t

ORIGIN

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 Best Local Similarity 99.9%; Pred. No. 2.3e-102;
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RESULT 7
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 ACCESSION IMAGE:4989312, mRNA, complete cds.
 BC034166
 KEYWORDS BC034166.1 GI:21706874
 MGC.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 1612)
 Strausberg, R.
 Direct Submission
 Submitted (02-JUL-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mdedpaxil@stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

FEATURES

source

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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 This clone was selected for full length sequencing because it
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CDS

BASE COUNT 417 a 424 c 420 g 351 t

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RESULT 8
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 ACCESSION AF239157
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 ORGANISM Rattus norvegicus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 Rattus.
 1 (bases 1 to 1616)
 Fang, M., Jaffrey, S.R., Sawa, A., Ye, K., Luo, X. and Snyder, S.H.
 Dextrasi: a G protein specifically coupled to neuronal nitric oxide

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JOURNAL synthase via CAPON
MEDLINE Neuron 28 (1), 183-193 (2000)
PUBMED 20537828
REFERENCE 11086993
AUTHORS 2 (bases 1 to 1616)
TITLE Fang, M., Jaffrey, S.R., Sawa, A., Ye, K. and Snyder, S.H.
JOURNAL Direct Submission
SUBMITTED (24-FEB-2000) Neuroscience, Johns Hopkins University, 725
N. Wolfe St, Baltimore, MD 21205, USA
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BASE COUNT 403 a 436 c 413 g 363 t 1 others
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Query Match 80.1%; Score 678; DB 10; Length 1616;
Best Local Similarity 88.4%; Pred. No. 2.3e-81;
Matches 748; Conservative 0; Mismatches 95; Indels 3; Gaps 1;
QY 1 ATGAAACTGCGCGGCGGCTGCTCAAGAGATGTCGCCGAGCTCGAGCTGATATCCG 60
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VERSION	AF009246.1	GI:2253712		
KEYWORDS				
SOURCE	Mus musculus.			
ORGANISM	Mus musculus			
REFERENCE	1 (bases 1 to 1623)			
AUTHORS	Kempainen,R.J. and Behrend,E.N.			
TITLE	Dexamethasone rapidly induces a novel ras superfamily member-related gene in AtT-20 cells			
JOURNAL	J. Biol. Chem. 273 (6), 3129-3131 (1998)			
MEDLINE	98123070			
PUBMED	9452419			
REFERENCE	2 (bases 1 to 1623)			
AUTHORS	Kempainen,R.J. and Behrend,E.N.			
TITLE	Direct Submission			
JOURNAL	Submitted (18-JUN-1997) Physiology & Pharmacology, Auburn University College of Veterinary Medicine, 213 Greene Hall, Auburn, AL 36849, USA			
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QY	361	ATCCTCGCACACCAAGCTCTGCTCAAGAAACAACCAAGGAAGAACGATGAGCTGGCCGCTG	420	
Db	502	ATCCCTAGACACCAAGTCCCTGTCTCAAGAAACAACCAAGGAAGATGTGAGCTGCCGCTG	561	
QY	421	GTCATCTGGGCGCACAAAGGTGACCGCGCACTTCTACCGGAGGTGAGACCGCGGAGATC	480	
Db	562	GTCATTTGGGCTTACAAAGGGGAGCCGGGCACTTCTACCGGAGGTGAGACCGCGGAGATTC	621	
QY	481	GAGCAGCTGTGTGGGAGAGACCCGAGCGCTGCGCTCTTCTGCATCTCGGCGCAAGAAAG	540	
Db	622	GAGCAGCTGTGTGGGAGAGACCCGAGCGCTGCGCTCTTCTGCATCTCGGCGCAAGAAAG	681	
QY	541	AACACAGAGCTGTGACAGATGTTCGCGCGGCTCTTCGCGCATGGCCAAAGTGTGCCACGCGAG	600	
Db	682	AACACAGAGCTGTGACAGATGTTCGCGCGGCTCTTCGCGCATGGCCAAAGTGTGCCACGCGAG	741	
QY	601	ATGAGCCCAAGACTGTGACCCGCAAGGTCTTGGTGTGACGTACTGCGGAGCTGCTGCACAAGAAAG	660	
Db	742	ATGAGCCCAAGACTGTGACCCGCAAGGTATTTGTGACGTACTGCGGAGCTGCTGCACAAGAAAG	801	
QY	661	GCGCTGCGGAAACAAGAGCTGTGCGGGGCGGACGCGCGCGCGCGGCGGCGACCCGAGC	720	
Db	802	GCTGTGAGGAAACAAGAGCTTGTGGGTGTGGGGCA---GCGGAGCGCGGGGCGGACCCAGCGC	858	
QY	721	GAGCGCTTGTGCGATGTGTGACCTCTTTCGCGCGCGCGCCAGCGGTACACAGGACCTCATG	780	
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QY	781	TATCATTCGCGAACAAGCGCGCGGACCGGCAAGGACCAAGGAGGCGTGTGCTCATC	840	
Db	919	TATCATTCGTGAATAAACAGTGTGCGGACCGCAGGCTTAAGACAAAGAGCGCTGTGTCTATC	978	
QY	841	AGCTAG 846		
Db	979	AGTTAG 984		
RESULT 10				
LOCUS	AF222979	4990 bp	DNA	linear
DEFINITION	Homo sapiens activator of G-protein signaling gene, complete cds.			
ACCESSION	AF222979			
VERSION	AF222979.1	GI:12004991		
KEYWORDS				
SOURCE	Homo sapiens			
ORGANISM	Homo sapiens			

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 4990)
AUTHORS Cismowski, M.J., Xie, X. and Duzic, E.
TITLE Genomic sequence of the human ras-related G-protein activator AGS1
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 4990)
AUTHORS Cismowski, M.J., Xie, X. and Duzic, E.
TITLE Direct Submission
Submitted (10-JAN-2000) OSI Pharmaceuticals, 777 Old Saw Mill River Road, Tarrytown, NY 10591, USA
JOURNAL Location/Qualifiers
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BASE COUNT 1049 a 1507 c 1509 g 925 t
ORIGIN

Query Match 73.9%; Score 625; DB 9; Length 4990;
Best Local Similarity 80.0%; Pred. No. 2.1e-74;
Matches 846; Conservative 0; Mismatches 0; Indels 211; Gaps 1;

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QY 61 GCCAAGATGCTATGATGATGATGATGATGATGATGATGATGATGATG 120
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Db 2963 GCCAAGATGCTATGATGATGATGATGATGATGATGATGATGATGATG 3022

QY 121 GTGTGGGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATG 180
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Db 3023 GTGTGGGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATG 3082

QY 181 CACCGCAAGTTCATGATGATGATGATGATGATGATGATGATGATGATGATG 240
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Db 3083 CACCGCAAGTTCATGATGATGATGATGATGATGATGATGATGATGATGATG 3142

QY 241 GGCAGACACCGTTCATGATGATGATGATGATGATGATGATGATGATGATG 284
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Db 3143 GGCAGACACCGTTCATGATGATGATGATGATGATGATGATGATGATGATG 3202

QY 285 ----- 284
Db 3203 GGCAGACGTCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 3262

QY 285 ----- 284
Db 3263 CCGGCTGCCCGCGCGAGTAGTGGCTTGGCCTTAGAGAGGCTAGCGGCCCGCG 3322

QY 285 ----- 284
Db 3323 GCGTCAAGTACAGCGCAGTTCCTGCGGCGGAGGAGGAGGAGGAGGAGGAGT 3382

QY 285 -----AGCAGACGTTTTCATCTGCTGTTCACTGTCGCAACCGGACTC 329
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Db 3383 CTCTGTGCCCCCTTCTGAGAGAGCTTTTCATCTGCTGTTCACTGTCGCAACCGGACTC 3442

QY 330 CTTCGAGAGGTGTCAGCGGCTCAGGACAGATCTCTGACACCAAGTCTGCTCAAGAA 389
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Db 3443 CTTCGAGAGGTGTCAGCGGCTCAGGACAGATCTCTGACACCAAGTCTTGGCTTCAGAA 3502

QY 390 CAAACCAAGAGAAAGTGGAGCTGCCCCGTGCTATCTGCGGCAACAAAGGTGACCGGCA 449
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Db 3503 CAAACCAAGAGAAAGTGGAGCTGCCCCGTGCTATCTGCGGCAACAAAGGTGACCGGCA 3562

QY 450 CTTCACGCGCGAGGTGGACACGCGAGATGACAGCTGTGTGGCGACACCGGACCG 509
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Db 3563 CTTCACGCGCGAGGTGGACACGCGAGATGACAGCTGTGTGGCGCGACCGGACCG 3622

QY 510 CTGCGCTACTCTGAGATGATGATGATGATGATGATGATGATGATGATGATG 569
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Db 3623 CTGCGCTACTCTGAGATGATGATGATGATGATGATGATGATGATGATGATG 3682

QY 570 GCTCTGCGCATGGCCAAAGCTGCCAGAGATGAGCCAGACCTGACCGCAAGGTCTC 629
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Db 3683 GCTCTGCGCATGGCCAAAGCTGCCAGAGATGAGCCAGACCTGACCGCAAGGTCTC 3742

QY 630 GGTGCAATCTGTCGACGCTGTCGACAGAGCGCTGCGGAAACAAAGCTGTGCGGCG 689
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Db 3743 GGTGCAATCTGTCGACGCTGTCGACAGAGCGCTGCGGAAACAAAGCTGTGCGGCG 3802

QY 690 CGGACG 749
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Db 3803 CGGACG 3862

QY 750 GCG 809
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Db 3863 GCG 3922

QY 810 CCAGGCCAAGAGCAAGAGAGCGCTGCGCTCATGCTAG 846
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Db 3923 CCAGGCCAAGAGCAAGAGAGCGCTGCGCTCATGCTAG 3959

RESULT 11
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LOCUS AC020558
DEFINITION Homo sapiens BAC clone RP11-524F11 from 17, complete sequence.
ACCESSION AC020558
VERSION AC020558.4 GI:13242397
KEYWORDS HTG.
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 183334)
AUTHORS Sulston, J.E. and Waterston, R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074
REFERENCE 2 (bases 1 to 183334)
AUTHORS Mulvaney, E., Maupin, R., Laplant, Y. and Bielicki, L.
TITLE The sequence of Homo sapiens BAC clone RP11-524F11
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 183334)
AUTHORS Waterston, R.H.
TITLE Direct Submission
Submitted (03-JAN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 4 (bases 1 to 183334)
AUTHORS Waterston, R.H.
TITLE Direct Submission
Submitted (07-MAR-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,

REFERENCE MO 63108, USA
 5 (bases 1 to 183334)
 AUTHORS Waterston, R.
 TITLE Direct Submission
 JOURNAL Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Mar 7, 2001 this sequence version replaced g117631041.

----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc>
 Contact: sapiens@wustl.wustl.edu
 ----- Summary Statistics
 Center project name: H_NH0524F11

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
 Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
 The RPCR-11 human BAC library was made from the blood of one male donor, as described by Osogawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tatenou, M., Catanese, J.J., and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries: Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://dpcpec.med.buffalo.edu>)
 VECTOR: pBACE3.6
 NEIGHBORING SEQUENCE INFORMATION:
 The clone sequenced to the left is AC073621. Actual start of this clone is at base position 1 of RPl1-524F11; actual end is at base position 183334 of RPl1-524F11.

The sequence from position 1987 to 2253 was derived from PCR product of RPl1-524F11 BAC DNA.

FEATURES
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 repeat_region 6583..6891 /rpt_family="Alu"
 repeat_region 6960..7153 /rpt_family="L1"
 repeat_region 7525..7838 /rpt_family="Alu"
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OY	61	GCCAAGAACTGCTATCGCATGTCATCCCTCGGCTGTCCAAAGTGGGCAAGACGGGCATC	120
Db	2020	GCCAAGAACTGCTATTCGATGTCATCTCGGCTGTCCAAAGTGGGCAAGACGGGCATC	1961
OY	121	GTGTGCGGCTTCTTCACCGGGCGGCTTGAGAGCCCTACACGGCTTACCATCGAGACTTC	180
Db	1960	GTGTGCGGCTTCTTCACCGGGCGGCTTGAGAGCCCTTACCATCGAGACTTC	1901
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Db	1840	GGCAACACACCCGTTCCCGSCATATGGGGGCGCTCTCCATCTCAACAGTGTGAGCCGGGGCC	1781
OY	285	-----	284
Db	1780	GGGCGAGTGGGGGAGGGAAGGGCGGGGAACCTCGGCCAAGGGCGCCCGGAGGGCGG	1721
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Db	1720	CCGGCTCCCGCGGCGAGTAGTGGCTTCCGCGTTAGAGAGGCTTACGCGCCCGCGGCG	1661
OY	285	-----	284
Db	1660	GCCTCAAAAGTCAGCCGCATCTTGCCTCGGGGGGCAACCCCTCACCTTCTCTTCTCTCT	1601
OY	285	-----ACGACAGCTTTTTCATCTCGTGGTTCAGTCGTGGCAACACCGGAGTCC	329
Db	1600	CTCTGTGCCCTCTTAAAGAAACGTTTTCACTCGGTGTCAAGTCTGACACACCGGAGATC	1541
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Db	1540	CTTGCAGAGGTGACGGGGCTCAAGGCAAGATCTCTGACACCAAGCTTGGCTTCAAGA	1481
OY	390	CAAAACCAAGGAAGAACTGGACGTGGCCCGTGCATCTGGGCAACAAAGGTGACCGGA	449
Db	1480	CAAAACCAAGGAAGAACTGGACGTGGCCCGTGCATCTGGGCAACAAAGGTGACCGGA	1421

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QY	510	CTGCGCCTACTTTCGAGATCTGGGCGCAAGNAAAGACGAGCTGGAGCCAGATGTTTCGCGC	569
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QY	570	GCTCTTCGCATGGCGCAAGCTGCGCAGAGATGAGCCAGACTGCAACGCGAAGGTCTC	629
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QY	690	CGGACACGAGCGGCGGCGGCGGACCGGCGACGCTTTGGCATGTGGCAACCTTTCG	749
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RESULT 12	AF262018	5141 bp	DNA	linear	PII 31-MAY-2000
LOCUS	AF262018				
DEFINITION	Homo sapiens dexamethasone-induced ras-related protein 1 (DEXRAS1) gene, complete cds.				
ACCESSION	AF262018				
VERSION	AF262018.1	GI:8118456			
KEYWORDS	.				
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 5141) Kempainen,R.J. and Behrend,E.N.				
AUTHORS	Human Dextral gene				
TITLE	Unpublished				
JOURNAL	2 (bases 1 to 5141)				
REFERENCE	Kempainen,R.J. and Behrend,E.N.				
AUTHORS	Direct Submission				
TITLE	Submitted (30-APR-2000) Anatomy & Physiology, Auburn University,				
JOURNAL	College of Veterinary Medicine, Auburn, AL 36832, USA				
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EIVLDGPOCAVFEISAKNSLIDOMERALFAMAKLPSSMSDILIRKYSVOYDVYLV
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Query Match	73.7%;	Score 623.4;	DB 9;	Length 5141;
Best Local Similarity	79.9%;	Pred. No. 3.4e-74;		
Matches 845; Conservative	0;	Mismatches 1;		

16

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GGCGGGGCCAAGCGCTATACAGCCACCTCATGTACATCCGCGAAGAGGCCAGGCCGCGAC	CCAGGCCAAGGACAAAGAGCGCTGCGCTCATCAGCTAG	
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RESULT 13
AC073621

LOCUS	58882 bp	DNA	linear	HTG 19-AUG-2002
DEFINITION	Homo sapiens chromosome 17 clone CND-3073J20 map 17, ***	SEQUENCING		
ACCESSION	AC073621			
	AC073621			

KEYWORDS	HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN
SOURCE	human.

REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE
1	(bases 1 to 58882)	Bliren, B., Nushbaum, C. and Lander, E.	Unpublished	2 (bases 1 to 58882)
2	(bases 1 to 58882)	Homo sapiens chromosome 17, clone CTD-3073J20.		

AUTHORS

TITLE

3 (bases 1 to 58882)

AUTHORS

TTT

JOURNAL

COMMENT

Research, 320 Charles Street, Cambridge, MA 02141, USA
On Aug 19, 2002 this sequence version replaced gi:22123632.
All repeats were identified using RepeatMasker:

Smilt, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
 Genome Center

COMMENT

FEATURES
SOURCE

Query Match	60.98;	Score 515;	DB 10;	Length 179124
Best Local Similarity	74.98;	Pred. NO. 4	5e-60;	
Matches 748				

Indels 156; Gaps 2;

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QY 61 GCCAAGAACTGCTATCCGATGTCATCCCTCGTCCAGAGTGGGCAAGACGGCCATC 120
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121 GGTGCGGGCTTTCAGGATGGTGCCATCCTCGGCTCAATCCAAAGTGGGCAAGACGGCCATT 122306

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QY 181 CACCGCAAGTCTTACTCCATCCGCGGCGAGTCTTACCAGCTGACATCCTGCACACGTC 240

241 GGCAACACCCGTTCCCGGCATCGCGGCGCTTCATCTCCAC-----

Db 122185 GGCATCATCGTTTCCCGCCCATGCGCGCTCTCTATCTCACAGGTGAGTGGGAGTC 122126

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Db 12185 AACAAACCAAGAGAACTGTGACGTCCCGCTGTGCATTTCGGTAAACAAGGGGACCGG 121826

448 GACTTCTACCGCGAGGTGGACCAGCGCGAGATCGAGCAGCTGTTGGCGAGCAGCCCCAC 507

Db 121825 GACTTCTACCGGAGTAGAGCAGCGGAGATTGACACAGTGTGGGTAGACGACCCCTCAG 121766

QY 508 CGCTGCGCCTACTTCGAGATCTCGGCCAGAGAGAACAGCAGCTTGCACCACTCTCTCCGCT

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db 121585 GCGGGCA---GCGGAGGCGGGGGCGAGCCACAGGCAAGTGGGCTTGGCATCGTGGACCCCTTC 747

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b121528 GCTCGACAGCCAGGCTGCACACCCGCCGGCAGCCGCCGC 807

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GAGTCTGGC 12146

008 AGCCAGGCGCAAGGACAGCGCGTCATCAGCTAG 846

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Search completed: December 28, 2002, 04:59:24
Job time : 2599.44 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 27, 2002, 22:19:47 ; Search time 3136 Seconds
(without alignments)
2607.745 Million cells updates/sec

Title: US-09-709-103-2
Perfect score: 1449
Sequence: 1 MFLAMIKKMCPSDBSLSP.....IREKASAGQAKDKRCVYS 281

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=xlp
-O=/cgn2.1/USPTO.spool/US09709103/runat_20122002.162405.805/app.query.fasta.1.455
-DB=GenEmbl -OFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsun62 -TRANS=human40.cdt -LIST=45
-DOCALLIGN=200 -THR_SCORE=pcr -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pic -NORR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USBR=US09709103.0CEN_1.1.3637_@runat_20122002.162405.805 -NCP=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMECUT=120
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Database : GenEmbl.*
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39: em_htgo_hum.*
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41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1449	100.0	846	9 AF498923	AF498923 Homo sapi
2	1449	100.0	979	9 AF172846	AF172846 Homo sapi
3	1449	100.0	1187	9 AF153192	AF153192 Homo sapi
4	1449	100.0	1740	9 AF069506	AF069506 Homo sapi
5	1449	100.0	1758	9 BC018041	BC018041 Homo sapi
6	1436	99.1	1746	9 AF177335	AF177335 Homo sapi
7	1405.5	97.0	1612	10 BC034166	BC034166 Mus muscu
8	1405.5	97.0	1623	10 AF009246	AF009246 Mus muscu
9	1399.5	96.6	1616	10 AF238157	AF238157 Rattus no
10	1387	95.7	4990	9 AF222979	AF222979 Homo sapi
11	1387	95.7	18334	9 AC020558	AC020558 Homo sapi
12	1384	95.5	5141	9 AF262018	AF262018 Homo sapi
13	1370	94.5	179124	10 AL603710	AL603710 Mouse DNA
14	1370	94.5	247899	2 AC025509	AC025509 Mus muscu
15	1356	93.6	183598	2 AC090608	AC090608 Homo sapi
16	1355	93.5	58882	2 AC073621	AC073621 Homo sapi
17	985	60.0	162504	2 AC122995	AC122995 Rattus no
18	893	61.6	2832	6 AX393244	AX393244 Sequence
19	893	61.6	2832	6 AF279143	AF279143 Homo sapi
20	893	61.6	2873	6 AX393267	AX393267 Sequence
21	893	61.6	3058	9 BC013419	BC013419 Homo sapi
22	867	59.8	3020	6 AX393362	AX393362 Sequence
23	867	59.8	3469	10 AF134409	AF134409 Rattus no
24	790	54.5	2699	9 HSM803172	ALB31936 Homo sapi
25	526	36.3	114771	9 H5669D19	AL022334 Human DNA
26	512	35.3	211071	10 AC076974	AC076974 Mus muscu
27	359.5	24.8	181528	3 AC010562	AC010562 Drosophila
28	359.5	24.8	207684	2 AC018039	AC018039 Drosophila
29	359.5	24.8	285495	3 AE003560	AE003560 Drosophila
30	359	24.8	2294	10 BC026377	BC026377 Mus muscu
31	342	23.6	4412	9 AB062937	AB062937 Macaca fa
32	334	23.1	1875	9 BC008065	BC008065 Homo sapi
33	334	23.1	2505	9 AB076889	AB076889 Homo sapi
34	334	23.1	4167	6 AX477382	AX477382 Sequence
35	334	23.1	143299	9 AL353619	AL353619 Human DNA
36	334	23.1	143857	9 AC021583	AC021583 Homo sapi
37	334	23.1	199612	9 AC021582	AC021582 Homo sapi
38	326	22.5	597	9 AY056037	AY056037 Homo sapi
39	326	22.5	597	9 AY059641	AY059641 Homo sapi
40	326	22.5	774	9 AB076888	AB076888 Homo sapi
41	326	22.5	2827	9 AK096600	AK096600 Homo sapi
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43	326	22.5	177540	2 AC006538	AC006538 Homo sapi
44	324	22.4	126801	9 AC091518	AC091518 Mus muscu
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ALIGNMENTS

RESULT 1


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AF498923      846 bp  mRNA  linear  PRI 01-MAY-2002
LOCUS         Homo sapiens activator of G protein signaling (RASD1) mRNA,
DEFINITION   complete cds.
ACCESSION    AF498923
VERSION      AF498923.1 GI:20379021
KEYWORDS
SOURCE       Homo sapiens.
ORGANISM     Homo sapiens.
REFERENCE    1 (bases 1 to 846)
AUTHORS     Puhl, H.L., Ikeda, S.R. and Aronstam, R.S.
TITLE       Direct Submission
JOURNAL     Submitted (05-APR-2002) cDNA Resource Center, Guthrie Research
            Institute, One Guthrie Square, Sayre, PA 18840, USA

FEATURES
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            EQLVGDPPORCAFEISAKNSSLIDQFRALFMAKLPSEMSPDILHRKVSQYCDVLIH
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            RCVIS"

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 EOLVGDPORCAYFEISAKKNSLDOMFALPMARKIPSEMSPDILHRKSYOCDYIH
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 RCVIS"

BASE COUNT 195 a 347 c 284 g 153 t
 ORIGIN

Alignment Scores:

Pred. No.: 1,69e-127 Length: 979
 Score: 1449.00 Matches: 281
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-709-103-2 (1-281) x AF172846 (1-979)

QY 1 MetLysLeuAlaMetIleLysLysMetCysProSerAspSerGluLeuSerIlePro 20
 DB 64 ATGAAGCTGGCCGATGATCAAGAAGATGCGCCGAGAGCTGGAGCTGATATCCCG 123
 QY 21 AlalysAsnGlyTyrArgMetValIleLeuGlySerSerLysValGlyTyrAlaIle 40
 DB 124 GCCAAGAAGCTGATGCAAGTGCATCTGCTCTCCCAAGGTGGGCAAGAGCCCATC 183
 QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
 DB 184 GTGTGGCTTCTCTACACGGCCCTTCGAGAGACGCTTACACGCTTACCTCGAGAGCTTC 243
 QY 61 HisArgLysPheThrSerIleArgGlyValIleGluValIleGluAspIleLeuAspThrSer 80
 DB 244 CACCGAAGTTCATCTCACTCCGCGGAGAGTCTACAGCTGACATCTCGACAGCTCC 303
 QY 81 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIle 100
 DB 304 GGCACACACCGCTTCCCGCCATGCGCGCTCTCCATCTCCACAGAGACGCTTTCATC 363
 QY 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValIleGluAspIleArgGlnGln 120
 DB 364 CTGCTGTCTGCTGACACACCGCTCTCTGAGAGAGTGCAGGCTCAGGCAAG 423
 QY 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeu 140
 DB 424 ATCTCGACACCAAGTCTGCTCCAGAACAAACCAAGAGAGAGTGCAGCTGAGCCCTG 483
 QY 141 ValIleGlyGlyAsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIle 160
 DB 484 GTATCTGCGGCAACAGGCTGACCGCTTCTACCGGAGGTGACACGCGCGAGATC 543
 QY 161 GluGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerIleAlaLysLys 180
 DB 544 GACGACTGCTGGGACACACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 603
 QY 181 AsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGlu 200
 DB 604 AACAGAGAGCTGAGCAGATGTTCCGCGGCTCTGCGCATGAGCCAAAGTGGCCACGAG 663
 QY 201 MetSerProAspLeuHisArgLysValSerValGlnTyrCysAspValLeuHisLysLys 220
 DB 664 ATGAGCCACAGCTGACCGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 723
 QY 221 AlalysAsnGlyTyrArgMetValIleLeuGlySerSerLysValGlyTyrAlaIle 240
 DB 724 GCGCTGGGAAACAAGAGCTGCTGCGGCGGAGAGGCGGCGGCGGCGGCGGCGGCGGCGG 783
 QY 241 AspAlaPheGlyIleValAlaProPheAlaArgArgProSerValHisSerAspLeuMet 260
 DB 784 GACGCTTGGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 843

QY 261 TyrIleArgGluLysAlaSerAlaGlySerGlnAlaLysAspLysGluArgCysValIle 280
 DB 844 TACATCCGCGAAGAGCCGCGCCGACCGCAAGCAAGAGAGAGCGCTGCTATC 903
 QY 281 Ser 281
 DB 904 AGC 906

RESULT 3 AF153192 1187 bp mRNA linear PRI 02-JUN-1999
 LOCUS AF153192
 DEFINITION Homo sapiens ras-related protein mRNA, complete cds.
 ACCESSION AF153192
 VERSION AF153192.1 GI:4960166
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens.
 Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS Kempainen, R.J.
 TITLE Identification of human pituitary Dextral
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1187)
 AUTHORS Kempainen, R.J.
 TITLE Direct Submission
 JOURNAL Submitted (20-MAY-1999) Anatomy & Physiology, Auburn University,
 College of Veterinary Medicine, Auburn, AL 36849, USA

FEATURES
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 RCVIS"

BASE COUNT 249 a 396 c 362 g 180 t
 ORIGIN

Alignment Scores:

Pred. No.: 2.13e-127 Length: 1187
 Score: 1449.00 Matches: 281
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-709-103-2 (1-281) x AF153192 (1-1187)

QY 1 MetLysLeuAlaMetIleLysLysMetCysProSerAspSerGluLeuSerIlePro 20
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 DB 61 GCCAAGAAGCTGATGCAAGTGCATCTGCTCTCCCAAGGTGGGCAAGAGCCCATC 120
 QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
 DB 121 GTGTGGCTTCTCTACACGGCCCTTCGAGAGACGCTTACACGCTTACCATGAGAGCTTC 180

QY 61 HisArgLysPheTyrSerIleArgLysValTyrGlnLeuAspIleLeuAspThrSer 80
 DB 181 CACGGCAAGATTCTACTCCATCCGGCGAGGTCTACACAGCTCGACATCTCGACAGCTCC 240
 QY 81 GlysHisPheProPheProAlaMetArgLeuSerIleLeuThrGlyAspValPheIle 100
 DB 241 GGCACACACCCGTTCCCGCATCGGCGCTCTCCATCTCCACAGAGACGTTTTCATC 300
 QY 101 LeuValPheSerIleuAspAsnArgAspSerPheGlnGluValGlnArgLeuArgGlnGln 120
 DB 301 CTGGTGTTCACCTTGGACACACCGGACTCTTCACAGAGAGTGCAGCGCTCAGGACAG 360
 QY 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGlnAsnValAspValProLeu 140
 DB 361 ATCTCGACACCAAGTCTTGCTCCAGAACAAACCAAGGAGAACGTTGACCTGCCCTG 420
 QY 141 ValIleCysGlnAsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGlnIle 160
 DB 421 GTCACTCTCGGCAACAAAGGGGACCGGACTTTCACCGGAGGTGACACGCGAGATC 480
 QY 161 GluGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGlnIleSerAlaLysLys 180
 DB 481 GAGCAGCTGGTGGCGGACGACCCCGCTCGGCTCTGAGATCTCGGCGCAAGAG 540
 QY 181 AsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaLysLysLeuProSerGln 200
 DB 541 AACAGCAGCTCGACACAGATGTCTCGCGCTCTTCGCCATGCGCAAGCTGCCACGCGAG 600
 QY 201 MetSerProAspLeuHisArgLysValSerValGlnTyrCysAspValLeuHisLysLys 220
 DB 601 ATGAGCCCGACCTGACCGCGAAGGTCTCGGTGCAAGTCTGCGAGCTGCGACAAAGAG 660
 QY 221 AlaLeuArgAsnLysLysLeuLeuArgAlaGlySerGlnGlyGlyGlyGlyAspProGly 240
 DB 661 GCGCTGGCGAACAAGAGCTGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 720
 QY 241 AspAlaPheGlyIleValAlaPheProPheAlaArgArgProSerValHisSerAspLeuMet 260
 DB 721 GACGCGCTTGGCATCTGCGCACCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
 QY 261 TyrIleArgGlnLysAlaSerAlaGlySerGlnAlaLysAspLysGlnArgCysValIle 280
 DB 781 TACATCCCGGAGAAAGCTATC 840
 QY 281 Ser 281
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 RESULT 4
 AF069506 1740 bp mRNA linear PRI 10-JAN-2000
 LOCUS Homo sapiens activator of G protein signaling (AGS1) mRNA, complete cds.
 DEFINITION
 ACCESSION AF069506
 VERSION AF069506.1 GI:4959037
 KEYWORDS
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 Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1740)
 AUTHORS Cismowski,M.J., Takesono,A., Ma,C., Lizzano,J.S., Xie,X., Fuernkrantz,H., Lanier,S.M. and Duzic,E.
 TITLE Genetic screens in yeast to identify mammalian nonreceptor modulators of G-protein signaling
 JOURNAL Nat. Biotechnol. 17 (9), 878-883 (1999)
 MEDLINE 9940338
 PUBMED 10471929
 REFERENCE 2 (bases 1 to 1740)
 AUTHORS Cismowski,M.J., Fuernkrantz,H., Ma,C., Spruyt,M., Xie,X., Lanier,S.M. and Duzic,E.
 TITLE Direct Submission
 JOURNAL Submitted (01-JUN-1998) Receptor Pharmacology/Biochemistry, Cadus

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 ORIGIN
 Alignment Scores:
 Pred. No.: 3,37e-127 Length: 1740
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 DB 206 GCCAAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 265
 QY 41 ValSerArgPheLeuThrGlyArgPheGlnAspAlaTyrThrProThrIleGlnAspHe 60
 DB 266 GTGTGGGGTCTCTCAACGCGCGCTTGAAGAGCGCTTACAGCTGACATCTCGACAGCTTC 325
 QY 61 HisArgLysPheTyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSer 80
 DB 326 CACCGAAGTTCATCCATCCCGCGGCGAGGCTTACACCTGACATCTCGACAGCTTC 385
 QY 81 GlysHisPheProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIle 100
 DB 386 GGCACACACCGTTCCTCCCGCATGCGGCGCTCTCCATCTCCACAGAGACGTTTTCATC 445
 QY 101 LeuValPheSerLeuAspAsnArgAspSerPheGlnGluValGlnArgLeuArgGlnGln 120
 DB 446 CTGGTGTTCAGTGTGACAAACCGCGACTCTTGAAGAGGTGACGAGGCTCAGGACGAG 505
 QY 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGlnAsnValAspValProLeu 140
 DB 506 ATCTCGACACCAAGTCTTGCTCCAGAACAAACCAAGGAGAACGTTGACCTGCCCTG 565
 QY 141 ValIleCysGlnAsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGlnIle 160
 DB 566 GTCACTCTCGGCAACAAAGGTGACCGGACTTTCACCGGAGGTGACACGCGGAGATC 625
 QY 161 GluGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGlnIleSerAlaLysLys 180
 DB 626 GAGCAGCTGGTGGCGGACGACCCCGCTGCGCTCTGAGATCTCGGCGCAAGAG 685

QY 181 AsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGlu 200
 DB 686 AACAGCAGCCTGGACGAGATGTTCCGCGCTCTTCCGATGGCCAAAGCTGCCACCGAG 745
 QY 201 MetSerProAspLeuHisArgLysValSerValGlnTyrCysAspValLeuHisLysLys 220
 DB 746 ATAGGCCAGACTGACCGCAGAGTCTCGGTGCTACTGCGACCTGCTGCCAAGAG 805
 QY 221 AlaLeuArgAsnLysLysLeuLeuArgAlaGlySerGlyGlyGlyGlyGlyGlyGly 240
 DB 806 GCGCTGGCAAGAAAGAGTGTGCGGGCGGCGAGCGGGCGGGCGGGCGAGCCCGGG 865
 QY 241 AspAlaPheGlyLysValAlaProPheAlaArgArgProSerValHisSerAspLeuMet 260
 DB 866 GAGCGCTTGGCATCGTGGCAGCCCTTCCGCGCGCGCGCGCGCTACACAGCGACCTCATG 925
 QY 261 TyrIleArgLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 280
 DB 926 TACATCCGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 985

QY 281 Ser 281
 DB 986 AGC 988

RESULT 5
 BC018041 1758 bp mRNA linear PRI 06-DEC-2001
 LOCUS
 DEFINITION Homo sapiens, RAS, dexamethasone-induced 1, clone MGC:26290
 IMAGE:497482, mRNA, complete cds.

ACCESSION BC018041
 VERSION BC018041.1 GI:17390075

KEYWORDS MGC.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1758)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (03-DEC-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgapsb@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shihaki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www.shgc.stanford.edu>
 Contact: (Dickson, Mark) modpaxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 32 Row: f Column: 11.

FEATURES
 source
 Location/Qualifiers

1..1758
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 /db_xref="taxon:9606"
 /db_xref="taxon:9606"
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 /tissue_type="Brain, hypothalamus"
 /clone_id="NH_MGC_96"
 /lab_host="DH10b"
 /note="Vector: pBluescript"
 213..1058
 /codon_start=1
 /product="RAS, dexamethasone-induced 1"

BASE COUNT 387 a 576 c 501 g 294 t
 ORIGIN

Alignment Scores:

Pred. No.: 3,42e-127 Length: 1758
 Score: 1449.00 Matches: 281
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0

US-09-709-103-2 (1-281) x BC018041 (1-1758)

QY 1 MetLysLeuAlaAlaMetLysLysMetCysProSerAspSerGluLeuSerIlePro 20
 DB 213 ATGAAGACCTGGCGGATGATCAAGAAAGATGTCGCGAGGACTCGGAGCTGATCCG 272
 QY 21 AlaLysAsnCysTyrArgMetValIleLeuGlySerSerLysValGlyLysThAlaIle 40
 DB 273 GCCAAGACAGTGTATCGCATGCTGATCCCTGCTGTCACAGGTGGGAGAGCGGCATC 332
 QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspHe 60
 DB 333 GTTGGCGCTTCTTCTACCGCGCGCTTCCGAGCGCTTACAGCGCTTACACCTGAGACTTC 392
 QY 61 HisArgLysPheTyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSer 80
 DB 393 CACCGCAATTTCTACATCCATCCGCGCGAGGCTACACCTGACATCTCTGACACGTC 452
 QY 81 GlyAsnHisProPheProAlaMetArgLysSerIleLeuThrGlyAspValPheIle 100
 DB 453 GGGACACACCGCTTCCCGCCCATGCGCGCGCTCTCATCTCAGAGACACCTTTTCATC 512
 QY 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValAlaArgLeuArgGln 120
 DB 513 CTGGTTTCACTGTGACACACCGCATCTCTTCCGAGAGGTGACGCGCTCAGGACGAG 572
 QY 121 IleLeuAspThrLysSerCysLeuLysAsnLysTyrLysGluAsnValAspValProLeu 140
 DB 573 ATCTGTGACACCAAGTCTGCTCAAGAACAAACCAAGAGAGAGAGAGAGAGAGAGAG 632
 QY 141 ValIleCysGlyAsnLysGlyAspArgAspPheTyrArgGluValAlaAspGlnArgLys 160
 DB 633 GTTCATCTGGGGCAACAGGGGTGACCGGACCTTCTACCGGAGGTGACAGCGGAGATC 692
 QY 161 GluGlnLeuValGlyLysAspProGlnArgCysAlaTyrPheGlnIleSerAlaLysLys 180
 DB 693 GAGCAGCTGTGGGCGACACACCGCCAGCGCTGCTTCTGAGATCTCGGCGCAAGAG 752
 QY 181 AsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGlu 200
 DB 753 AACAGCAGCCTGGACGAGATGTTCCGCGCGCTCTTGGCCATGGCCAAAGTCCAGCGAG 812
 QY 201 MetSerProAspLeuHisArgLysValSerValGlnTyrCysAspValLeuHisLysLys 220
 DB 813 ATAGGCCAGACTGACCGCAGAGTCTCGGTGCTACTGCGACCTGCGACAGAGAG 872
 QY 221 AlaLeuArgAsnLysLysLeuLeuArgAlaGlySerGlyGlyGlyGlyGlyGlyGly 240
 DB 873 GCGCTGGCAAGAAAGTCTGCGCGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCG 932
 QY 241 AspAlaPheGlyLysValAlaProPheAlaArgArgProSerValHisSerAspLeuMet 260
 DB 933 GAGCGCTTGGCATCGTGGACACCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 992

[illegible]

DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcdick@paxill.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 58 Row: 9 Column: 5
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6677672.

FEATURES

source

1. 1612
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 /db_xref="taxon:10090"
 /map="FVB/N"
 /clone="MGC:36188 IMAGE:4989112"
 /issue_type="Colon, normal, 5 month old male mouse."
 /clone_lib="NCI_CGAP_Co24"
 /lab_host="DH10B"
 /note="Vector: PCMV-SPORT6"
 108. 950
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 FSLNDRDSFEVQRKQOILIDTRSCILKNTKENVDPVLTGKNGDRDYREVQREI
 EQLVGDPPQRCAYFEISAKNSLDMPALPAMAKLPSEMSPDILARKVSVQCVLH
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 CVTS"

CDS

BASE COUNT 417 a 424 c 420 g 351 t
 ORIGIN

Alignment Scores:

Pred. No.: 3.88e-123 Length: 1612
 Score: 1405.50 Matches: 274
 Percent Similarity: 98.58% Conservative: 3
 Best Local Similarity: 97.51% Mismatches: 1
 Query Match: 97.00% Indels: 1
 DB: 10 Gaps: 1

US-09-709-103-2 (1-281) x BC034166 (1-1612)

QY 1 MetLysLeuAlaMetLysLysMetCysProSerAspSerGluLeuSerIlePro 20
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 Db 108 ATGAACCTGCGCGGATGATCAAGAAATGTCGCCAAGCGACTCTGAACAGATATCCCG 167
 QY 21 AlalysAncysYrArGmetValIleLeuGlySerSerLysValGlyLysThrAlaIle 40
 |||||
 Db 168 GCCAAGAACGCTACAGAGATGCTATCTCGCTCATCCAAAGGGGCAAGCGCCATT 227
 QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
 |||||
 Db 228 GTTCGGGCTCTCCACGGGCGCTTTCGAGGATCTTACACCCCTACCATTCAGAGACTTC 287
 QY 61 HisArgLysPheLysSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspPheSer 80
 |||||
 Db 288 CACGAAAGTTTACTGATCCCGGCGGCAAGTTCACAGATGACATTCGACACATTC 347
 QY 81 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIle 100
 |||||
 Db 348 GGCATATCATCGTTCCCGCATCGCGGCTCTCTATCTCTACACAGAGAGAGCTTTTATT 407
 QY 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGln 120
 |||||
 Db 408 CTGGTGTTCAGCTTACACACCGGCACTCATTCGAAAGAGGTGCAAAAGCTCAACACAGAC 467
 QY 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeu 140
 |||||

Db 468 ATCTAGACACCACTCTCTCTCAAGAACAAACCAAGAGATGTGACGCTGCCCTG 527
 QY 141 ValIleCysGlyAsnLysGlyAspArgAspPheLysArgLysValAspGlnArgGluIle 160
 |||||
 Db 528 GATCTTGGGTGAACAAAGGGGACCGGGACTTCTACCGGGAAAGTAGACACGGGAGATT 587
 QY 161 GluGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLys 180
 |||||
 Db 588 GAGCAGCTGGTGGTGGAGCAGCCCTCAGCGTGTGCTCTCTCATGATCTCAGCCAAAGAG 647
 QY 181 AsnSerLeuAspGlnPheArgLysLeuPheAlaLeuPheAlaLysLeuProSerGlu 200
 |||||
 Db 648 AACAGAGCTTGGACCAAGATGTTCCGTGGCTTGGCCATAGGCCAACGCTGCTAGCGAG 707
 QY 201 MetSerProAspLeuHisArgLysValSerValGlnTyrCysAspValLeuHisLysLys 220
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 Db 708 ATGAGCCCGGATTCGACCGCAAGATATCTGTGAGTACTGCGAGCTACTGACACAAAG 767
 QY 221 AlAlaLeuAsnLysLysLeuLeuArgAlaGlySerGlyGlyGlyGlyAspProGly 240
 |||||
 Db 768 GCTGTGAGGACAAAGAGAGCTTCTGCGTGGCGGACG--GGAGGGGGGGGACACACGCG 824
 QY 241 AspAlaPheGlyIleValAlaProPheAlaArgArgProSerValHisSerAspLeuMet 260
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 Db 825 GATGCTTGGCATCTTGCGCGCTTGGCTGCGACAGCCAGGCTGCACAGGACCTCATG 884
 QY 261 TyrIleArgGlyAlaLysAlaSerAlaGlySerGlnAlaLysAspLysGluArgCysValIle 280
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 Db 885 TCATTCGTGGAAAAAACAGCTGCGGACCGACGAGGTAAAGAACAGAGCGGTGTCTATC 944
 QY 281 Ser 281
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 Db 945 AGT 947

RESULT 8

AF009246

LOCUS

AF009246

DEFINITION

Mus musculus ras-related protein (DEXRAS1) mRNA, complete cds.

ACCESSION

AF009246.1 GI:2253712

VERSION

AF009246.1 GI:2253712

KEYWORDS

Mus musculus.

SOURCE

Mus musculus.

ORGANISM

Mus musculus.

REFERENCE

1 (bases 1 to 1623)

AUTHORS

Kempainen, R.J. and Behrend, E.N.

TITLE

Dexamethasone rapidly induces a novel ras superfamily

JOURNAL

J. Biol. Chem. 273 (6), 3129-3131 (1998)

MEDLINE

98123070

PUBMED

9452419

REFERENCE

2 (bases 1 to 1623)

AUTHORS

Kempainen, R.J. and Behrend, E.N.

TITLE

Direct Submission

JOURNAL

Submitted (18-JUN-1997) Physiology & Pharmacology, Auburn

FEATURES

Location/Qualifiers

source

1. 1623

gene

1. 1623

CDS

142. 984

/organism="Mus musculus"
 /db_xref="taxon:10090"
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 1. 1623
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 /note="DEXRAS1"
 /note="induced by dexamethasone"
 /codon_start=-1
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 /protein_id="AAC5338.1"
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 EQLVDDPQRCATFEISAKKNSLDQFRALPSESPDLHRKVSQYCDVLH
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 CVIS"

BASE COUNT 412 a 437 c 417 g 357 t
 ORIGIN

Alignment Scores:

Pred. No.: 3,91e-123 Length: 1623
 Score: 1405.50 Matches: 274
 Percent Similarity: 98.58% Conservative: 3
 Best Local Similarity: 97.51% Mismatches: 3
 Query Match: 97.00% Indels: 1
 Gaps: 10

US-09-709-103-2 (1-281) x AF009246 (1-1623)

QY 1 MetLysLeuAlaAlaMetIleLysLysMetCysProSerAspSerGluLeuSerIlePro 20
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 Db 142 ATGAAGTGGCGCGCATATCAAGAAAGTGGCCCAACGCTGTGAATGATATCCCG 201
 QY 21 AlAlysAsnCysTyrArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIle 40
 |||
 Db 202 GCCAAGAACTGCTACAGATGATGATCTCCGCTCATCCAAAGTGGCAAGCGCCATT 261
 QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
 |||
 Db 262 GTGTGCGCCCTCCACCGGCGGCTTCGAGGATGCTTACACCCCTACCATGAGACTTC 321
 QY 61 HsArgLysPheTyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSer 80
 |||
 Db 322 CACGAAAGTTTCTGATCGAGCGGCAAGTTCACAGTGGACATAGTGAACATCC 381
 QY 81 GLysAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIle 100
 |||
 Db 382 GGCATATATCGGTTCCCGCATCGGCGCTCTCTATCCCAAGAGAGAGATTTCATT 441
 QY 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuAspGlnGln 120
 |||
 Db 442 CTGGGTTCACCTTAGACACACCGGACTCATTCGAAAGGTGCAAAAGCTCAACACACAG 501
 QY 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGlnValAspValProLeu 140
 |||
 Db 502 ATCTTAGACACCAAGTCTCTGTCAGAAACAAACCAAGAAATGGAGCGCTG 561
 QY 141 ValIleCysGlyAsnLysGlyAspArgAspPheTyrArgGluValAspArgGluIle 160
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 Db 562 GTCAATTCGCGTAAACAAAGGAGCGGAGACTTACCGGGAAGTAAAGACGCGGAGATT 621
 QY 161 GluGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLys 180
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 Db 622 GAGAGCTGGTGGTGAACGACCTCAGCTGTGCTCCTACTTCGAGATCTGACCAAGAG 681
 QY 181 AsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGlu 200
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 Db 682 AACGACGACTTGGACCGAGATGTTCCGTGCGCTCTTCCATGGCAAGGCTCCAGGAG 741
 QY 201 MetSerProAspLeuHisArgLysValSerValGlnTyrCysAspValIleHisLysLys 220
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 Db 742 ATGAGCCCGGCTGACCGCAAGGATGTCGTGACGTACGCGAGCTACGCAACAGAG 801
 QY 221 AlaLeuArgAsnLysLysLeuLeuArgAlaGlySerGlyGlyGlyLysAspProGly 240
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 Db 802 GCTGTGAGGAACAAGAGCTTCTGCGCGGCGAGC---GAGAGCGGCGGCGACCAAG 858
 QY 241 AspAlaPheGlyIleValAlaIleProPheAlaArgArgProSerValHisSerAspLeuMet 260
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 Db 859 GATCCCTTTGGCATCTTGGCGCCCTTGTGCGAGACCCAGCGGCAACGACCTCATG 918
 QY 261 TyrIleArgGluLysAlaSerAlaGlySerGlnAlaLysAspLysGluValIle 280
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 Db 919 TACATTCGTGAAAAAACACAGTGTGCGGAGCGACGCTAAGACCAAGAGCGCCCTGTGTCATC 978

QY 281 Ser 281
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 Db 979 AGT 981

RESULT 9
 AF239157

LOCUS AF239157 1616 bp mRNA linear ROD 06-JUL-2001

DEFINITION Rattus norvegicus DEXRAS1 (Dextras1) mRNA, complete cds.

ACCESSION AF239157

VERSION AF239157.1 GI:7230767

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

gene

CDS

1.1616
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 /db_xref="taxon:10116"
 1.1616
 /gene="Dextras1"
 118..960
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 KKALRNKRLNRAGSGGHDGDAFGIILAPFARRPSVSHDLMYIREKTSVSOAKDKER
 CVIS"

BASE COUNT 403 a 436 c 413 g 363 t 1 others
 ORIGIN

Alignment Scores:

Pred. No.: 1.43e-122 Length: 1616
 Score: 1399.50 Matches: 273
 Percent Similarity: 98.22% Conservative: 3
 Best Local Similarity: 97.15% Mismatches: 4
 Query Match: 96.58% Indels: 1
 Gaps: 10

US-09-709-103-2 (1-281) x AF239157 (1-1616)

QY 1 MetLysLeuAlaAlaMetIleLysLysMetCysProSerAspSerGluLeuSerIlePro 20
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 QY 21 AlAlysAsnCysTyrArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIle 40
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 Db 178 GCCAAGAACTGCTACAGATGATGATCTCCGCTCATCCAAAGTGGCAAGCGCCATT 237
 QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
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Db 238 GTGTGGCGCTTCTCAGAGGCGCTTGAAGACCTTACACCCCTTACACCTTGAAGACTTC 297
 Qy 61 HisArgLysPheTyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSer 80
 Db 298 CACGGAAGAGTTTACTGATGATCCGCGGAGAGTGTACAGTGTGACATCTGACACATCT 357
 Qy 81 GlysAsnHisProPheProAlaMetLarGArgLeuSerIleLeuThrGlyAspValPheIle 100
 Db 358 GGCACATCATCCCTTCCCGGACCGCGCTCTCATCTCAGAGAGACGCTTTTCATT 417
 Qy 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGln 120
 Db 418 CTGGTGTGCTTGAACAACCGGACCTCTTGAAGAGGTGCAAGGCTCAACAGACAG 477
 Qy 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGlnAsnValAspValProLeu 140
 Db 478 ATCTAGACACCAAGTCTCTCTCAACAAACCAAGAGATGTGACGTCGCGCTG 537
 Qy 141 ValIleCysGlyAsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIle 160
 Db 538 GTCATTTGCGGTAAACAAGGGGACCGGACTTCTACCGCAAGTGAAGACGCGAGATT 597
 Qy 161 GluGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLys 180
 Db 598 GACACAGCTGTGGGCGGAGACCTCAGCTGTGCTTCTGAGATCTCGCCAAAGAG 657
 Qy 181 AsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGlu 200
 Db 658 AATAGCGCCTTGACGAGATGTTCCGTGGCTCTTGGCCATGGCCAAAGCTGCTAGCGAG 717
 Qy 201 MetSerProAspLeuHisArgLysValSerValGlnTyrCysAspValLeuHisLysLys 220
 Db 718 ATGAGCCCTGACTTGCACCCCAAGGTGTCTGTGACAGTGTGACGCTGCACAAAG 777
 Qy 221 AlaLeuArgAsnLysLysLeuLeuArgAlaGlySerGlyGlyGlyGlyValAspProGly 240
 Db 778 GCTTGTGAGAACAGAGCTTCTGCGGAGGAC--GAGAGTGGGGGCGACACGGA 834
 Qy 241 AspAlaPheGlyIleValAlaProPheAlaArgArgProSerValHisSerAspLeuMet 260
 Db 835 GATGCTTTGGCATCTGGGCGCTTGTGTCGACAGCTAGCGTGCATACGACCTCATG 894
 Qy 261 TyrIleArgGlyLysAlaSerAlaGlySerGlnAlaLysAspLysGluArgCysValIle 280
 Db 895 TACATTCGTGAGAAACAGTGTGACGACGAGCTAAGGACAAAGAGCGCTGTGCATC 954
 Qy 281 Ser 281
 Db 955 AGT 957
 RESULT 10
 AF222979 4990 bp DNA linear PRI 02-JAN-2001
 LOCUS Homo sapiens activator of G-protein signaling gene, complete cds.
 DEFINITION AF222979
 ACCESSION AF222979.1 GI:12004991
 VERSION
 KEYWORDS
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 4990)
 Cismowski, M.J., Xie, X. and Duzic, E.
 Genomic sequence of the human ras-related G-protein activator AGS1
 Unpublished
 JOURNAL 2 (bases 1 to 4990)
 Cismowski, M.J., Xie, X. and Duzic, E.
 Direct Submission
 TITLE Submitted (10-JAN-2000) OSI Pharmaceuticals, 777 Old Saw Mill River
 JOURNAL Road, Tarrytown, NY 10591, USA
 FEATURES
 SOURCE 1..4990
 /organism="Homo sapiens"

mRNA
 CDS
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 /note="chromosomal localization verified by fluorescence
 in-situ hybridization analysis"
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 join(2903..3188,3400..3959)
 /note="ras-related protein; AGS1"
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 KCVLS"
 BASE COUNT 1049 a 1507 c 1509 g 925 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 8,38e-121 Length: 4990
 Score: 1387.00 Matches: 281
 Percent Similarity: 79.83% Conservative: 0
 Best Local Similarity: 79.83% Mismatches: 0
 Query Match: 95.72% Indels: 71
 Gaps: 1
 US-09-709-103-2 (1-281) x AF222979 (1-4990)
 Qy 1 MetLysLeuAlaAlaMetIleLysLysMetCysProSerAspSerGluLeuSerIlePro 20
 Db 2903 ATGAACACTGGCGCGATGATCAAGAAAGATGTCGCGAGGATCGAGTGTATCCG 2962
 Qy 21 AlaLysAsnCysTyrArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIle 40
 Db 2963 GCCAAGACCTGATCGATGTCATCTCGGCTGTCCAAAGTGGGCAAGCGGCATC 3022
 Qy 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspHe 60
 Db 3023 GTGTGCGCTTCTCTCAACCGCGCTTGAAGAGGCTTACAGCTTACACATCTGACAC 3082
 Qy 61 HisArgLysPheTyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSer 80
 Db 3083 CACCGCAAGTCTACTCCATCCGCGGAGGAGTCTACACCTGACATCTCTGACACGTC 3142
 Qy 81 GlysAsnHisProPheProAlaMetLarGArgLeuSerIleLeuThr----- 95
 Db 3143 GGCACACCCCGTCCCGCCCAATGCGCGCTCTCCATCTCAGAGTGAAGCGGCGCC 3202
 Qy 95 ----- 95
 Db 3203 GGGCAGGTGCGGAGGAGGAAAGCGGGGAACCTCGGCGAGGGCGCCCGCGCGCT 3262
 Qy 95 ----- 95
 Db 3263 CGGGCTGCGCGCGCGGAGTGTGCGCTTGAAGAGGCTTGAAGAGGCGCGCGCGG 3322
 Qy 95 ----- 95
 Db 3323 GCCTCAAGTCAACCCGACTGTCCCTGGCGCGCCACCTCACCCTTCTGTGCT 3382
 Qy 96 -----GlyAspValPheIleLeuValPheSerLeuAspAsnArgAsp 110
 Db 3383 CTCTGTGCCCCCTCTAGAGAGCTTTTCTCTGCTTCTGATCTGACACCGGACCTC 3442
 Qy 110 rPheGluGluValGlnArgLeuArgGlnIleLeuAspThrLysSerCysLeuLysAs 130
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Score:          1387.00      Matches:      281
Percent Similarity: 79.83%      Conservative: 0
Best Local Similarity: 79.83%      Mismatches: 0
Query Match:    95.72%      Indels:      71
DB:              Gaps:      1

US-09-709-103-2 (1-281) x AC020558 (1-183334)

QY      1      MetLysLeuAlaAlaMetIleLysMetCysProSerAspSerGluLeuSerIlePro 20
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QY      21      AlAlAsnCyStyArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIle 40
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QY      41      ValSerArgPheLeuThrGlyArgPheGluAspAlaIleTyrProThrIleGluAspPhe 60
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DB      1960      GGTGTGGCTTCTCACCAGCGCTTCAGAGACGCTTCACAGCCCTACCATCGAGACTTC 1901

QY      61      HisArgLysPheTyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspPheSer 80
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DB      1900      CACCCGAGTTTACTCATTCGCGGCGGAGGTCTTACCAAGCTTGGACATCTCGACACGTCC 1841

QY      81      GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThr----- 95
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QY      95      ----- 95
DB      1780      GGGCAGGTGGGAGGAGGAGGGGGAACCTTCGCGCAGGCGCGCCCGCGAGCGCGGT 1721

QY      95      ----- 95
DB      1720      CCGGCTGGCGGCGCGGAGTAGTGCGCTTCGCGCTTACAGAGGCTAGCGGCCCGCGCG 1661

QY      95      ----- 95
DB      1660      GCCTCAAAAGTAGCCGAGCTTGCCTCGGCGGCGACCTCACCCTTCTCTTCTGCT 1601

QY      96      -----GlyAspValPheIleLeuValPheSerLeuAspAsnArgAspSe 110
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QY      110      rPheGluGluValGlnArgLeuArgGlnGlnIleLeuAspPheThrLysSerCysLeuLysAs 130
DB      1540      CTTGAGAGAGGTGACGCGGTACAGGACAGATCTCTGACACCAAGCTTGGCTCAAGAA 1481

QY      130      nLysThrLysGluAsnValAspValProLeuValIleCysGlyAsnLysGlyAspArgAs 150
DB      1480      CAAACCAAGAGAAACGAGGAGCTGCCCCCTGGTCACTCGCGGCAACAGGATGACCGCGA 1421

QY      150      pPheTyrArgGluValAspGlnArgGluIleGlnGluLeuValGlyAspAspProGlnArg 170
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QY 170 GCSAlaTyrPheGluIleSerAlaLysAsnSerSerLeuAspGlnMetPheArgAl 190
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 QY 190 aleuphealmetalaLysLeuProSerGlnMetSerProAspLeuHisArgLysValSe 210
 Db 1300 GCTCTTCGCCATGCCAAGTGTGCCAGGATGAGCCAGACCTGCACCCGCAAGGTCTTC 1241
 QY 210 rValGlnTyrCysAspValLeuHisLysLysAlaLeuArgAsnLysLysLeuLeuArgAl 230
 Db 1240 GGGCGAGTACTGCGAGCTGTGCACAAGAGCGCTGCGGACACAAAGCTGCTGCGGCGC 1181
 QY 230 aglySerGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 250
 Db 1180 CGGACAGC 1121
 QY 250 aatgAtgProSerValHisSerAspLeuMetTyrIleArgGluLysAlaSerAlaGlySe 270
 Db 1120 GC 1061
 QY 270 rGlnAlaLysAspLysGluArgGlyValIleSer 281
 Db 1060 CCAGGCCAAGAGACAGAGCGCTGCTCATACAC 1027

RESULT 12

AF262018 5141 bp DNA linear PRI 31-MAY-2000
 LOCUS AF262018
 DEFINITION Homo sapiens dexamethasone-induced ras-related protein 1 (DEXRAS1)
 gene, complete cds.

ACCESSION AF262018
 VERSION AF262018.1 GI:8118456

KEYWORDS

SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 5141)
 AUTHORS Kempainen, R.J. and Behrend, E.N.
 TITLE Human Dexas1 gene
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 5141)
 AUTHORS Kempainen, R.J. and Behrend, E.N.
 TITLE Direct Submission
 JOURNAL Submitted (30-APR-2000) Anatomy & Physiology, Auburn University,
 College of Veterinary Medicine, Auburn, AL 36832, USA

FEATURES

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BASE COUNT

1090 a 1579 c 1522 g 950 t

Alignment Scores:

Pred. No.: 1.67e-120 Length: 5141
 Score: 1384.00 Matches: 280
 Percent Similarity: 79.83% Conservative: 1
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 Query Match: 95.51% Indels: 71
 DB: 9 Gaps: 1

US-09-709-103-2 (1-281) x AF262018 (1-5141)

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 QY 21 AlalysAsnCysTyrArgMetValIleLeuGlySerSerLysValGlyLysThalalle 40
 Db 2608 GCCAAGACTGCTATTCGATGATGATGATGATGATGATGATGATGATGATGATGATG 2667
 QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
 Db 2668 GTGTGCGCTTCCTTCACCGCGCGCTTCGAGGACCGCTACAGCCTACAGGAGACTTC 2727
 QY 61 HisArgLysPheTyrSerIleArgGlyValValTyrGlnLeuAspIleLeuAspThrSer 80
 Db 2728 CACCGAAGTCTTACTCATCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 2787
 QY 81 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThr 95
 Db 2788 GGCACACACCGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 2847
 QY 95 2848 GGGCAGTCCGCGAGAGAGAGGCGGGGAAACCTCGCGCGCGCGCGCGCGCGCGGT 2907
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 QY 95 2968 GCGTCAAGTACG 3027
 QY 96 3028 CTCTGTGCCCGCTTACGAGAGAGCTTTCATCTGTGTTCAGTGTGCGCAACCGGACTC 3087
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 Db 3088 CTTCAGAGAGGTGACGCGCGCTCAACGACGAGATCTCGACACCAAGCTTTCCTCAAGAA 3147
 QY 130 nLysThrLysGluAsnValAspValProLeuValIleCysGlyAsnLysGlyAspArgAs 150
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 QY 170 gCysAlaTyrPheGluIleSerAlaLysLysAsnSerSerLeuAspGlnMetPheArgAl 190
 Db 3268 CTGGCGCTACTTCGAGATGTGGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3327
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 QY 230 aglySerGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 250
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Db 3508 GCCCGCCGCCACGACGACGACCTCATGATCCGCGAGAACGCCAGCGCGGACG 3567
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RESULT 13
AL603710/c 179124 bp DNA linear ROD 05-APR-2002
LOCUS Mouse DNA sequence from clone Rp23-247B13 on chromosome 11,
DEFINITION complete sequence.
ACCESSION AL603710 GI:20068514
VERSION AL603710.8
KEYWORDS HTG.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS 1 Almeida, J.
JOURNAL Direct Submission
Submitted (04-APR-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humqueres@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 7, 2002 this sequence version replaced gi:18070899.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em, EMBL; Sw,
SWISSPROT; Tr, TrEMBL; Wp, WormPEP; Information on the WormPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep Rp23-247B13 is
from the RPCI-23 Mouse PAC library
constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBAC3.6.
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Best Local Similarity: 82.53% Mismatches: 3
Query Match: 94.55% Indels: 52
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US-09-709-103-2 (1-281) x AL603710 (1-179124)
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QY 21 AlalysanCysTyrTrpMetValIleLeuGlySerSerLysValGlyLysThrAlaIle 40
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Db 122365 GCCAAGAACTGCTACAGAGATGGTCACTCCGCTCATCAAGAGGCGAGCCATC 122306
QY 41 ValSerArgPheIleuThrGlyArgPheGluAspAlaTyrTrpProThrIleGluAspPhe 60
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QY 61 HisArgLysPheTyrSerIleArgGlyValuValTyrGlnLeuAspIleLeuAspThrSer 80
Db 122245 CACCGAAGTTTACTGATCATCCGCGCGCAAGTCTACACGTTGGACATACAGACATCC 122186
QY 81 GlysNHISProPheProAlaMetArgArgLeuSerIleLeuThr----- 95
Db 122185 GGCATCATCGCTTCCCGCATGGGCGGCTCTATCTCAGACAGTGAAGTGGGAGTC 122126
QY 95 ----- 95
Db 122125 GACGGGATAGGGGACCGGAGTCTTGAGGGGAGTGAGTGGGCTGTGTGCTTG 122066
QY 95 ----- 95
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QY 230 AlaGlySerGlyGlyGlyGlyAspProGlyLysPheGlyIleValAlaIleProPhe 249
Db 121585 GCGGGGACAC---GGAGGGGGGGGCGACCGCCATGCTTGGCATCTTGGCCCTTT 121529
QY 250 AlaArgArgProSerValHisSerAspLeuMetTyrIleArgGluLysAlaSerAlaGly 269
Db 121528 GCTCGCAGACCCAGCGCTGCAAGCGACCTCATGTACATTCCTGAAAAAACCAAGTGTGCGC 121469
QY 270 SerGlnAlaLysAspLysGluArgCysValIleSer 281
Db 121468 AGCCAGGCTAAGGACAAAGACGCTGTCTCATCAGT 121433
RESULT 14
LOCUS AC025909 247899 bp DNA linear HTG 27-JUN-2001
DEFINITION Mus musculus chromosome 11 clone Rp23-82E8, WORKING DRAFT SEQUENCE,
AC025909 6 unordered pieces.
ACCESSION AC025909 GI:14547761
VERSION AC025909.28
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

QY 95 ----- 95
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QY 96 -----GlyAspValPheIleuValPheSerLeuAspAsnArgAspSe 110
Db 181988 CTCTGTGCCCTCTAGGAGACGTTTTCATCTGTGTTTCAGTCTGGACACACCGGACTC 182047
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Db 182468 GCGCGCCGCGCCAGCGCTACACAGGACCTCATGTACATCCGGAAGAGCCAGCGCGCGC 182527
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Search completed: December 28, 2002, 02:13:33
Job time : 3319 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus.p2n model

Run on: December 30, 2002, 14:39:31 ; Search time 353 Seconds
(without alignments)
1799.047 Million cell updates/sec

Title: US-09-709-103-1f1

Perfect score: 1450
Sequence: 1 MKLAMITKMKCPDSELSIP.....REKASAGSOAKDXERCVIS. 282

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blom62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pcio -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=TRANSUS0709103 @cgn 1.1 79 @runat.30122002.143925.20642 -NCPU=6 -ICPU=3
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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELop=6 -DELEXt=7

Database :

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24: /SID32/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1449	99.9	846	21	AAZ36892
2	1449	99.9	1740	21	AAZ36914
3	1449	99.9	1801	21	AAZ36893
4	1449	99.9	1841	20	AAZ23022
5	1441	99.4	1776	21	AAA49177
6	1399.5	96.5	1689	20	AAZ23024
7	1387	95.7	3986	20	AAZ23023
8	1343	92.6	8379	20	AAZ23025
9	893	61.6	3037	21	AAZ36913
10	893	61.6	2832	24	ABL92076
11	893	61.6	2973	24	ABL92087
12	893	61.6	3427	24	ABK71563
13	867	59.8	3020	24	ABL92134
14	717	49.4	951	23	AA590571
15	615	42.4	1305	23	ABL07789
16	494	34.1	624	24	ABO28318
17	494	34.1	624	24	ABO28319
18	459	31.7	624	24	ABO28320
19	459	31.7	624	24	ABO28321
20	370	25.5	368	22	ABA51382
21	370	25.5	368	22	ABA69388
22	370	25.5	368	22	ABA36323
23	370	25.5	368	22	AAK17661
24	370	25.5	368	22	AAK43477
25	370	25.5	368	22	AA124259
26	370	25.5	368	22	AA149541
27	370	25.5	368	22	AA109818
28	370	25.5	368	24	AB517600
29	359.5	24.8	4543	23	AB107788
30	334	23.0	1087	22	AA160838
31	334	23.0	1108	22	AA159052
32	334	23.0	4167	24	AAD37605
33	330.5	22.8	960	23	AB125241
34	332	22.2	3061	24	AB072648
35	307.5	21.2	702	23	AB114159
36	305	21.0	1144	22	AAH90075
37	305	21.0	4933	22	AAK81235
38	305	21.0	4934	22	AAK81234
39	304	21.0	1249	24	ABO72525
40	302	20.8	558	11	AAO03212
41	302	20.8	3300	22	AA158569
42	301	20.8	2205	24	AB150199
43	301	20.8	2205	24	AB150231
44	301	20.8	2277	24	AB150202
45	301	20.8	2277	24	AB150234

ALIGNMENTS

RESULT 1
AAZ36892
ID AAZ36892 standard; cDNA, 846 BP.
XX AAZ36892;
AC
XX
DT 13-MAR-2000 (first entry)
XX
DE cDNA encoding an activator of G protein signalling (AGS) protein.
XX
XX Activator of G protein signalling; AGS; ras-related G protein;
XX GTP hydrolysis; G protein activity; pheromone response pathway;
KW G protein-coupled signal transduction; G-gamma selectivity;
KW cellular signal transduction; ss.
XX
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers

XX Cismowski M, Duzic E;
 XX MPI: 2000-072337/06.
 DR P-PSDB; AAY53924.

PT A new activator of G protein signalling used to treat disorders
 characterized by an aberrant AGS protein activity -

PS Disclosure: Page 146-148, 162pp; English.

XX The present sequence encodes an activator of G protein signalling (AGS)
 CC protein. The cDNA sequence was isolated from a human liver cDNA
 CC library. The AGS protein exhibits homology to ras-related G proteins,
 CC and contains alterations in conserved amino acids consistent with a
 CC deficiency in GTP hydrolysis activity. AGS stimulates G protein
 CC activity, G protein-coupled signal transduction and the pheromone
 CC response pathway in a receptor-independent manner. The AGS protein
 CC also shows G-gamma selectivity, as measured by growth assays in
 CC yeast expressing various mammalian G-gamma constructs, and
 CC tissue-specific expression, as measured by Northern blot analysis.
 CC The AGS protein can be used to screen for compounds that modulate
 CC cellular signal transduction. The protein is used to treat disorders
 CC characterized by an aberrant AGS protein activity or AGS nucleic acid
 CC expression.

XX Sequence 1740 BP; 422 A; 546 C; 483 G; 289 T; 0 other;

Alignment Scores:

Pred. No.: 1,93e-157 Length: 1740
 Score: 1449.00 Matches: 281
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.93% Indels: 0
 DB: 21 Gaps: 0

US-09-709-103-1f1 (1-282) x AA236914 (1-1740)

QY 1 MetLysLeuAlaMetLysMetCysProSerAspSerGluLeuSerIlePro 20
 DB 146 ATGAACTGCGCCGATGATCAAGAGATGTGCCGAGCACTCGAGCTGAGTATCCCG 205
 QY 21 ALlysAsnCySTyTrArgMetValIleLeuGlySerSerLysValGlyThrAlaIle 40
 DB 206 GCCAAGACGCTATGCGATGATCCTCGGCTCGTCCAAAGTGAGGCAAGCGCCATC 265
 QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
 DB 266 GTGTGCGGCTTCTCAACCGCGCTTCGAGAGCGCTACACGCTTCACTCGAGACTTC 325
 QY 61 HisArgPhePheTyrSerIleArgGlyGluValTyrGluLeuAspIleLeuAspThrSer 80
 DB 326 CACCGCAAGTTCATCTCATCCGGCGAGGTCCTACAGCTTCACATCTTCGACAGCTTC 385
 QY 81 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIle 100
 DB 386 GGCACCAACCGCTTCCCGCATCGCGCGCTCTCCATCTTCACAGAGACGTTTTCATC 445
 QY 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGln 120
 DB 446 CTGGTGTTCAGTCTGCAACCGGACTCTCTTCGAGAGAGTGCAGCGGCTCAGGCAAGCAG 505
 QY 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeu 140
 DB 506 ATCTTCACACCAAGTCTTGGCTTCAGACAAACCAAGAGAACTGGACGTGCCCTG 565
 QY 141 ValIleCysGlyAsnLysGlyAspArgAspPheTyrArgIleValAspGlnArgGlnIle 160
 DB 566 GTATCTCGCGCAACCAAGGAGACCGGACTTTCACCGGAGGAGCCAGCGCGAGATC 625
 QY 161 GluGluLeuValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLys 180
 DB 626 GAGCAGCTGTGGGCGAGACCCCAAGCGCTGCGCTTCACTTCAGATCTCGGCAAGAG 685

QY 181 AsnSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGlu 200
 DB 686 AACAGACGCTCGACCAAGATGTTCCGCGCTCTTCGCGCATGCGCAAGCTGCCAGGAG 745
 QY 201 MetSerProAspLeuHisArgGlyValSerValGlnTyrCysAspValLeuHisLysLys 220
 DB 746 ATGAGCCAGACCTCGACCCGCAAGTCTCGGTGAGTACGACGCTGCGACCAAGAG 805
 QY 221 AlaLeuArgAsnLysLysLeuLeuArgAlaGlySerGlyGlyGlyGlyAspProGly 240
 DB 806 CGCGTCCGAACAAAGAGCTCTCGGCGCGGCAAGCGCGCGCGCGCGCGCGCGCG 865
 QY 241 AspIlePheGlyIleValAlaProPheAlaArgArgProSerValHisSerAspLeuMet 260
 DB 866 GACGCGTTCGATCGTGGACACCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 925
 QY 261 TyrIleArgGlyLysAlaSerAlaGlySerGlnAlaLysAspLysGluArgCysValIle 280
 DB 926 TACATCCCGCAAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCATC 985
 QY 281 Ser 281
 DB 986 AGC 988

RESULT 3

ID AA236893 standard; cDNA; 1801 BP.

AC AA236893;

DT 13-MAR-2000 (first entry)

DE cDNA encoding an activator of G protein signalling (AGS) protein.

KW Activator of G protein signalling; AGS; ras-related G protein;

KW GTP hydrolysis; G protein activity; pheromone response pathway;

KW cellular signal transduction; G-gamma selectivity;

OS Homo sapiens.

FA Key Location/Qualifiers

FT 5'UTR 7..153

FT CDS /*tag= a

FT /*tag= b

FT /product= "activator of G protein signalling (AGS)

FT 3'UTR 1000..1801

FT /*tag= c

PN W09958670-A1.

PD 18-NOV-1999.

PF 07-MAY-1999; 99WO-US10151.

PR 08-MAY-1998; 98US-0084842.

PR 07-OCT-1998; 98US-0103355.

PA (CADU-) CADUS PHARM CORP.

PI Cismowski M, Duzic E;

DR MPI: 2000-072337/06.

DR P-PSDB; AAY53921.

XX A new activator of G protein signalling used to treat disorders

XX characterized by an aberrant AGS protein activity -

XX Claim 3; Page 133-135, 162pp; English.

CC The present sequence encodes an activator of G protein signalling (AGS)
 CC protein. The cDNA sequence was isolated from a human liver cDNA
 CC library. The AGS protein exhibits homology to ras-related G proteins,
 CC and contains alterations in conserved amino acids consistent with a
 CC deficiency in GTP hydrolysis activity. AGS stimulates G protein
 CC activity, G protein-coupled signal transduction and the pheromone
 CC response pathway in a receptor-independent manner. The AGS protein
 CC also shows G-gamma selectivity, as measured by growth assays in
 CC yeast expressing various mammalian G-gamma constructs, and
 CC tissue-specific expression, as measured by Northern blot analysis.
 CC The AGS protein can be used to screen for compounds that modulate
 CC cellular signal transduction. The protein is used to treat disorders
 CC characterized by an aberrant AGS protein activity or AGS nucleic acid
 CC expression.
 XX

SQ Sequence 1801 BP; 437 A; 561 C; 500 G; 303 T; 0 other;

Alignment Scores:

Pred. No.: 2.02e-157 Length: 1801
 Score: 1449.00 Matches: 281
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.93% Indels: 0
 DB: 21 Gaps: 0

US-09-709-103-1F1 (1-282) x AAZ23022 (1-1841)

QY 1 MetLysLeuAlaAlaMetIleLysMetCysProSerAspSerGluLeuSerIlePro 20
 DB 154 ATGAACCTGGCGCGATGATCAAGAAGATGTCCCGAGCGACTCGAGTATCCCG 213
 QY 21 AlaLysAsnCysTyrArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIle 40
 DB 214 GCCAAGAAGTCTATCGCATGTCTATCTCGCTCGTCCAAAGGTGGCAAGCGGCATC 273
 QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
 DB 274 GTGTGCGCTTCTCCACCGCGCTTCGAGGACGCTACAGCGCTACCATCGAGACTTC 333
 QY 61 HisArgLysPheTyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSer 80
 DB 334 CACCGCAAGTTCTACTCCATCCGCGGAGGTCTACAGCTCGACATCTCCGACACGTCC 393
 QY 81 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIle 100
 DB 394 GGCACACACCGTTCCTCCCGCGCTCGCGGCTCTCCATCTCAGGAGACGTTTCATC 453
 QY 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGln 120
 DB 454 CTGGTGTTCAGTCTGGACAACCGCGACTCTCTTCGAGGAGGTGCGCGCTCAGCAGCAG 513
 QY 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeu 140
 DB 514 ATCTCTGACACCAAGTCTTGTCTCAAGAACAAACCAAGGAGAACGTGGACGTGCCCTG 573
 QY 141 ValIleCysGlyAsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIle 160
 DB 574 GTCATCTCGCGCAACAAGGGTACCGGACCTTCTACCGGAGGTGGACCGCGAGATC 633
 QY 161 GluGlnLeuValGlyAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLys 180
 DB 634 GAGCAGCTGTGTGGCGGACGACCCCGCGCTGCGCTTCTCGAGATCTCGGCNAGAAG 693
 QY 181 AsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGlu 200
 DB 694 AACAGACGCTGGACACAGATCTTCGCGCGCTCTTCGCCATGGCCAAAGCTGCCAGCGAG 753
 QY 201 MetSerProAspLeuHisArgLysValSerValGlnTyrCysAspValLeuHisLysLys 220
 DB 754 ATGAGCCAGACCTTCACCGCAAGGTCTCGGTGCAGTACTGCCGACGTGTCACAGAAG 813
 QY 221 AlaLeuArgAsnLysLysLeuLeuArgAlaGlySerGlyGlyGlyGlyAspProGly 240

DB 814 GCGCTCGGAAACAAGAAGTCTGCTGGGCGCGCAGCGCGCGCGGCGACCCGGGC 873
 QY 241 AspAlaPheGlyIleValAlaProPheAlaArgArgProSerValHisSerAspLeuMet 260
 DB 874 GACGCTTTTGGCATCGTGGCACCCCTTGGCGCGCGCGCGCGGTACACAGCGACCTCATG 933
 QY 261 TyrIleArgGluLysAlaSerAlaGlySerGlnAlaLysAspLysGluArgCysValIle 280
 DB 934 TACATCCGCGAGAAGCCAGCCGCGCAGCCAGGCAAGGACCAAGAGCGCTGCGTCATC 993
 QY 281 Ser 281
 DB 994 AGC 996
 RESULT 4
 AAZ23022
 ID AAZ23022 standard; cDNA; 1841 BP.
 XX
 AC AAZ23022;
 XX
 DT 17-JAN-2000 (first entry)
 XX
 DE Human kd312 polypeptide encoding cDNA.
 XX
 KW kd312 polypeptide; cancer; immunodeficiency disorder; AIDS; stroke;
 KW heart attack; head trauma; neurodegenerative disease; human;
 KW Parkinson's disease; Alzheimer's disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO950288-A2.
 XX
 PD 07-OCT-1999.
 XX
 PF 30-MAR-1999; 99WO-US06993.
 XX
 PR 31-MAR-1998; 98US-0053374.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Yen K;
 XX
 DR WPI: 1999-601322/51.
 DR P-PSDB; AAY42693.
 XX
 PT kd312 polypeptides useful for treating diseases and disorders
 PS associated with alterations in cell proliferation and cell death
 XX
 PS Claim 1; Fig 8; 85pp; English.
 CC
 CC The invention provides nucleic acid molecules encoding human and rat
 CC kd312 polypeptides. The kd312 polypeptides can be expressed by standard
 CC recombinant methodology. The kd312 sequences, and the antibodies against
 CC the proteins may be used to treat or diagnose the presence or progression
 CC of various diseases, e.g. cancer, immunodeficiency disorders (e.g. AIDS),
 CC stroke, heart attack, head trauma, and neurodegenerative diseases (e.g.
 CC Parkinson's disease and Alzheimer's disease). The present sequence
 CC represents the human kd312 cDNA sequence.
 SQ Sequence 1841 BP; 398 A; 605 C; 530 G; 308 T; 0 other;

Alignment Scores:
 Pred. No.: 2.09e-157 Length: 1841
 Score: 1449.00 Matches: 281
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.93% Indels: 0
 DB: 20 Gaps: 0

US-09-709-103-1F1 (1-282) x AAZ23022 (1-1841)

QY 1 MetLysLeuAlaAlaMetIleLysMetCysProSerAspSerGluLeuSerIlePro 20
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Db 255 ATGAACTGCGCCGATGATCAAGAAAGATGTCGCGAGCTCGAGCTGAGTATCCCG 314
QY 21 AAlAsnCySerTyArgMetValIleuGlySerSerValGlyThrAlaIle 40
Db 315 GCCAAGAACTGCGATGCGATGCGATCCTCGGCTCGTCCAAAGTGGGCAAGCGCCATC 374
QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
Db 375 GTGTGCGCTTCTCTCAACCGCGCTTCGAGGACGCTTACACCCCTTACATCAGAGACTTC 434
QY 61 HisArgGlyPheThrSerIleArgGlyGluValTyrGlnIleuAspIleuAspThrSer 80
Db 435 CACCGCAAGTCTACTCCATCCGCGCGAGTCTCAAGCTGAGATCCTCGACACGCTCC 494
QY 81 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIle 100
Db 495 GGCACACCAACCGCTTCCCGCCCATGGCGGCGCTCTCCATCTCACAGGAGAGCTTTTCACTC 554
QY 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGln 120
Db 555 CTGGTGTTCAGTCTGGACAAACCGCACTCTCTCGAGAGTGCACGCGCTCAGCAGCAG 614
QY 121 IleuAspThrThySerSerValLeuAsnValThrThrGlyAsnValAspValProLeu 140
Db 615 ATCTTGACACCAAGTCTGCTCAAGAAACAAACCAAGACGAGTGGACGCTGCCCTG 674
QY 141 ValIleCysGlyAsnLysGlyAspArgPheTyrArgGlyValAspGlnArgGlnIle 160
Db 675 GTCATCTGGCGCAACAGGCTGACCGGCACTTCTTACCGGAGGTGGACCAAGCGCAGATC 734
QY 161 GlnGlnIleuValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLys 180
Db 735 GAGCAGCTGTGGCGACGACCCCGAGCGCTGCGCTTACTGAGATCTCGGCGCAAGAG 794
QY 181 AsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGln 200
Db 795 AACAGAGAGCTGACCAAGATGTTCCGCGGCTCTTCCGATGCGCAAGCTGCCCGCAGAG 854
QY 201 MetSerProAspLeuHisArgLysValSerValGlnTyrCysAspValIleuHisLysLys 220
Db 855 ATGAGCGCCGACCTGCAACCGGCAAGGCTCTGCTGCGAGTCTGCGAGCTGCGACAAAGAG 914
QY 221 AlaLeuArgAsnLysLysLeuLeuArgAlaGlySerGlyGlyGlyGlyAspProGly 240
Db 915 GCGCTGCGGAACAAAGAGCTGCTGCGGCGCGGACGCGGCGGCGGCGGCGGCGGCG 974
QY 241 AspAlaPheGlyIleValAlaProPheAlaArgArgProSerValHisSerAspLeuMet 260
Db 975 GACGCTTGTGGATCGTGGACCCCTTCGCGCGCGCGCCGACGCTACACGCACTCATG 1034
QY 261 TyrIleArgGlyLeuValSerAlaGlySerGlnAlaLysAspLysGluArgCysValIle 280
Db 1035 TACATCCGCGAAGAGCCGCGCGCGGCAACCGGCGCAAGAGAGCGCTCATC 1094
QY 281 Ser 281
Db 1095 AGC 1097

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RESULT 5
AAA49177
ID AAA49177 standard; cDNA, 1776 BP.
XX
AC AAA49177;
XX
DT 03-NOV-2000 (first entry)
XX
DE cDNA encoding human GTPase associated protein-7.
XX
KW Guanine nucleotide binding protein; GMP-binding protein; G-protein;
KW GTPase; GTPase associated protein; GTPAP; cell proliferation;
KW autoimmune; inflammatory; immune system disorder; cancer; AIDS;
KW acquired immune deficiency syndrome; asthma; atherosclerosis;
KW arthritis; systemic lupus erythematosus; psoriasis; human; ss.

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XX OS Homo sapiens.
XX Location/Qualifiers
XX Key 180..1025
XX FT CDS
XX FT /tag= a
XX FT /product= GTPAP7
XX
XX MO200031263-A2.
XX
PD 02-JUN-2000.
XX
PF 23-NOV-1999; 99MO-US28013.
XX
PR 23-NOV-1998; 98US-0109592.
PR 04-FEB-1999; 99US-0118610.
PR 06-APR-1999; 99US-0127990.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Hillman JL, Tang YT, Bandman O, Lal P, Yue H, Lu DAM, Baughn MR;
PI Yang J, Azimzai Y.
XX
XX MPI; 2000-400073/34.
XX
XX P-PSDB; AAY99655.
XX
PT Human GTPase associated proteins, polynucleotides, and antibodies,
PT useful for diagnosing, preventing and treating various diseases such as
PT atherosclerosis, cancer, acquired immune deficiency syndrome (AIDS),
PT asthma, and autoimmune diseases -
XX
XX Claim 9; Page 125-126; 144p; English.
XX
CC Human cDNA libraries from various tissues were screened for GTPase
CC associated proteins (GTPAP). The present sequence is cDNA encoding
CC human GTPAP-7. This sequence was derived from a cDNA library of the
CC brain tumour tissue from the parietal lobe of a female.
CC This protein is expressed in reproductive, nervous and
CC gastrointestinal tissue. The GTPAP proteins may be used to define
CC agonists and antagonists of GTPAP activity and to generate antibodies
CC to GTPAP. This means the GTPAP proteins may be useful for treatment or
CC prevention of diseases associated with GTPAP such as cell proliferation
CC disorders, autoimmune disorders, inflammatory disorders, immune system
CC disorders, cancer, AIDS, asthma, atherosclerosis, arthritis, systemic
CC lupus erythematosus and psoriasis.
XX
SQ Sequence 1776 BP, 430 A, 565 C, 490 G, 291 T; 0 other;

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Alignment Scores:

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Pred. No.: 1,67e-156 Length: 1776
Score: 1441.00 Matches: 280
Percent Similarity: 99.64% Conservative: 0
Best Local Similarity: 99.64% Mismatches: 1
Query Match: 99.38% Indels: 0
DB: 21 Gaps: 0

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US-09-709-103-1f1 (1-282) x AAA49177 (1-1776)

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QY 1 MetLysLeuAlaAlaMetIleLysLysMetCysProSerAspSerGluLeuSerIlePro 20
Db 180 ATGAACTGCGCCGATGATCAAGAAAGATGTGCGCGAGCACTCGAGCTGAGTATCCCG 239
QY 21 AAlAsnCySerTyArgMetValIleuGlySerSerValGlyThrAlaIle 40
Db 240 GCCAAGAACTGCGATGCGATGCGATCCTCGGCTCGTCCAAAGTGGGCAAGACGCGCATC 299
QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
Db 300 GTGTGCGCTTCTCTCAACCGCGCGCTTCGAGGAGAGCTTACACGCTTACATCAGAGCTTC 359
QY 61 HisArgLysPheTyrSerIleArgGlyGluValTyrGlnIleuAspIleuAspThrSer 80
Db 360 CACGCAAGTCTTACTTCATCCGCGCGGAGGTCTACACAGCTCGACATCTCTCGACACGCTCC 419

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Qy 81 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIle 100
Db 420 GGCAACACCCGTTCCCGCCCATCGGTGCTCTCCATCTCTCACAGAGACGTTTTCATC 479
Qy 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGln 120
Db 480 CTGTGTTCAGTCTGGACAAACCGGACTCTCTCGAGAGGTGCGAGCGCTCAGCGAGCAG 539
Qy 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeu 140
Db 540 ATCTCTGACACCAAGTCTTGCTCTCAAGACAAACACCAAGAGACGTTGGAGTGGCCCTG 599
Qy 141 ValIleCysGlyAsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIle 160
Db 600 GTCATCTGCGGCAACAAGGGTGACCGGACTTCTTACCGCGAGGTGGACGACGCGAGATC 659
Qy 161 GluGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLys 180
Db 660 GAGCAGCTGGTGGCGGACGACCCGACGCTGCGCCTTACTTCGAGATCTCGGCCAAGAAG 719
Qy 181 AsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGlu 200
Db 720 AACAGCAGCTGGACAGATGTTCCGCGCGTCTTCGCCATGGCCAAAGCTGCCAGCGAG 779
Qy 201 MetSerProAspLeuHisArgLysValSerValGlnTyrCysAspValLeuHisLysLys 220
Db 780 ATGAGCCAGACCTGCACCGCAAGGTCTCGGTGCGAGTACTGCGACGTGCTGCACAAGAAG 839
Qy 221 AlaLeuArgAsnLysLysLeuLeuArgAlaGlySerGlyGlyGlyGlyAspProGly 240
Db 840 CGCTGCGGAACAAGAGCTCTCGCGCGCGGACGCGCGCGCGCGCGCGCGCGCGCGCG 899
Qy 241 AspAlaPheGlyIleValAlaProPheAlaArgArgProSerValHisSerAspLeuMet 260
Db 900 CAGCGCTTTGGCATCGTGGCACCTTTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 959
Qy 261 TyrIleArgGluLysAlaSerAlaGlySerGlnAlaLysAspLysGluArgCysValIle 280
Db 960 TACATCCGCGAAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1019
Qy 281 Ser 281
Db 1020 AGC 1022

RESULT 6
AAZ23024
ID AAZ23024 standard; cDNA; 1689 BP.
XX
AC AAZ23024;
XX
XX
DT 17-JAN-2000 (first entry)
XX
DE Rat kd312 polypeptide encoding cDNA.
XX
KW kd312 polypeptide; cancer; immunodeficiency disorder; AIDS; stroke;
KW heart attack; head trauma; neurodegenerative disease; rat;
KW Parkinson's disease; Alzheimer's disease; ss.
XX
OS Rattus sp.
XX
PN W09950288-A2.
XX
XX
PD 07-OCT-1999.
XX
PF 30-MAR-1999; 99WO-US06993.
XX
XX
PR 31-MAR-1998; 98US-0053374.
XX
PA (AMGE-) AMGEN INC.
XX
PI Yen K;
XX

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DR WPI: 1999-601322/51.
DR P-PSDB; AA42694.
XX
PT kd312 polypeptides useful for treating diseases and disorders
PT associated with alterations in cell proliferation and cell death -
XX
PS Claim 2; Fig 9; 85pp; English.
XX
CC The invention provides nucleic acid molecules encoding human and rat
CC kd312 polypeptides. The kd312 polypeptides can be expressed by standard
CC recombinant methodology. The kd312 sequences, and the antibodies against
CC the proteins may be used to treat or diagnose the presence or progression
CC of various diseases, e.g. cancer, immunodeficiency disorders (e.g. AIDS),
CC stroke, heart attack, head trauma, and neurodegenerative diseases (e.g.
CC Parkinson's disease and Alzheimer's disease). The present sequence
CC represents the rat kd312 cDNA sequence.
XX
SQ Sequence 1689 BP; 417 A; 462 C; 434 G; 376 T; 0 other;

```

```

Alignment Scores:
Pred. No.: 9.87e-152 Length: 1689
Score: 1399.50 Matches: 273
Percent Similarity: 98.22% Conservative: 3
Best Local Similarity: 97.15% Mismatches: 4
Query Match: 96.52% Indels: 1
DB: 20 Gaps: 1

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US-09-709-103-1F1 (1-282) x AAZ23024 (1-1689)
Qy 1 MetLysLeuAlaAlaMetIleLysLysMetCysProSerAspSerGluLeuSerIlePro 20
Db 132 ATGAACCTGGCGCGCATGATCAAGAAGATGTGCCAAGACTCTGAACCTGAGTATCCCG 191
Qy 21 AlaLysAsnCysTyrArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIle 40
Db 192 GCCAAGACTGCTACAGATGGTCTATCTCGCTCATCAAGTGGGCAAGCGCCATC 251
Qy 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
Db 252 GTGTGCGCGTTCCTCACGGCGGCTTCGAGGACGCTTACACCCCTACCATTTGAAGACTC 311
Qy 61 HisArgLysPheTyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSer 80
Db 312 CACCGAAAGTTTTACTCGATCCGCGGCAAGTCTACCAAGTTGGACATACCTGACACATCT 371
Qy 81 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIle 100
Db 372 GGCAATCATCTCGTTTCCCGCCCATCGCGCTCTCTATCTCTCACAGAGACGTTTTCATT 431
Qy 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGln 120
Db 432 CTGGTGTTCAGCTTAGACAACCGCGACTCTTCGAGGAGGTGCAAAAGGCTCAAAACAGCAG 491
Qy 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeu 140
Db 492 ATCTTAGACACCAAGTCTCTCTCAAGAACAAACCAAGAGAAATGTGGACGTGCGCGTG 551
Qy 141 ValIleCysGlyAsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIle 160
Db 552 GTCATTTGCGGTAAACAAGGGGACCGGACTTCTACCGCGAAGTGGAGCAGCGGAGATT 611
Qy 161 GluGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLys 180
Db 612 GAGCAGCTGGTGGCGGATGACCCCTCAGCGTTTGTGCTACTTTCGAGATCTCGGCCAAGAAG 671
Qy 181 AsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGlu 200
Db 672 AATAGCAGCTGGACCAAGATGTTCCGTGCGCTCTTTGCGCATGGCCCAAGCTCGCTAGCCAG 731
Qy 201 MetSerProAspLeuHisArgLysValSerValGlnTyrCysAspValLeuHisLysLys 220
Db 732 ATGAGCCCTGACTTGCACCGCAAGGTGCTGTGCAAGTACTGTGACGCTGTCACAAAAAG 791

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AAZ23025
ID AAZ23025 standard; DNA; 3079 BP.

AC AAZ23025;
XX

DT 17-JAN-2000 (first entry)

XX Rat kd312 genomic DNA sequence.

XX kd312 polypeptide; cancer; immunodeficiency disorder; AIDS; stroke;

KW heart attack; head trauma; neurodegenerative disease; rat;

KW Parkinson's disease; Alzheimer's disease; ss.

XX Rattus sp.

XX WO950288-A2.

XX 07-OCT-1999.

XX 30-MAR-1999; 99WO-US06993.

XX 31-MAR-1998; 98US-0053374.

XX (AMGE-) AMGEN INC.

XX Yen K;

XX WPI; 1999-601322/51.

XX P-PSDB; AAY42694.

XX kd312 polypeptides useful for treating diseases and disorders

PT associated with alterations in cell proliferation and cell death

PT Claim 2; Fig 7; 85pp; English.

XX The invention provides nucleic acid molecules encoding human and rat

CC kd312 polypeptides. The kd312 polypeptides can be expressed by standard

CC recombinant methodology. The kd312 sequences, and the antibodies against

CC the proteins may be used to treat or diagnose the presence or progression

CC of various diseases, e.g. cancer, immunodeficiency disorders (e.g. AIDS),

CC stroke, heart attack, head trauma, and neurodegenerative diseases (e.g.

CC Parkinson's disease and Alzheimer's disease). The present sequence

CC represents the rat kd312 genomic DNA sequence.

XX SQ Sequence 3079 BP; 708 A; 843 C; 829 G; 699 T; 0 other;

Alignment Scores:

Pred. No.: 7,99e-145 Length: 3079

Score: 1343.00 Matches: 272

Percent Similarity: 84.10% Conservative: 3

Best Local Similarity: 83.18% Mismatches: 5

Query Match: 92.62% Indels: 48

DB: 20 Gaps: 2

US-09-709-103-1F1 (1-282) x AAZ23025 (1-3079)

Qy 1 MetLysLeuAlaMetIleLysLysMetCysProSerAspSerGluLeuSerIlePro 20

Db 303 ATGAACTGGCGGATGATCAAGAAGATGTGCCAAGCGACTCTGAAGTATCCCG 362

Qy 21 AlalysAsnCysTyrAcMetValIleLeuGlySerLysValGlyLysThrAlaIle 40

Db 363 GCCAAGAAGTCTGATCAGATGGTATCTCCGCTCATCCAAAGTGGGCAAGCGCCATC 422

Qy 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60

Db 423 GTGTGCGCTTCTCTCACGGCGCTTCAGAGCGCTTACACCCCTACCATTTGAAGACTTC 482

Qy 61 HisArgLysPheTyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSer 80

Db 483 CACCCAAAAGTTTACTCGATCCGCGGAAAGTCTACCAAGTTGGACATACCTGGACACATCT 542

Qy 81 GlyAsnHisProPheProAlaMetArgLeuSerIle----- 93

Db 543 GGCAATCATCGTTTCCCGCATCGCGGCTCTCTATCTCAGAGTGTGGGGACC 602

Qy 93 ----- 93

Db 603 GACAGGACCGTGGGAGGAATCTCGGGAGCGGATGGGGCGGTGTGTGTGCTTTGGG 662

Qy 94 -----Leu 94

Db 663 GCTGTGCTGTCTGCTGCTCCGTGCTGGCAGCTGCCCTCACCTTTCACCTGCTTCCTTTG 722

Qy 95 ThrGlyAspValPheIleLeuValPheSerLeuAspAsnArgAspSerPheGluGluVal 114

Db 723 TA-GGAGACGTTTTCATCTCTGCTTTCAGCTTAGCAACCGGACTCTCTCGAGAGGTG 781

Qy 115 GlnArgLeuArgGlnGlnIleLeuAspThrLysSerCysLeuLysAsnLysThrLysGlu 134

Db 782 CAAAGGCTCAACAGCAGATCTTAGACACCAAGTCTCTCAAGAACAAACCAAGAG 841

Qy 135 AsnValAspValProLeuValIleCysGlyAsnLysGlyAspArgAspPheTyrArgGlu 154

Db 842 AATGTGGACGTGCCGCTGGTTCATTTGGGTAAACAAAGGGGACCGGACTTCTACCGGAA 901

Qy 155 ValAspGlnArgGluIleGluGlnLeuValGlyAspAspProGlnArgCysAlaTyrPhe 174

Db 902 GTGGAGCAGCGGAGATTGACAGCTGGTGGCCGATGCCCTCAGCGTTGTGCTACTTC 961

Qy 175 GluIleSerAlaLysLysAsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMet 194

Db 962 GAGATCTCGGCCAAGAGATAGCAGCTGGTGGCCGATGGTCCGTGGGCTCTTTGCCATG 1021

Qy 195 AlalysLeuProSerGluMetSerProAspLeuHisArgLysValSerValGlnTyrCys 214

Db 1022 GCCAAGCTGCCTAGCAGATGAGCCCTGACTTGCCCAAGGTGTCTGTGCTACTGT 1081

Qy 215 AspValLeuHisLysLysAlaLeuArgAsnLysLysLeuLeuArgAlaGlySerGlyGly 234

Db 1082 GACGTGCTGCACAAAGAGCTCTGAGGAACAAAGAGCTTCTGCGTGGGCGCAGC--GGA 1138

Qy 235 GlyGlyGlyAspProGlyAspAlaPheGlyIleValAlaProPheAlaArgArgProSer 254

Db 1139 GGTGGGGCGCACCGAGATGCTTTGGCATCTTGGCGCCCTTTGCTCGCAGACCTAGC 1198

Qy 255 ValHisSerAspLeuMetTyrIleArgGluLysAlaSerAlaGlySerGlnAlaLysAsp 274

Db 1199 GTGCATAGCGACCTCATGTATCTGTGAGAAACACAGTGTTCAGCAGCGCTAAGGAC 1258

Qy 275 LysGluArgCysValIleSer 281

Db 1259 AAGGAGCGCTGTGTATCAGT 1279

RESULT 9

AAZ36913

ID AAZ36913 standard; DNA; 837 BP.

XX AAZ36913;

XX AC AAZ36913;

XX DT 13-MAR-2000 (first entry)

XX DE DNA encoding a homologue of activator of G protein signalling AGS1.

XX KW Activator of G protein signalling; AGS; ras-related G protein;

XX KW GTP hydrolysis; G protein activity; pheromone response pathway;

XX KW G protein-coupled signal transduction; G-gamma selectivity;

XX KW cellular signal transduction; AGS1 homologue; ss.

XX OS Homo sapiens.

XX XX Location/Qualifiers

XX FH Key 1..837

XX CDS /*tag= a

XX FT /product= "AGS1 homologue"

XX FT

XX XX

PN MO9958670-A1.
 XX 18-NOV-1999.
 PD
 XX 07-MAY-1999; 99WO-US10151.
 PF
 XX 08-MAY-1998; 98US-0084842.
 PR 07-OCT-1998; 98US-0103355.
 XX
 PA (CADU-) CADUS PHARM CORP.
 XX
 PI Cismoweki M, Duzic E;
 XX WPI: 2000-072337/06.
 DR P-PSDB; AAY53923.
 XX
 PT A new activator of G protein signalling used to treat disorders
 PT characterized by an aberrant AGS protein activity -
 XX
 PS Example 15, Page 143-144; 162pp; English.
 XX
 CC The present sequence encodes a homologue of a human AGS1 (activator
 CC of G protein signalling (AGS)) protein. The AGS cDNA sequence was
 CC isolated from a human liver cDNA library. The AGS protein exhibits
 CC homology to ras-related G proteins, and contains alterations in
 CC conserved amino acids consistent with a deficiency in GTP hydrolysis
 CC activity. AGS stimulates G protein activity, G protein-coupled signal
 CC transduction and the pheromone response pathway in a receptor-independent
 CC manner. The AGS protein also shows G-gamma selectivity, as measured by
 CC growth assays in yeast expressing various mammalian G-gamma constructs,
 CC and tissue-specific expression, as measured by Northern blot analysis.
 CC The AGS protein can be used to screen for compounds that modulate
 CC cellular signal transduction. The protein is used to treat disorders
 CC characterized by an aberrant AGS protein activity or AGS nucleic acid
 CC expression.
 XX
 SO Sequence 837 BP; 177 A; 272 C; 233 G; 155 T; 0 other;
 50
 Alignment Scores:
 Pred. No.: 1.46e-93 Length: 837
 Score: 893.00 Matches: 174
 Percent Similarity: 78.14% Conservative: 44
 Best Local Similarity: 62.37% Mismatches: 45
 Query Match: 61.59% Indels: 16
 DB: 21 Gaps: 4

US-09-709-103-1f1 (1-282) x AA236913 (1-837)

QY 5 AlaMetIleLysLysMetCysProSerAspSerGluLeuSerIleProAlaLysAsnGys 24
 Db 34 GCCATGATGAAGACTTTGTCCAGCGGAATGCAAGCTCAGTGTGCGCCGCAAAAATCA 93
 QY 25 TyrArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIleValSerArgPhe 44
 Db 94 TACCGCATGTGTGTCTGAGTGTCTCTCGGGTGGCAAGACTCCATGTCGTCTCGCTTC 153
 QY 45 LeuThrGlyArgPheGluAspAlaIleThrProThrIleGluAspPheAsxLysPhe 64
 Db 154 CTCATGCGCGCTTTGAGACGACGACACACCCACATCGAGACTTCCACCGTAAGGTA 213
 QY 65 TyrSerIleArgGlyGluValIleGluLeuAspIleLeuAspThrSerGlyAsnHisPro 84
 Db 214 TACAACATCCCGCGGCGCATGTACGACGCTGACATCTGTGATACCTGTGGCACACCCC 273
 QY 85 PheProAlaMetArgArgLeuSerIleLeuThrGlyAspValIlePheIleLeuValPheSer 104
 Db 274 TTCCTGGCATGCGAGGCTGTCTCTCAAGGGAGTGTCTTCATCTCGTGTTCAGC 333
 QY 105 LeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGlnIleLeuAspThr 124
 Db 334 CTGATTAACCGGAGCTCTTCATGATAGGTCAAGCCCTTCGAAAGACATCTGAGAGTC 393
 QY 125 LysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeuValIleCysGly 144

Db 394 AAGTCTCGCTGAAGAAACAAGACCAAGGCGCGGAGCTGCGCATGTCTGTGCG 453
 QY 145 AsnLysGlyAspArg---AspPheTyrArgGluValAspGlnArgGluIleGluGlnLeu 163
 Db 454 AACCAAGAACGACGAGCGCTGTGCTGCGCAGGTGCCACCAACCGAGCGTGTG 513
 QY 164 ValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLysAsnSerSer 183
 Db 514 GTGTGCGGCGAC---GAGAACTGCGCTTACTTGAGAGTGTGCGCAAGAAAGAACCAAC 570
 QY 184 LeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGluMetSerPro 203
 Db 571 GTGACAGAGATGTTCTTACCGTCTTCAAGATGCGCAAGCTGCCACAGAGATGAGCCCC 630
 QY 204 AspLeuHisArgLysValSerValGlnTyrCysAspValLeuHisLysLys-----Ala 221
 Db 631 GCCCTGATCGCAAGATCTTCGTCGAGTACGGTGAAGCGCTTCCACCCGCGCTTCTGC 690
 QY 222 LeuArgAsnLysLysLeuLeuArgAlaGlySerGlyGlyGlyAspProGlyAsp 241
 Db 691 ATGCGCGCGCTCAAGAGATG-----GAC 714
 QY 242 AlaPheGlyTleValAlaProPheAlaArgArgProSerValHisSerAspLeuMetTyr 261
 Db 715 GCTATGAGCATGTGTCTGCGCTTGCCTGCGCGCGCCGACGCTCAACAGTACCTCAAGTAC 774
 QY 262 IleArgGluLysLysLeuArgAlaGlySerGlnAlaLysAspLysGluArgCysValIle 280
 Db 775 ATCAAGGCCAAGGTCTCTCGGGAAGCGCAGCGCTGAGAGGAGCAAGTGCACCATC 831

RESULT 10
 ABL92076
 ID ABL92076 standard; cDNA; 2832 BP.
 XX
 AC ABL92076;
 XX
 DT 30-MAY-2002 (first entry)
 XX
 DE Human Tumour Endothelial Marker polynucleotide SEQ ID NO 174.
 XX
 KW Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
 KW normal endothelial marker; pan-endothelial marker; immunostimulant;
 KW antiangiogenic; tumour; neovascularization; vasculatured tumour;
 KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
 KW psoriasis; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200210217-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 01-AUG-2001; 2001WO-US24031.
 XX
 PR 02-AUG-2000; 2000US-222599P.
 PR 11-AUG-2000; 2000US-224360P.
 PR 11-APR-2001; 2001US-282850P.
 XX
 PA (UYUO) UNITV JOHNS HOPKINS.
 XX
 PI St Croix B, Kinzler KW, Vogelstein B;
 XX
 DR WPI; 2002-291856/33.
 XX
 PT An isolated molecule comprising an antibody variable region which
 PT specifically binds to an extracellular domain of a tumor endothelial
 PT marker (TEM) protein, useful for inhibiting tumor growth -
 XX
 PS Disclosure; Page 119-120; 331pp; English.
 XX
 CC The invention relates to an isolated molecule comprising an antibody
 CC variable region which specifically binds to an extracellular domain of a

CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
 CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
 CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
 CC They are useful for inhibiting tumour growth, neoangiogenesis in
 CC subjects bearing a vascularised tumour, polycystic kidney disease,
 CC diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse
 CC and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and
 CC ABB90721-ABB90789) are disclosed, as are marker oligonucleotide
 CC sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and
 CC ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074;
 CC and pan-endothelial markers (PEM) ABL91903-ABL91995.

XX Sequence 2832 BP; 602 A; 891 C; 727 G; 612 T; 0 other;

Alignment Scores:

Pred. No.: 8.3e-93 Length: 2832
 Score: 893.00 Matches: 174
 Percent Similarity: 78.14% Conservative: 44
 Best Local Similarity: 62.37% Mismatches: 45
 Query Match: 61.59% Indels: 16
 DB: 24 Gaps: 4

US-09-709-103-1F1 (1-282) x ABL92076 (1-2832)

Qy 5 AlaMetIleLysLysMetCysProSerAspSerGluLeuSerIleProAlaLysAsnCys 24
 Db 34 GCCATGATGAAGACTTTGTCCAGCGGAAGTGCAGCTGTGCGCCGCAAAACTCA 93
 Qy 25 TyrArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIleValSerArgPhe 44
 Db 94 TACCCGATGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT 153
 Qy 45 LeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPheHisArgLysPhe 64
 Db 154 CTCAATGCCCGCTTTAGGACCACTACACACCCACCATCCAGGACTTCCACCCGTAAGGTA 213
 Qy 65 TyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisPro 84
 Db 214 TACAACATCCGCGGACATGTACACATCTGCATCTGATACCTTGGCAACCAACCC 273
 Qy 85 PheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSer 104
 Db 274 TTCCCGCCATGCCAGGTGTCTCATCTCACAGGGATGTCTTCATCTCTGGTTCAGC 333
 Qy 105 LeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnIleLeuAspThr 124
 Db 334 CTGGATAACCGGAGTCTCTCGATGAGTCAAGCGCTTCAGAAGCAGATCCTGGAGTC 393
 Qy 125 LysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeuValIleCysGly 144
 Db 394 AAGTCTCTGCTGAAGAACCAAGACCAAGGCGCGGAGGTGCCATGGTCATCTGTGGC 453
 Qy 145 AsnLysGlyAspArg---AspPheTyrArgGluValAspGlnArgGluIleGluGlnLeu 163
 Db 454 AACAAAGAACACACCGGAGTGTGGCGGAGTGTGGCGGAGTGTGGCGGAGTGTGGCG 513
 Qy 164 ValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLysAsnSerSer 183
 Db 514 GTGTCCGGCGAC---GAGAACTGGCGCTACTTTCAGGTGTGGCGGAGGAGCAACCAAC 570
 Qy 184 LeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGluMetSerPro 203
 Db 571 GTGGACGAGATGTTCTTACGTCTCTTACGATGCTGCAAGTGTGCCACACGAGATGAGCCC 630
 Qy 204 AspLeuHisArgLysValSerValGlnTyrCysAspValLeuHisLysLys-----Ala 221
 Db 631 GCCCTGTCATCGAGATCTCGGTGAGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT 690
 Qy 222 LeuArgAsnLysLysLeuLeuArgAlaGlySerGlyGlyGlyGlyGlyAspProGlyAsp 241
 Db 691 ATGCCCGCGTCAGGAGATG-----GAC 714
 Qy 242 AlaPheGlyIleValAlaProPheAlaArgProSerValHisSerAspLeuMetTyr 261

Db 715 GCCTATGCGATGGTCTCGCCCTTCCGCGCGCCGCGCCAGCTCAACAGTCAAGTAC 774
 Qy 262 IleArgGluLysAlaSerAlaGlySerGlnAlaLysAspLysGluArgCysValIle 280
 Db 775 ATCAAGGCCAAGTCTCTCGGGAAGGCCGCGCGTGGAGGGGCAAGTGCACCATC 831

RESULT 11

ABL92087
 ID ABL92087 standard; cDNA; 2973 BP.

XX ABL92087;

XX 30-MAY-2002 (first entry)

XX Human Tumour Endothelial Marker polynucleotide SEQ ID NO 197.

XX Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
 KW normal endothelial marker; pan-endothelial marker; immunostimulant;
 KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
 KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
 KW psoriasis; gene; ss.

XX Homo sapiens.

XX WO200010217-A2.

XX 07-FEB-2002.

XX 01-AUG-2001; 2001WO-US24031.

XX 02-AUG-2000; 2000US-222599P.

XX 11-AUG-2000; 2000US-224360P.

XX 11-APR-2001; 2001US-282850P.

XX (UVJO) UNIV JOHNS HOPKINS.

XX St Croix B, Kinzler KW, Vogelstein B;

XX WPI; 2002-291856/33.

XX P-PSDB; ABB90733.

XX An isolated molecule comprising an antibody variable region which
 PT specifically binds to an extracellular domain of a tumor endothelial
 PT marker (TEM) protein, useful for inhibiting tumor growth -

XX Claim 65; Page 152-153; 33pp; English.

XX The invention relates to an isolated molecule comprising an antibody
 CC variable region which specifically binds to an extracellular domain of a
 CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
 CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
 CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
 CC They are useful for inhibiting tumour growth, neoangiogenesis in
 CC subjects bearing a vascularised tumour polycystic kidney disease,
 CC diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse
 CC and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and
 CC ABB90721-ABB90789) are disclosed, as are marker oligonucleotide
 CC sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and
 CC ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074;
 CC and pan-endothelial markers (PEM) ABL91903-ABL91995.

XX Sequence 2973 BP; 596 A; 967 C; 787 G; 623 T; 0 other;

Alignment Scores:

Pred. No.: 8.89e-93 Length: 2973
 Score: 893.00 Matches: 174
 Percent Similarity: 78.14% Conservative: 44
 Best Local Similarity: 62.37% Mismatches: 45
 Query Match: 61.59% Indels: 16
 DB: 24 Gaps: 4

US-09-709-103-1F1 (1-282) x ABL92087 (1-2973)

QY 5 AlameTlleYslysmwCysProSerAspSerGluLeuSerlleProAlaYsancys 24
 DB 205 GCCATGATGAAGACTTGTTCACAGCGGAACTGACGCTCAGTGTGCGCCCAAAAACCTCA 264
 QY 25 TyrArgMetValIleLeuEnlYsSerlyServalGlyVtThAlaIleValSerArgPhe 44
 DB 265 TACCGCATGTGTGTCTGGTGTCTCTCGGGTGGCGCAAGATCTCCATCTGTCTGTCTTC 324
 QY 45 LeuThGlyArgPheGluAspAlaTyrThrProThrIleGluAspPheHisArglySph 64
 DB 325 CTCGAATGGCCGCTTTAGAGACCACTACACACCCATGAGAGACTTCCACCGTAAGTA 384
 QY 65 TyrSerIleArgGlyGluValYlYrGluLeuAspIleLeuAspThrSerGlyAsnHisPro 84
 DB 385 TACAAATCCGCGGACATGTATCCAGCTCGACATCTGTATACCTCTGCAACCAACCC 444
 QY 85 PheProAlaMetArgArgLeuSerlleLeuThrglyAspValPheIleLeuValPheSer 104
 DB 445 TTCCTCCGATGGCGAGGCTGTCTTCATCTCAACAGGGAGTCTTCACTCTGTGTCTGAC 504
 QY 105 LeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnIleLeuAspThr 124
 DB 505 CTGGATAAACGGGAGCTTTCATGAGGTCAAGCCCTTCAAGAGCATCTTGAAGGTC 564
 QY 125 YrSerCysLeuYsAsnYsThrlySgluAsnValAspValProLeuValIleCysgly 144
 DB 565 AAGTCTGCTGAAAGAACAAAGCAAGAGGCGGCGGAGCTGCCATGTCTGTGTG 624
 QY 145 AsnlySglYAspArg---AspPheTyrArgGluValAspGlnArgGluIleGluLeu 163
 DB 625 AACCAAGAACGACACCGGCGAGCTGTGCCCGCAGGTGCCACCAACGAGCGCAGCTGTG 684
 QY 164 ValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaYslyAsnSerSer 183
 DB 685 GTGTGGGGGAC---GAGAACTGCCCTTCTTGAGGTCTCGCAAGAGAACACCAAC 741
 QY 184 LeuAspGlnMetPheArgAlaLeuPheAlaMetAlaYsLeuProSerGluMetSerPro 203
 DB 742 GTGAGCAGATGTCTTACGCTGCTTCAAGCATGGCCAACTGCCACAGAGATGAGCC 801
 QY 204 AspLeuHisArgLyValSerValGlnTyrCysAspValLeuHisLyS---Ala 221
 DB 802 GCCCTGCATCGGAAGTCTCCGTGCAAGTACGCGCTTCACCCAGCCCTTCTGC 861
 QY 222 LeuArgAsnlySlyLeuLeuArgAlaGlySerGlyGlyGlyAspProIlyAsp 241
 DB 862 ATGCCCGCGCTCAAGGACATG-----GAC 885
 QY 242 AlaPheGlyIleValAlaProPheAlaArgArgProSerValHisSerAspLeuMetTyr 261
 DB 886 GCGTATGGCATGTCTCGCCCTTCCGCCGCCGCCAGGCTCAACAGTACCTCAAGTAC 945
 QY 262 IleArgGluYsAlaSerAlaGlySerGlnAlaYsAspLySgluArgCysValIle 280
 DB 946 ATCAAGGCCAAGTCTTCTCGGAAGGCCGCGCGTGAAGGAGCAAGTGCACCATC 1002
 RESULT 12
 ABK71563
 ID ABK71563 standard; cDNA, 3427 BP.
 XX ABK71563;
 DT 30-JUL-2002 (first entry)
 DE Human dithp polynucleotide #29.
 XX
 KW Human; dithp; diagnostic and therapeutic polynucleotide; gene; ss; bone;
 KW cell proliferative disorder; cancer; tumour; autoimmune disorder; brain;
 KW inflammatory disorder; viral infection; bacterial infection; seizure;
 KW fungal infection; parasitic infections; developmental disorder; breast;
 KW endocrine disorder; metabolic disorder; neurological disorder; cervix;
 KW gastrointestinal disorder; transport disorder; gene therapy; kidney;

KW adrenal gland; bone marrow; lung; ovary; pancreas; prostate; spleen;
 KW skin; testis; thymus.
 OS Homo sapiens.
 XX
 FN W0200220754-A2.
 XX
 PD 14-MAR-2002.
 XX
 PF 29-AUG-2001; 2001MO-US27127.
 XX
 PR 05-SEP-2000; 2000US-229747P.
 PR 05-SEP-2000; 2000US-229748P.
 PR 05-SEP-2000; 2000US-229749P.
 PR 05-SEP-2000; 2000US-229750P.
 PR 05-SEP-2000; 2000US-229751P.
 PR 05-SEP-2000; 2000US-230583P.
 PR 06-SEP-2000; 2000US-230505P.
 PR 06-SEP-2000; 2000US-230514P.
 PR 06-SEP-2000; 2000US-230515P.
 PR 06-SEP-2000; 2000US-230517P.
 PR 06-SEP-2000; 2000US-230518P.
 PR 06-SEP-2000; 2000US-230519P.
 PR 06-SEP-2000; 2000US-230595P.
 PR 06-SEP-2000; 2000US-230597P.
 PR 06-SEP-2000; 2000US-230598P.
 PR 06-SEP-2000; 2000US-230599P.
 PR 06-SEP-2000; 2000US-230610P.
 PR 06-SEP-2000; 2000US-230655P.
 PR 06-SEP-2000; 2000US-230685P.
 PR 07-SEP-2000; 2000US-230988P.
 PR 07-SEP-2000; 2000US-230951P.
 PR 07-SEP-2000; 2000US-231163P.
 PR 07-SEP-2000; 2000US-231167P.
 XX
 PA (INCR-) INCTE GENOMICS INC.
 XX
 PI Stuart J, Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JL;
 PI Jones AU, Yu JY, Wright RJ, Gierzen D, Liu TF, Yap PE, Dahl CR;
 PI Motiyama MG, Bradley DL, Rohatgi SD, Harris B, Roseberry AM;
 PI Gerstein EH, Peralta CH, David MH, Panzer SR, Florese V, Daffo A;
 PI Marwaha R, Chen AV, Chang SC, Au AP, Inman RR;
 XX
 DR WPI; 2002-383054/41.
 DR P-PSDB; ABG59971.
 XX
 PT An isolated polynucleotide useful in diagnostics and therapeutics -
 XX
 PS Claim 1; Page 419-420; 686pp; English.
 XX
 CC The invention relates to human diagnostic and therapeutic (dithp)
 CC polynucleotides and their associated polypeptides (DITHP polypeptides).
 CC The sequences of the invention are used in the treatment and diagnosis of
 CC cell proliferative disorders (e.g. atherosclerosis, cirrhosis), cancers
 CC (e.g. tumours of the adrenal gland, bone, bone marrow, brain, breast,
 CC cervix, kidney, lung, ovary, pancreas, prostate, skin, spleen, testis or
 CC thymus), autoimmune/inflammatory disorders (e.g. asthma, bronchitis,
 CC psoriasis, osteoporosis), viral infections, bacterial infections, fungal
 CC infections, parasitic infections, developmental disorders (e.g. anaemia,
 CC epilepsy), seizure disorders (e.g. cerebral palsy, spina bifida),
 CC endocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders
 CC (e.g. obesity, diabetes), neurological disorders (e.g. stroke,
 CC amyotrophic lateral sclerosis, multiple sclerosis), gastrointestinal
 CC disorders (e.g. ulcerative colitis, lysinuria) and transport disorders
 CC (e.g. myotonic dystrophy, catatonias, peripheral neuropathy). Sequences
 CC ABK71535-ABK71809 represent human dithp polynucleotides of the invention.
 XX
 SQ Sequence 3427 BP; 682 A; 1145 C; 935 G; 665 T; 0 other;
 Alignment Scores:
 Pred. No.: 1 09e-92 Length: 3427
 Score: 893.00 Matches: 174
 Percent Similarity: 78.14% Conservative: 44
 Best Local Similarity: 62.37% Mismatches: 45

QY 195 AlalysLeuProSerGluMetSerProAspLeuHisArgLysValSerValGlnTyrCys 214
 DB 649 GCCAAGCTGCCACAGAGATGAGCCCGCTGCATCGCAGATCTCCGTCGACGAGTACGGT 708
 QY 215 AspValLeuHisLysLys-----AlaLeuArgAsnLysLysLeuLeuArgAlaGlySer 232
 DB 709 GAGCGCTTCCACCCAGGCGCTTGTGCATCGCGCGCTCAAGGAGATG----- 756
 QY 233 GlyGlyGlyGlyGlyAspProGlyAspAlaPheGlyLeuValAlaProPheAlaArgAtg 252
 DB 757 -----GAGCGCTATGGCATGGTCTCGCCCTTCGCGCGCTTCGCGCGCGCG 792
 QY 253 ProSerValHisSerAspMetTyrIleArgGluLysAlaSerAlaGlySerGlnAla 272
 DB 793 CCCAGCGTCAACAGTACCTCAAGTACATCAAGCCCAAGGTCCTTCGCGGAAGGCCAGGCC 852
 QY 273 LysAspLysGluArgCysValile 280
 DB 853 CGTGAGAGGACAAAGTGCAACATC 876
 RESULT 15
 ABL07789
 ID ABL07789 standard; cDNA; 1305 BP.
 XX AC ABL07789;
 XX DT 26-MAR-2002 (first entry)
 XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 17849.
 DE Drosophila; developmental biology; cell signalling; insecticide;
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ss.
 XX OS Drosophila melanogaster.
 XX WO200171042-A2.
 XX 27-SEP-2001.
 XX 23-MAR-2001; 2001WO-US09231.
 XX 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX (PEKE) PE CORP NY.
 PA Venter JC, Adams M, Li PWD, Myers EW;
 PI WPI; 2001-656860/75.
 DR P-PSDB; ABB63686.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX Claim 1; SEQ ID NO 17849; 21pp + Sequence Listing; English.
 PS The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABBS7737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 1305 BP; 313 A; 390 C; 336 G; 266 T; 0 other;

Alignment Scores: 4.04e-61 Length: 1305
 Pred. No.:

Score: 615.00 Matches: 134
 Percent Similarity: 64.42% Conservative: 38
 Best Local Similarity: 50.19% Mismatches: 26
 Query Match: 42.41% Indels: 26
 DB: 23 Gaps: 6
 US-09-709-103-1F1 (1-282) x ABL07789 (1-1305)
 QY 18 SerIlePro---AlaLysAsnCysTyrArgMetValIleLeuGlySerSerLysValGly 36
 DB 475 AGCCTGCCATCGGCGCAAACTGCTATCGATGTTATGCTCGGCTCATCACGCGCGCG 534
 QY 37 LysThrAlaIleValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThr 56
 DB 535 AAGTCATCGATTGTGGCAGCTTCTCTGGGCAATCGTTTCGAGGAGGCTTACGCGCGACC 594
 QY 57 IleGluAspPheHisArgLysPheTyrSerIleArgGlyGluValTyrGlnLeuAspIle 76
 DB 595 ATCGAGGAGTTCACCGCAATTTGATCGCATACGAATGAAGTCTTCAATTGGATATT 654
 QY 77 LeuAspThrSerGlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGly 96
 DB 655 TTGGATACCTCTGGCTATCATCCGTTTCCGCAATGCGACGTTTATCATTTCTAACTGGG 714
 QY 97 AspValPheIleLeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArg 116
 DB 715 GATCTCTTCATCTCTGCTTTCAGCATGGATTCCCGCGAGTCTTTCGAGGAGGTGGTTCG 774
 QY 117 LeuArgGlnGlnIleLeuAspThrLysSerCysLeuLysAsn-----Lys 131
 DB 775 CTGCGGGAGACATCTGGAGACCAAGTGGGCTGCATAAATCCCGGCTCCCGGTTTAAAG 834
 QY 132 ThrLysGluAsnValaspValProLeuValIleCysGlyAsnLysGlyAspArgPhe 151
 DB 835 AAGAGAGTCTTCCAAAGATACCCATGATATTTGGCGGGAATAAATGTGATCGAGACITT 894
 QY 152 TyrArgGluValaspGlnArgGluIleGluGlnLeuValGlyAspAspProGlnArgCys 171
 DB 895 ---AAACTGTTCAAGTGACGAGGTGAGGTGCTACATCGTGGCCAGGACAACTGCTGC 951
 QY 172 AlaTyrPheGluIleSerAlaLysLysAsnSerSerLeuAspGlnMetPheArgAlaLeu 191
 DB 952 ACCTTTGTGGAGTGCTCGGCTCGTCAGAATTACCGCATCGATGACCTATTCCACTCGCTG 1011
 QY 192 PheAlaMetAlaLysLeuProSerGluMetSerProAspLeuHisArgLys---ValSer 210
 DB 1012 TTTACGCTCTCCAATCTCGCGCTGGAGATGACCCCAATCATCATCTGTTGGTCTCC 1071
 QY 211 ValGlnTyrCysAspValLeuHisLysLysAlaLeuArgAsnLysLysLeuLeuArgAla 230
 DB 1072 GTTTTGGGCGGCC-----TCGCCACTCCCAACCCACAC 1104
 QY 231 GlySerGlyGlyGlyGlyAspPro-----GlyAsp 241
 DB 1105 GGAATCTCGGTGGCGGCGGCAAGAAAGATGCCCTCTCCATCAAGAGAGATTACCGCAT 1164
 QY 242 AlaphedylleValAlaProPheAlaArgArgProSerValHisSerAspLeuMetTyr 261
 DB 1165 GCCTGCGGTGTGTGACGCGCAACGCGAGGAGACCCGACGATCCGACCGATCTCAATCTG 1224
 QY 262 IleArgGluLysAlaSerAla 268
 DB 1225 ATGAGATCCAGAGCGATGGCG 1245

Search completed: December 30, 2002, 14:45:52
 Job time : 366 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus.p2n model

Run on: December 27, 2002, 22:15:03 ; Search time 353 Seconds
(without alignments)
1792.667 Million cell updates/sec

Title: US-09-709-103-2
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-DB=NCBI.GeneSeq.101002 -OPMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPT=0
-LOOPT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pcr -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-MARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1449	100.0	846	AA236892	CDNA encoding an a
2	1449	100.0	1740	AA236914	CDNA encoding an a
3	1449	100.0	1801	AA236893	CDNA encoding an a
4	1449	100.0	1841	AA236922	Human kd312 polyep
5	1441	99.4	1776	AAA49177	CDNA encoding huma
6	1399.5	96.6	1689	AA233024	Rat kd312 polyep
7	1387	95.7	3986	AA233023	Human kd312 genom
8	1343	92.7	3079	AA233025	Rat kd312 genomic
9	893	61.6	837	AA236913	CDNA encoding a hom
10	893	61.6	2832	ABL92076	Human Tumour Endot
11	893	61.6	2973	ABL92087	Human Tumour Endot
12	893	61.6	3427	ABK71563	Human dltip polynu
13	867	59.8	3020	ABL92134	Mouse Tumour Endot
14	717	49.5	951	AA590571	DNA encoding novel
15	615	42.4	1305	ABL07789	Drosophila melanog
16	494	34.1	624	ABO28318	Oligonucleotide fo
17	494	34.1	624	ABO28319	Oligonucleotide fo
18	459	31.7	624	ABO28320	Oligonucleotide fo
19	459	31.7	624	ABO28321	Oligonucleotide fo
20	370	25.5	368	ABAS1382	Human breast cell
21	370	25.5	368	ABAS6388	Human foetal liver
22	370	25.5	368	ABAS6323	Probe #14789 for g
23	370	25.5	368	AAK17661	Human brain expres
24	370	25.5	368	AAK43477	Human bone marrow
25	370	25.5	368	AAI24259	Probe #14192 for g
26	370	25.5	368	AAI49541	Probe #18227 used
27	370	25.5	368	AAI09818	Probe #9809 used t
28	370	25.5	368	ABSI17600	Human genome-deriv
29	359.5	24.8	4543	ABL07788	Drosophila melanog
30	334	23.1	1087	AAI60838	Human polynucleoti
31	334	23.1	1108	AAI59052	Human polynucleoti
32	334	23.1	1167	AAI59052	Human polynucleoti
33	330.5	22.8	960	ABL22541	Human intracellular
34	322	22.2	3061	ABO72648	Drosophila melanog
35	307.5	21.2	702	ABL14159	Human MDT encodin
36	305	21.0	1144	AAH90075	Drosophila melanog
37	305	21.0	4933	AAK81235	Human bone marrow
38	305	21.0	4934	AAK81234	Human immune/haema
39	304	21.0	1249	ABO72525	Human MDT encodin
40	302	20.8	3300	AAI58569	RAP2 Gene encoding
41	302	20.8	2205	ABL50219	Human polynucleoti
42	301	20.8	2205	ABL50231	Human Rapla, c-Raf
43	301	20.8	2277	ABL50231	Human Rapla, c-Raf
44	301	20.8	2277	ABL50232	Human Rapla, c-Raf
45	301	20.8	2277	ABL50234	Human Rapla, c-Raf

ALIGNMENTS

RESULT 1
AA236892
AA236892 standard; cDNA; 846 BP.

AC AA236892;

DT 13-MAR-2000 (first entry)

DE CDNA encoding an activator of G protein signalling (AGS) protein.

KW Activator of G protein signalling; AGS; ras-related G protein;

KW GTP hydrolysis; G protein activity; pheromone response pathway;

KW G protein-coupled signal transduction; G-gamma selectivity;

KW cellular signal transduction; ss.

OS Homo sapiens.
XX Location/Qualifiers
FH Key

XX Cismowski M, Duzic E;
 XX MPI: 2000-072337/06.
 DR P-PSDB: AAY53924.
 XX
 PT A new activator of G protein signalling used to treat disorders
 PT characterized by an aberrant AGS protein activity -
 XX
 PS Disclosure: Page 146-148; 162pp; English.
 XX
 CC The present sequence encodes an activator of G protein signalling (AGS)
 CC protein. The cDNA sequence was isolated from a human liver cDNA
 CC library. The AGS protein exhibits homology to ras-related G proteins,
 CC and contains alterations in conserved amino acids consistent with a
 CC deficiency in GTP hydrolysis activity. AGS stimulates G protein
 CC activity, G protein-coupled signal transduction and the pheromone
 CC response pathway in a receptor-independent manner. The AGS protein
 CC also shows G-gamma selectivity, as measured by growth assays in
 CC yeast expressing various mammalian G-gamma constructs, and
 CC tissue-specific expression, as measured by Northern blot analysis.
 CC The AGS protein can be used to screen for compounds that modulate
 CC cellular signal transduction. The protein is used to treat disorders
 CC characterized by an aberrant AGS protein activity or AGS nucleic acid
 CC expression.
 CC
 SQ Sequence 1740 BP; 422 A; 546 C; 483 G; 289 T; 0 other;

Alignment Scores:
 Pred. No.: 1,93e-157 Length: 1740
 Score: 1449.00 Matches: 281
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0

US-09-709-103-2 (1-281) x AA236914 (1-1740)

QY 1 MetSerLeuAlaMetIleLysMetCysProSerAspSerGluLeuSerIlePro 20
 DB 146 ATGAAATCGCCGCGATGATCAAGAAAGATGTGCCCGAGCAGCTCGAGTATCCCG 205
 QY 21 AAlaLysAncCysTyrArgMetValIleLeuGlySerSerIysValGlyThrAlaIle 40
 DB 206 GCCAAGAACACTGATCATCGATCTCGCTCGCCAAAGTGGGCAAGAGCCCATC 265
 QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaIleThrProThrIleGluAspPhe 60
 DB 266 GTGTGGCGCTTCCACCGCGCTTCGAGAGACGCTTACACGCTTACCAAGAGAGACTTC 325
 QY 61 HisArgLysPheLeuSerIleArgGlyGluValIleGlnLeuAspIleLeuAspThrSer 80
 DB 326 CACCGCAAGTTCTACTCATCCGCGGAGAGTCTACACAGCTCGACATCTCGACAGCTCC 385
 QY 81 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIle 100
 DB 386 GGCACACACCCGCTCCCGGCATCGCGGCTCTCCATCTCACAGAGACGTTTTCATC 445
 QY 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGln 120
 DB 446 CTGGTGTTCAGTCTGGCAACCCGCGACTCTTCGAGAGAGTGGCGCGCTCAGGACAG 505
 QY 121 IleLeuAspThrLysSerCysIleuLysAsnLysThrLysGlnLysValAspValProLeu 140
 DB 506 ATCTCGACACCAAGTCTTGCTCAAGAACAAACCAAGGAGACGTGAGAGTCCCTG 565
 QY 141 ValIleCysGlyAsnLysGlyAspArgAspPheThrArgGluValAspGlnArgGluIle 160
 DB 566 GTCACTTCGCGCAACAGGAGTACCGGACTTTCACCGGAGGAGGACGCGGAGATC 625
 QY 161 GluGlnLeuValGlyAspAspProGlnArgCysAlaIleThrPheGluIleSerAlaLysLys 180
 DB 626 GAGCAGCTGTGGGCGAGACCCCGCAGCTGCTTCTGAGATCTCGCCCAAGAG 685

QY 181 AsnSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGlu 200
 DB 686 AACACAGAGCTTGACACAGATGTTCGCGCGCTCTTCGCGATGCGCAAGCTCCAGCGAG 745
 QY 201 MetSerProAspLeuHisArgLysValSerValGlnTyrCysAspValLeuHisLysLys 220
 DB 746 ATGACCCCAAGACTTCCACCGCAAGGCTTCGCGTCACTGCGAGCTCTCCACAAAGAG 805
 QY 221 AlaLeuArgAsnLysLysLeuLeuArgAlaGlySerGlyGlyGlyValGlyAspProGly 240
 DB 806 GCGCTGCGGACCAAGAGTCTGCGGCGCGGACGCGCGCGCGCGCGCGCGCGCGCG 865
 QY 241 AspAlaPheGlyIleValAlaProPheAlaArgArgProSerValHisSerAspLeuMet 260
 DB 866 GACGCTTGGCATCTGGACACCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 925
 QY 261 TyrIleArgGluLysAlaSerIleArgGlnAlaLysAspLysGluArgCysValIle 280
 DB 926 TACATCCCGGAGAGGCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGT 985
 QY 281 Ser 281
 DB 986 AGC 988

RESULT 3
 AA236893
 ID AA236893 standard; cDNA; 1801 BP.

AC AA236893;
 XX
 DT 13-MAR-2000 (first entry)
 XX
 DE cDNA encoding an activator of G protein signalling (AGS) protein.
 XX
 KW Activator of G protein signalling; AGS; ras-related G protein;
 KW GTP hydrolysis; G protein activity; pheromone response pathway;
 KW G protein-coupled signal transduction; G-gamma selectivity;
 KW cellular signal transduction; ss.
 XX
 OS Homo sapiens.
 XX

XX Key Location/Qualifiers
 FH 7..153
 FT 5'UTR
 FT CDS
 FT /*tag= a
 FT /*tag= b
 FT /product= "activator of G protein signalling (AGS)
 FT 3'UTR 1000..1801
 FT /*tag= c
 FT
 PN WO9958670-A1.
 XX

PD 18-NOV-1999.
 XX
 PF 07-MAY-1999; 99WO-US10151.
 XX
 PR 08-MAY-1998; 98US-0084842.
 PR 07-OCT-1998; 98US-0103355.
 XX
 PA (CADU-) CADUS PHARM CORP.
 XX

XX Cismowski M, Duzic E;
 XX MPI: 2000-072337/06.
 DR P-PSDB: AAY53921.
 XX

PT A new activator of G protein signalling used to treat disorders
 PT characterized by an aberrant AGS protein activity -
 XX
 PS Claim 3; Page 133-135; 162pp; English.
 XX

DB 255 ATGAACTGGCCGATGATCAAGAAAGATGTGCCCGACGAGCTGGAGTATCCG 314
 QY 21 AlAlAsnAsnCysTyrArgMetValIleLeuGlySerSerLysValGlyThrAlaIle 40
 DB 315 GCCAAGAAAGTATGTCATGTCATGTCGCTGCTCCAGGATGGGCAAGAGCCATC 374
 QY 41 ValSerThrPheLeuThrGlyArgPheGluAspAlaIleTyrThrProThrIleGluAspPhe 60
 DB 375 GTGTGGGCTTCTCCACCGCCGCTCGAGAGAGCCCTACACGCTTACATCGAGGAGCTTC 434
 QY 61 HisArgLysPheThrSerIleLeuGlyGluValTyrGlnLeuAspIleLeuAspThrSer 80
 DB 435 CACCGCAAGTCTACTTCATCCCGGCGAGGCTTACACAGCTCCATCTCCGACAGCTCC 494
 QY 81 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIle 100
 DB 495 GGGCAACACCCGTTCCCGGATCGCGGCTCTCCATCTCCACAGAGAGAGCTTTTCATC 554
 QY 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGln 120
 DB 555 CTGGTGTTCAGTCTGCAACACCGGAGCTCTTCCAGAGAGTGCAGCGGCTCAGGACAG 614
 QY 121 IleLeuAspThrLysSerLysSerLysValAsnLysThrLysGluAsnValAspValProLeu 140
 DB 615 ATCTCGACACCAAGTCTTCCCTCAGACAAACCAAGAGAGACGTGGACGTGCCCTG 674
 QY 141 ValIleCysGlyAsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIle 160
 DB 675 GTCATTCGCGCAACAGAGGTGACCGGACTTCTACCGGAGGTGACAGCCGAGATC 734
 QY 161 GluGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLys 180
 DB 735 GAGAGGTGTGGGCGGAGACCCCGAGCGTGGCTTCTGAGATCTTGGGCAAGAG 794
 QY 181 AsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGlu 200
 DB 795 AACGAGAGCTGAGACCAAGATGTTCCGCGCTCTTCCCATGGCCAAAGTGGCCAGAG 854
 QY 201 MetSerProAspLeuHisArgLysValSerValGlnTyrCysAspValLeuHisLysLys 220
 DB 855 ATGAGCCCAAGACCTGCACCGCAAGGTCTCGGTGAGTACTGACAGCGTGTGCACAAAG 914
 QY 221 AlaLeuArgAsnLysLysLeuLeuArgAlaGlySerLysLysLysLysLysLysLysLys 240
 DB 915 GCGGTGGGAAACAGAGAGCTGCTGGGCGGCGGACGCGGCGGCGGCGGCGGCGGCG 974
 QY 241 AspAlaPheGlyIleValAlaProPheAlaArgArgProSerValHisSerAspLeuMet 260
 DB 975 GAGCGCTTTGGCATGTCGGACCTTGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCG 1034
 QY 261 TyrIleArgGluLysAlaSerAlaGlySerGlnAlaLysAspLysGluArgCysValIle 280
 DB 1035 TACATCCGCGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1094
 QY 281 Ser 281
 DB 1095 AGC 1097
 DB 1095 AGC 1097
 RESULT 5
 AAA49177
 ID AAA49177 standard; cDNA; 1776 BP.
 AC AAA49177;
 XX 03-NOV-2000 (first entry)
 DE cDNA encoding human GTPase associated protein-7.
 XX
 KW Guanine nucleotide binding protein; GTP-binding protein; G-protein;
 KW GTPase; GTPase associated protein; GTPAP; cell proliferation;
 KW autoimmune; inflammatory; immune system disorder; cancer; AIDS;
 KW acquired immune deficiency syndrome; asthma; atherosclerosis;
 KW arthritis; systemic lupus erythematosus; psoriasis; human; ss.

XX OS Homo sapiens.
 XX Key Location/Qualifiers
 FH 180..1025
 FT CDS /tag=a
 FT /product= GTPAP7
 PN W0200031263-A2.
 XX
 PD 02-JUN-2000.
 XX
 PF 23-NOV-1999; 99WO-US28013.
 XX
 PR 23-NOV-1998; 98US-0109592.
 PR 04-FEB-1999; 99US-0118610.
 PR 06-APR-1999; 99US-0127990.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Hillman JT, Tang YT, Bandman O, Lai P, Yue H, Lu DM, Baughn MR,
 PI Yang J, Azimzai Y;
 DR MPI: 2000-400073/34.
 DR P-PSDB: AA99655.
 XX
 PT Human GTPase associated proteins, polynucleotides, and antibodies,
 PT useful for diagnosing, preventing and treating various diseases such as
 PT atherosclerosis, cancer, acquired immune deficiency syndrome (AIDS),
 PT asthma, and autoimmune diseases -
 PS Claim 9; page 125-126; 144pp; English.
 XX
 CC Human cDNA libraries from various tissues were screened for GTPase
 CC associated proteins (GTPAP). The present sequence is cDNA encoding
 CC human GTPAP-7. This sequence was derived from a cDNA library of the
 CC brain tumour tissue from the parietal lobe of a female.
 CC This protein is expressed in reproductive, nervous and
 CC gastrointestinal tissue. The GTPAP proteins may be used to define
 CC agonists and antagonists of GTPAP activity and to generate antibodies
 CC to GTPAP. This means the GTPAP proteins may be useful for treatment or
 CC prevention of diseases associated with GTPAP such as cell proliferation
 CC disorders, autoimmune disorders, inflammatory disorders, immune system
 CC disorders, cancer, AIDS, asthma, atherosclerosis, arthritis, systemic
 CC lupus erythematosus and psoriasis.
 XX
 SQ Sequence 1776 BP; 430 A; 565 C; 490 G; 291 T; 0 other;
 Alignment Scores:
 Pred. No.: 1,67e-156 Length: 1776
 Score: 1441.00 Matches: 280
 Percent Similarity: 99.64% Conservative: 0
 Best Local Similarity: 99.64% Mismatches: 1
 Query Match: 99.45% Indels: 0
 DB: 21 Gaps: 0
 US-09-709-103-2 (1-281) x AAA49177 (1-1776)
 QY 1 MetLysLeuAlaIleMetIleLysMetCysProSerAspSerGluLeuSerIlePro 20
 DB 180 ATGAACTGGCCGATGATCAAGAAAGATGTGCCCGACGAGCTGGAGTATCCG 239
 QY 21 AlAlAsnAsnCysTyrArgMetValIleLeuGlySerSerLysValGlyThrAlaIle 40
 DB 240 GCCAAGAAAGTATGTCATGTCATGTCGCTGCTCCAGGATGGGCAAGAGCCATC 299
 QY 41 ValSerThrPheLeuThrGlyArgPheGluAspAlaIleTyrThrProThrIleGluAspPhe 60
 DB 300 GTGTGGGCTTCTCCACCGCCGCTTCGAGAGAGCTTACACGCTTACACGAGAGCTTC 359
 QY 61 HisArgLysPheThrSerIleLeuGlyGluValTyrGlnLeuAspIleLeuAspThrSer 80
 DB 360 CACCGCAAGTCTACTTCATCCCGGCGAGGCTTACACAGCTCCATCTCCGACAGCTCC 419

QY 81 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIle 100
 DB 420 GGCAACACACCCGTCGCCGACGCGGTGCTCTCATCTCCACAGAGAGGAGTTTTCATC 479
 QY 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGln 120
 DB 480 CTGGGTTCAGTCTGGACACCGCGACCTTCGAGAGGTGCAGCCGCTCAGCGAGAG 539
 QY 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeu 140
 DB 540 ATCCCTGCACACCAAGTCTTCCCTCAAGAACAAACCAAGAGAGAGAGAGAGAGAGAGAG 599
 QY 141 ValIleCysGlyAsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIle 160
 DB 600 GTCACTCTCGGCGACACAGGAGTGCACCGGACCTTTCACCGCGAGGTGACACACCGAGATC 659
 QY 161 GluGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLys 180
 DB 660 GAGCAGCTGTGTGGGCGACGACCCCGCGGTGCGCTTACCTTCGAGATCTCGGCCAAGAG 719
 QY 181 AsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGlu 200
 DB 720 AACAGACACCTGCAGACACATGTCTCCGCGCTTCCGACATGCGCCAGAGTCCACAGCAG 779
 QY 201 MetSerProAspLeuHisArgLysValSerValGlnTyrCysAspValLeuHisLysLys 220
 DB 780 ATGAGCCCGACCTGCACCGCAGAGGTCTCGGTGCAAGTACTCGAGAGTCTCGACAAAGAG 839
 QY 221 AlaLeuArgAsnLysLysLeuLeuValGlySerGluGluGluGluGluGluGluGluGlu 240
 DB 840 GCGCTGCGGAAACAGAAAGCTCTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 899
 QY 241 AspAlaPheGlyIleValAlaProPheAlaArgArgProSerValHisSerAspLeuMet 260
 DB 900 GAGCGCTTGGCATCGTGGACCCCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 959
 QY 261 TyrIleArgGluLysAlaSerAlaGlySerGlnAlaLysAspLysGluArgCysValIle 280
 DB 960 TACATCCCGGAGAGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1019
 QY 281 Ser 281
 DB 1020 AGC 1022
 RESULT 6
 AA23024
 ID AA23024 standard; cDNA; 1689 BP.
 AC AA23024;
 XX
 DT 17-JAN-2000 (first entry)
 XX
 DE Rat kd312 polypeptide encoding cDNA.
 XX
 KW kd312 polypeptide; cancer; immunodeficiency disorder; AIDS; stroke;
 KW heart attack; head trauma; neurodegenerative disease; rat;
 KW Parkinson's disease; Alzheimer's disease; ss.
 XX
 OS Rattus sp.
 XX
 PN MO9950288-A2.
 XX
 PD 07-OCT-1999.
 XX
 PF 30-MAR-1999; 99MO-US06993.
 XX
 PR 31-MAR-1998; 98US-0053374.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Yen K;
 XX

DR WPI; 1999-601322/51.
 DR P-PSDB; AA42694.
 XX
 PT kd312 polypeptides useful for treating diseases and disorders
 PT associated with alterations in cell proliferation and cell death
 XX
 PS Claim 2; Fig 9; 85pp; English.
 XX
 CC The invention provides nucleic acid molecules encoding human and rat
 CC kd312 polypeptides. The kd312 polypeptides can be expressed by standard
 CC recombinant methodology. The kd312 sequences, and the antibodies against
 CC of various diseases, e.g. cancer, immunodeficiency disorders (e.g. AIDS),
 CC stroke, heart attack, head trauma, and neurodegenerative diseases (e.g.
 CC Parkinson's disease and Alzheimer's disease). The present sequence
 CC represents the rat kd312 cDNA sequence.
 XX
 SQ Sequence 1689 BP; 417 A; 462 C; 434 G; 376 T; 0 other;
 Alignment Scores:
 Pred. No.: 9, 87e-152 Length: 1689
 Score: 1399.50 Matches: 273
 Percent Similarity: 98.22% Conservative: 3
 Best Local Similarity: 97.15% Mismatches: 4
 Query Match: 96.58% Indels: 1
 DB: 20 Gaps: 1
 US-09-709-103-2 (1-281) x AA23024 (1-1689)
 QY 1 MetLysLeuAlaAlaMetIleLysLysMetCysProSerAspSerGluLeuSerIlePro 20
 DB 132 ATGAACTGGCCCCGATGATCAAGAGATGTGCCCAAGCGACCTGAACTGATTCGCCG 191
 QY 21 AlaLysAsnCysTyrArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIle 40
 DB 192 GCCAAGACTGCTACAGAGATGATCTCGGCTCATCCAAAGTGGGCAAGCGCCATC 251
 QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
 DB 252 GTGTGCGGCTCTCTCAACGCGCGCTTCGAGAGAGCTTACACCCCTTACCAACTTC 311
 QY 61 HisArgLysPheTyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSer 80
 DB 312 CACGAAAGTTTACTTCGATCCGCGCGGCAAGCTTACACCTTGACATGACACACACT 371
 QY 81 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIle 100
 DB 372 GGCAATCATCCGTTTCCCGCATGCGCGCTCTCTATCTCACAAGAGAGAGGTTTTCATT 431
 QY 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGln 120
 DB 432 CTGGTGTTCAGTTAGACACAGCGGACCTCTTCGAGAGAGTGCACAAAGGCTCAACAGCAG 491
 QY 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeu 140
 DB 492 ATCCCTGCACACCAAGTCTTCCCTCAAGAACAAACCAAGAGAGAGAGAGAGAGAGAG 551
 QY 141 ValIleCysGlyAsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIle 160
 DB 552 GTCACTCTCGGCGACACAGGAGCGGAGCTTCTACCCGAGAGTGCAGCGAGAGATT 611
 QY 161 GluGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLys 180
 DB 612 GAGCAGCTGTGTGGGCGACGATGACCTCGCTGTGCTACTTGAAGATCTCGGCCAAGAG 671
 QY 181 AsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGlu 200
 DB 672 AATGACAGCTGAGCAGATGTTCCGTGCGCTTTCGATGCGCAACCTGCTGAGCAG 731
 QY 201 MetSerProAspLeuHisArgLysValSerValGlnTyrCysAspValLeuHisLysLys 220
 DB 732 ATGAGCCCTGACTTGACCGCAAGGTGTCTGTGCAAGTACTGTGACGCTCTGCACAAAG 791

QY 221 AlaLeuArgAsnLysLysLeuLeuArgAlaGlySerGlyGlyGlyGlyAspProGly 240
 DB 792 GCTCTGGAGCAAGAACAGCTTCTGCGTGGCGCAGC---GAGAGTGGGGCGCCACCGA 848
 QY 241 AspAlaPheGlyIleValAlaProPheAlaArgProSerValHisSerAspLeuMet 260
 DB 849 GATGCGCTTGGCATCTTGGCGCCCTTGTCTGCAACCTAAGCTGCAATGCACTCATG 908
 QY 261 TyrIleArgGlyLysAlaSerAlaGlySerGlnAlaLysAspLysGluArgCysValIle 280
 DB 909 TACATTCGTGAGAAACCAAGCTGTCAGCAGCCAGCCTAAGAGCAAGAGCGCTGTGCATC 968
 QY 281 Ser 281
 DB 969 AGT 971

RESULT 7
 AA23023
 ID AA23023 standard; DNA: 3986 BP.
 AC AA23023;
 XX 17-JAN-2000 (first entry)
 XX 17-JAN-2000 (first entry)

DE Human kd312 genomic DNA sequence.

XX kd312 polypeptide; cancer; immunodeficiency disorder; AIDS; stroke;
 KW heart attack; head trauma; neurodegenerative disease; human;
 KW Parkinson's disease; Alzheimer's disease; ss.

OS Homo sapiens.

PN WO950288-A2.

PD 07-OCT-1999.

PF 30-MAR-1999; 99WO-US06993.

PR 31-MAR-1998; 98US-0053374.

XX (AMGE-) AMGEN INC.

PA Yuen K.

XX WPI; 1999-601322/51.

DR P-PSDB; AA42693.

XX kd312 polypeptides useful for treating diseases and disorders
 PT associated with alterations in cell proliferation and cell death -

PS Claim 1; Fig 5; 85pp; English.

XX The invention provides nucleic acid molecules encoding human and rat
 CC kd312 polypeptides. The kd312 polypeptides can be expressed by standard
 CC recombinant methodology. The kd312 sequences, and the antibodies against
 CC the proteins may be used to treat or diagnose the presence or progression
 CC of various diseases, e.g. cancer, immunodeficiency disorders (e.g. AIDS),
 CC stroke, heart attack, head trauma, and neurodegenerative diseases (e.g.
 CC Parkinson's disease and Alzheimer's disease). The present sequence
 CC represents the human kd312 genomic DNA sequence.

XX Sequence 3986 BP; 856 A; 1226 C; 1172 G; 732 T; 0 other.

SO Alignment Scores:

Pred. No.: 9.36e-150 Length: 3986
 Score: 1387.00 Matches: 281
 Percent Similarity: 79.83% Conservative: 0
 Best Local Similarity: 79.83% Mismatches: 0
 Query Match: 95.72% Indels: 71
 DB: 20 Gaps: 1

US-09-709-103-2 (1-281) x AA23023 (1-3986)

QY 1 MetLysLeuAlaIleMetIleLysMetCysProSerAspSergluLeuSerIlePro 20
 DB 774 ATGAACACTGGCCGCGATGATCAAGAAAGATGGCCGAGCGACTCGAGCTAGATCCG 833
 QY 21 AlaLysAsnCysTyrArgMetValIleLeuGlySerSerLysValGlySerThrAlaIle 40
 DB 834 GCCAAGACGTGTATCGCATGGTCACTCGCTGCTGCCAAGTGGGCAACAGCGCATC 893
 QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
 DB 894 GTGCGCGCTTCTCAGCGCGCTTCCAGAGACGCTACAGCCCTACCATCGAGACTTC 953
 QY 61 HisArgLysPheTyrSerIleArgGlyValTyrGlnLeuAspIleLeuAspThrSer 80
 DB 954 CACCGCAAGTTCTACTCCATCCGCGCGAGGTCTACAGCTGAGACTCGACACGTCC 1013
 QY 81 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThr----- 95
 DB 1014 GGCAACACACCGCTTCCCGGCATGGCGGCGCTCTCATCTTCACAGGTGAGCGGGGCGC 1073
 QY 95 ----- 95
 DB 1074 GGGCAGGTGCGGGAGGAGGAGGCGGGGAAACCTCGGCCAGGGCGCCGACGCCGCT 1133
 QY 95 ----- 95
 DB 1134 CCGGCTGCTGGCGCGCGAGTACTGCGCTTCCGCTTACAGAGCCTAGCGCGCGCGCG 1193
 QY 95 ----- 95
 DB 1194 GCCTCAAAAGTCAAGCCGACTTGGCCCTGGGGGCGCACCCCTACCTTCTCTTCTGCT 1253
 QY 96 -----GlyAspValPheIleLeuValPheSerLeuAspAsnArgAspSe 110
 DB 1254 CTTCTGCCCCCTCTAGAGAGAGCTTTTCACTCGGTTCACCTGCACTGCAACCGCGACTC 1313
 QY 110 rPheGluGluValGlnArgLeuArgGlnGlnIleLeuAspThrLysSerCysLeuLysAs 130
 DB 1314 CTTGAGAGAGGTGCAGCGGCTCAGCGAGAGATCTCGACACCAAGAGTCTGCTCAAGAA 1373
 QY 130 pLysThrLysGluAsnValAspValProLeuValIleCysGlyAsnLysGlyAspArgAs 150
 DB 1374 CAABAACCAAGAGAAAGTGGAGGTGCCCTGGTCACTCGCGCAACAGGTGACCGGCA 1433
 QY 150 rPheTyrArgGluValAspGlnArgGluIleGlnIleLeuValGlyAspAspProGlnArg 170
 DB 1434 CTTCTACCGCGAGGTGACAGCGGCGAGATCGACAGCTGTGGGCGAGACGCCAGCG 1493
 QY 170 rCysAlaTyrPheGluIleSerAlaLysLysAsnSerSerLeuAspGlnMetPheArgIle 190
 DB 1494 CTGCGCTTCTTGGAGATCTCGGCGCCAAAGAAACAGACAGCTGTGAGACAGATGTTCCGCGC 1553
 QY 190 AlaPheAlaMetAlaLysLeuProSerGluMetSerProAspLeuHisArgLysValSe 210
 DB 1554 GCTCTGCGCATGCGCAAGGTGCCAGAGATGAGACCCAGACTCTCACCGCAAGGTCTC 1613
 QY 210 rValGlnTyrCysAspValLeuHisLysLysAlaLeuAsnLysLysLeuLeuArgIle 230
 DB 1614 GGTGCACTACTGCGAGCTGTGCACAAGAGGCGGTGCGGAACAAACAACTCTGCGGGC 1673
 QY 230 aGlySerGlyGlyGlyGlyGlyAspProGlyAspAlaPheGlyIleValAlaProPheAl 250
 DB 1674 CGGCAAGCGGGCGGGCGCGCGCGCGCACCCGCGACGCTTGGCATCGTGGACCTTCCG 1733
 QY 250 aArgArgProSerValHisSerAspLeuMetTyrIleArgGlyLysAlaSerAlaGlySe 270
 DB 1734 GCGCGCGCGCCAGGCTACACAGCACTCATGTACATCCCGAAGGCGCAGCGCGCGAG 1793
 QY 270 rGlnAlaLysAspLysGluArgCysValIleSer 281
 DB 1794 CCAAGCCCAAGACAAAGAGCGCTGCGTCAATCAGC 1827

RESULT 8

AA23025
 ID AA23025 standard; DNA; 3079 BP.
 AC AA23025;
 XX
 DT 17-JAN-2000 (first entry)
 XX
 DE Rat kd312 genomic DNA sequence.
 DE
 KM kd312 polypeptide; cancer; immunodeficiency disorder; AIDS; stroke;
 KM heart attack; head trauma; neurodegenerative disease; rat;
 KM Parkinson's disease; Alzheimer's disease; ss.
 XX
 OS Rattus sp.
 XX
 PN W09950288-A2.
 XX
 PD 07-OCT-1999.
 XX
 PF 30-MAR-1999; 99WO-US06993.
 XX
 PR 31-MAR-1998; 98US-0053374.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Yen K;
 XX
 DR WPI; 1999-601322/51.
 DR P-PSDB; AAY42694.
 XX
 PT kd312 polypeptides useful for treating diseases and disorders
 associated with alterations in cell proliferation and cell death
 XX
 PS Claim 2; Fig 7; 85pp; English.
 XX
 CC The invention provides nucleic acid molecules encoding human and rat
 CC kd312 polypeptides. The kd312 polypeptides can be expressed by standard
 CC recombinant methodology. The kd312 sequences, and the antibodies against
 CC the proteins may be used to treat or diagnose the presence or progression
 CC of various diseases, e.g. cancer, immunodeficiency disorders (e.g. AIDS),
 CC stroke, heart attack, head trauma, and neurodegenerative diseases (e.g.
 CC Parkinson's disease and Alzheimer's disease). The present sequence
 CC represents the rat kd312 genomic DNA sequence.
 XX
 SQ Sequence 3079 BP; 708 A; 843 C; 829 G; 699 T; 0 other;
 Alignment Scores:
 Pred. No.: 7.99e-145 Length: 3079
 Score: 1343.00 Matches: 272
 Percent Similarity: 84.10% Conservative: 3
 Best Local Similarity: 83.18% Mismatches: 5
 Query Match: 92.68% Indels: 48
 DB: 20 Gaps: 2
 US-09-709-103-2 (1-281) x AA23025 (1-3079)
 QY 1 MetLysLeuAlaMetIleLysLysMetCysProSerAspSerGluLeuSerIlePro 20
 DB 303 ATGAAGCTGGCGGATGATCAAGAAAGATGGCCCAAGCACTGTGAACAGATATCCG 362
 QY 21 AlAlAsnCySyrArMetValIleLeuGlySerSerLysValGlyLysThrAlaIle 40
 DB 363 GCCAAGAACTGCTACAGATGCTATCTCTGGCTCATCCAAAGTGGGCAAGAGCCCATC 422
 QY 41 ValSerArpHeuThrGlyArgpHeGluAspAlaTyrThrProThrIleGluAspHe 60
 DB 423 GTGTCCGCTTCCACAGGCGCTTCGAGAGACCTTACACCCCTACCATTTGAAGACTTC 482
 QY 61 HisArgLysPheTyrSerIleArgGlyGluValTyrGluLeuAspIleLeuAspThrSer 80
 DB 483 CACCGAAAGTTTACTGATCCGGGCGAAGCTTACACATGTGACATCTGACACATCT 542
 QY 81 GlyAsnHisProPheProAlaMetArgLargLeuSerIle----- 93

DB 543 GGCATATCATCGCTTCCCGGCATCGCGCCCTCTCTATCTCACAGSTGATGGGGACC 602
 QY 93 ----- 93
 DB 603 GACAGGACCGTGGGAGGAAATCTCGGGAGCGGATGGGGCGTGTGTGTGG 662
 QY 94 -----Leu 94
 DB 663 GCTGTGCTGTGCTGCTCCGTGCTGGAGCTGCCCTCACCTTTCACCTGTTCCCTTG 722
 QY 95 ThrGlyAspValPheIleLeuValPheSerLeuAspAsnArgAspSerPheGluIleVal 114
 DB 723 TA-GGAGACGTTTTCATTTCTGGTTGAGCTTGAGACACCGGACCTCTTCGAGGAGTG 781
 QY 115 GluArgLeuArgGlnGlnIleLeuAspThrLysSerCysLeuLysAsnLysThrLysGlu 134
 DB 782 CAAAGGCTCAAGACAGCATCTAGACACCAAGTCTCTCAAGAACAAACCAAGAG 841
 QY 135 AsnValAspValProLeuValIleGlyAsnLysGlyAspArgAspPheTyrArgGlu 154
 DB 842 AATGTGACGTGCGCGCTGTCATTTGGGTACAAAGGAGCGGACTTCTACCGCGAA 901
 QY 155 ValAspGlnArgGluIleGluGlnLeuValGlyAspAspProGlnArgCysAlaTyrPhe 174
 DB 902 GTGGAGCAGCGGAGATTGAGCAGCTGTGGCGGATGACCCCTAGCGTTGTGCTACTTC 961
 QY 175 GluIleSerAlaLysLysAsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMet 194
 DB 962 GAGATCTCGGCGCAAGAAAGATACACCTGGACCAATGTTCCGTCCGTCTTGGCCATG 1021
 QY 195 AlAlAsnLeuProSerGluMetSerProAspLeuHisArgLysValSerValGlnTyrCys 214
 DB 1022 GCCAAGCTGCTGACGAGATGAGACCTGACTTCACCCGAAAGGTGTCTGTGCAGTACTGT 1081
 QY 215 AspValLeuHisLysLysAlaLeuArgAsnLysLysLeuLeuArgAlaGlySerGlyGly 234
 DB 1082 GACGTGCTGACAAAAGGCTGTGAGGAACAAGAACTCTGCGTGGCGGAGC---GGA 1138
 QY 235 GlyGlyGlyAspProGlyAspAlaPheGlyTyrIleValAlaProPheAlaArgProSer 254
 DB 1139 GTGGGGGCGACACCGAGAGTGGCTTGGCATCTTGGCGCCCTTGGCGAGACCTTAC 1198
 QY 255 ValHisSerAspLeuMetTyrIleArgGluLysAlaSerAlaGlySerGlnAlaLysAsp 274
 DB 1199 GTGCATAGCGACCTCATGTACATTCGTGAGAAACAGTGTACAGCAGCCAGCTAAGGAC 1258
 QY 275 LysGluArgCysValIleSer 281
 DB 1259 AAGGAGCGCTGTGTCACTAGT 1279
 RESULT 9
 AA236913
 ID AA236913 standard; DNA; 837 BP.
 XX
 AC AA236913;
 XX
 DT 13-MAR-2000 (first entry)
 XX
 DE DNA encoding a homologue of activator of G protein signalling AGS1.
 DE
 KM Activator of G protein signalling; AGS; ras-related G protein;
 KM GTP hydrolysis; G protein activity; pheromone response pathway;
 KM G protein-coupled signal transduction; G-gamma selectivity;
 KM cellular signal transduction; AGS1 homologue; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 1..837
 FT CDS
 FT /*tag= a
 FT /product= "AGS1 homologue"

OY	5	AlaMetIleuLySlysMetCysProSerAspSerGluIleuSerIleProAlaLysAsnGlyCys	24
Db	205	GCCTATGATGAAGAACTTTGTCCACGCGGGAACCTGCACGCTCAAGTGTGCCCGCCAAAACCTCA	264
OY	25	TyrArgMetValIleIleuGlySerSerLysValGlyLysThrAlaIleValSerArgphe	44
Db	265	TACCGCATGGTGGTGTGGTGCCCTCCGGGTGGGGAAGAGCTCCATCGTGTCCGCTTC	324
OY	45	LeuThrGlyArgPheGluAspAlaTyrThrProThrIleLysAspPheHisArgLysPhe	64
Db	325	CTCATATGGCCCCCTTTGGAGACCACTATACACACCACTTCAGAGACTTCCACCGCTAAGGTA	384
OY	65	TyrSerIleArgGlyGlyIleValTyrGluIleuAspIleLeuAspPheSerGlyAsnHisPro	84
Db	385	TACACATCCCGCGCGCGCATGTATCCACGCTGACATCTGTGATACCTCTGGCAACCAACCC	444
OY	85	PheProAlaMetArgArgLysSerIleLeuThrGlyAspValPheIleLeuValPheSer	104
Db	445	TTCCCCCGCATGCCAGAGCTGTCCATCTCCACAGGGAGTGTTCATCCGTGTGTCCAG	504
OY	105	LeuAspAsnAlaGlyAspSerPheGluGluIleValGlnArgLeuArgGlnGlnIleLeuAspThr	124
Db	505	CTGATTAACCCGGAGGCTCTTCGATGAGGTCAAGGCGCTTGAAGAAGACGATCTGGAGGTC	564
OY	125	LysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeuValIleCysGly	144
Db	555	AAGTCTCTCCCTGAAGAACACAGACCAAGAGAGCGCGGAGCTGCCCATGATCTGTGGC	624
OY	145	AsnLysGlyAspArg--AspPheTyrArgGluIleValAspGlnArgGluIleGluGlnLeu	163
Db	625	AACAAGAACACGACCCAGCGAGCTGTGCCGCGAGGTGCCACCAACCGAGCGGAGCTGTG	684
OY	164	ValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysAsnSerSer	183
Db	665	GTGTGCGGCGCAG--GAGAACTGCGCTTACTTCAAGGTGTGGCCAAAGAAACACCAAC	741
OY	184	LeuAspGlnMetPheArgAlaIlePheAlaMetAlaLysLeuProSerGluMetSerPro	203
Db	742	GTGAGACGAGATGTTCTACGTCCTCTTCAGCATGGCCAAAGTGGCCACACGAGATGAGGCC	801
OY	204	AspLeuHisArgLysValSerValGlnTyrCysAspValLeuHisLysLys-----Ala	221
Db	802	GCCCTGCATCTCCACAAATCTCCGTACAGTACCGTACGCCCTTCCACCCCAAGCCCTTCTGC	861
OY	222	LeuArgAsnLysLysLeuLeuArgAlaGlySerGlyGlyGlyGlyLysProGlyAsp	241
Db	862	ATGCCCCCGCTCACAGCATG-----GAC	885
OY	242	AlaPheGlyIleValAlaProPheAlaArgArgProSerValHisSerAspLeuMetTyr	261
Db	886	GGCTATGGCATGGTGTGCGCTTGCGCCGCGCCGACCGCATCAAGTGAACCTCAAGTAC	945
OY	262	IleArgGlyLysAlaSerAlaGlySerGlnAlaLysAspLysGlyArgCysValIle	280
Db	946	ATCAAGGCCAAGGTCTTCGGGAAGCGCACGCCCGTGAAGAGGACAAGTGCACCATC	1002
RESULT 12			
ABK71563			
ID	ABK71563 standard; cDNA; 3427 BP.		
XX	ABK71563;		
AC			
XX			
DT	30-JUL-2002 (first entry)		
XX			
DE	Human dithp polynucleotide #29.		
XX			
KW	Human; dithp; diagnostic and therapeutic polynucleotide; gene; ss; bone		
KW	cell proliferative disorder; cancer; tumour; autoimmune disorder; brain;		
KW	inflammatory disorder; viral infection; bacterial infection; seizure;		
KW	fungal infection; parasitic infections; developmental disorder; breast;		
KW	endocrine disorder; metabolic disorder; neurological disorder; cervix;		
KW	gastrointestinal disorder; transport disorder; gene therapy; kidney;		

KW	adrenal gland; bone marrow; lung; ovary; pancreas; prostate; spleen;
KM	skin; testis; thymus.
XX	
OS	Homo sapiens.
XX	
PN	W0200220754-A2.
XX	
PD	14-MAR-2002.
XX	
PE	29-AUG-2001; 2001MO-US27127.
XX	
PR	05-SEP-2000; 2000US-229747P.
PR	05-SEP-2000; 2000US-229748P.
PR	05-SEP-2000; 2000US-229749P.
PR	05-SEP-2000; 2000US-229750P.
PR	05-SEP-2000; 2000US-229751P.
PR	06-SEP-2000; 2000US-230583P.
PR	06-SEP-2000; 2000US-230585P.
PR	06-SEP-2000; 2000US-230586P.
PR	06-SEP-2000; 2000US-230587P.
PR	06-SEP-2000; 2000US-230588P.
PR	06-SEP-2000; 2000US-230598P.
PR	06-SEP-2000; 2000US-230599P.
PR	06-SEP-2000; 2000US-230610P.
PR	06-SEP-2000; 2000US-230865P.
PR	06-SEP-2000; 2000US-230988P.
PR	07-SEP-2000; 2000US-230951P.
PR	07-SEP-2000; 2000US-231163P.
PR	07-SEP-2000; 2000US-231167P.
XX	
PA	(INCYTE -) INCYTE GENOMICS INC.
XX	
PI	Stuart J, Lincoln SE, Altus CW, Dufour GE, Chalup MS, Hillman JL,
PI	Jones AL, Yu YJ, Wright RJ, Gietzen D, Liu TF, Yap PE, Dahl CR,
PI	Moniyama MG, Bradley DL, Kohatgi SD, Harris B, Roseberry AM,
PI	Gerstl EH, Peralta CH, David MH, Panzer SR, Flores V, Datto A;
PI	Matwaha R, Chen AV, Chang SC, Au AP, Imman RR;
XX	
DR	WPI; 2002-383054/41.
DR	P-PSDB; ABG59971.
PT	
XX	An isolated polynucleotide useful in diagnostics and therapeutics -
XX	
PS	Claim 1; Page 419-420; 686pp; English.
XX	
CC	The invention relates to human diagnostic and therapeutic (dthp)
CC	polynucleotides and their associated polypeptides (DTHP polypeptides).
CC	The sequences of the invention are used in the treatment and diagnosis of
CC	cell proliferative disorders (e.g. atherosclerosis, cirrhosis), cancers
CC	(e.g. tumors of the adrenal gland, bone, bone marrow, brain, breast,
CC	cerxix, kidney, lung, ovary, pancreas, prostate, skin, spleen, testis or
CC	thymus), autoimmune/inflammatory disorders (e.g. asthma, bronchitis,
CC	psoriasis, osteoporosis), viral infections, bacterial infections, fungal
CC	infections, parasitic infections, developmental disorders (e.g. anaemia,
CC	epilepsy), seizure disorders (e.g. cerebral palsy, spina bifida),
CC	endocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders
CC	(e.g. obesity, diabetes), neurological disorders (e.g. stroke,
CC	amyotrophic lateral sclerosis, multiple sclerosis), gastrointestinal
CC	disorders (e.g. ulcerative colitis, lysinuria) and transport disorders
CC	(e.g. myoclonic dystrophy, cataracts, peripheral neuropathy). Sequences
CC	ABK1555-ABK1809 represent human dthp polynucleotides of the invention.
XX	
SQ	Sequence 3427 BP; 682 A; 1145 C; 935 G; 665 T; 0 other;
XX	
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Pred. No.:	1.09e-92
Score:	893.00
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Matches:	174
Conservative:	44
Percent Similarity:	78.14%
Best Local Similarity:	62.37%
Mismatches:	45

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 QY 215 AsPValleuHisLysLys-----AlaLeuArgAsnLysLysleuLeuArgAlaGlySer 232
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 Db 709 GACGCGCTCCACGCCCTTCCTGCTGCGCGCGCGCGCGCGAGATG----- 756
 QY 233 GlyGlyGlyGlyGlyAsPProGlyAsPAlaPheGlyIleValAlaProPheAlaArg 252
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 Db 757 -----GACGCTATGCGATGCTGCGCTCGCGCGCGCGCGCGCGCGCGCGCG 792
 QY 253 ProSerValHisSerAspleuMetIleArgGlyValSerAlaGlySerGlnAla 272
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 Db 793 CCCAAGCTCAACAGTACCTCAAGTACCAAGGCCAAGTCTTCGGGAAGGCCAGCGC 852
 QY 273 LysAsPlyGluArgCysValIle 280
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 ID ABL07789 standard; cDNA; 1305 BP.
 XX
 AC ABL07789;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 17849.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ss.
 XX
 OS Drosophila melanogaster.
 XX
 PN W0200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 FA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI: 2001-656660/75.
 DR P-PSDB; ABB63686.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Claim 1: SEQ ID NO 17849; 21pp + Sequence Listing; English.
 XX
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pat_sequences.
 CC
 XX Sequence 1305 BP; 313 A; 390 C; 336 G; 266 T; 0 other;
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 Alignment Scores: 4.04e-61 Length: 1305
 Pred. No.: 1305

Score: 615.00 Matches: 134
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 Best Local Similarity: 50.19% Mismatches: 69
 Query Match: 42.44% Indels: 26
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 QY 37 LysThrAlaIleValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThr 56
 |||||
 Db 535 AAGCATCGATGATGGGCGCTTCCTGGGCATTCGCTGAGAGGCGCTTACACGCGGACG 594
 QY 57 IleGluAspPheHisArgLysPheTyrSerIleArgGlyValIleArgGluLeuAspIle 76
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 Db 595 ATCGAGAGTTCACCGCCAAATGATCGCATCGGAAATGATGATGATGATGATGATGAT 654
 QY 77 LeuAspThrSerGlyAsnHisProPheProAlaMetArgIleuSerIleLeuThrGly 96
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 Db 655 TTGATATCTTCTGCGTATCATCGGTTCCCGCAATGCGAGCGTATCATTTCTAATCGG 714
 QY 97 AspValPheIleLeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArg 116
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 Db 715 GATCTCTTCATCTCGTCTTCACAGATGATGCCGAGATCTTCGAGAGGTGTTCGC 774
 QY 117 LeuArgGlnIleLeuAspThrLysSerCysLeuLysAsn-----Lys 131
 |||||
 Db 775 CTGCGGAGAACATCTGGAGACCAAGTGGGCTGCATTAATCCGCGCTCCGCGTTTAA 834
 QY 132 ThrLysGluAsnValAspValProLeuValIleCysGlyAsnLysGlyAspArgAspPhe 151
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 Db 835 AAGAAAGCTCTCCAAAGATACCATGATATGCGGGAATTAATGATGAGAGCTTT 894
 QY 152 TyrArgGluValAspGlnArgIleGluGluLeuValGlyAspAspProGlnArgCys 171
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 Db 895 ---AAACTGTTCAGGTGAGGAGGTGATGGCTACATCTGCGCCAGAACATCTGCTGC 951
 QY 172 AlaTyrPheGluIleSerAlaLysAsnSerSerLeuAspGlnMetPheArgAlaLeu 191
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 Db 952 ACCTTTGTGAGTGTCTGCGCTCGTCAAAATTTACCGCATGCACTTATTCACCTGCTG 1011
 QY 192 PheAlaMetAlaLysleuProSerGluMetSerProAspleuHisArgly--ValSer 210
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 Db 1012 TTACGCTCTCAATCTGCGCGTGAAGATGACCCCAATCATCATCTGATGCTGCTCC 1071
 QY 211 ValGlnTyrCysAspValIleHisLysLysAlaLeuArgAsnLysLysleuLeuArgAla 230
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 Db 1072 GTTTTGGGGCGCC-----TCGCCACTCCGCCACAC 1104
 QY 231 GlySerGlyGlyGlyGlyAsPPro-----GlyAsP 241
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 Db 1105 GGAATCTCGGTGGCGCGGAGCAAGAAATGCCCTGCTCATCAGAGAGATTCACGCGAT 1164
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 QY 262 IleArgGluLysAlaSerAla 268
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 Db 1225 ATGAGATCAAGAGATGAGCGG 1245

Search completed: December 28, 2002, 01:18:14
 Job time : 366 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 28, 2002, 01:13:57 ; Search time 87 Seconds

(without alignments)
1312.090 Million cell updates/sec

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Perfect score: 1449
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 363474 seqs, 203117208 residues

Total number of hits satisfying chosen parameters: 726948

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -LOOPEXT=0 -UNITS-bits -START=1 -END=1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE-pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODELOCAL -OUTFMT-pct -NORR-ext -HEAPSIZE=500 -MITLEN=0
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-FCAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_NA:*

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13: /cgnt2_6/prodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgnt2_6/prodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	883	60.9	3082	10	US-09-778-963A-1
2	526	36.3	11221	10	US-09-778-963A-3
3	485	33.5	405	10	US-09-960-352-10273
4	370	25.5	368	10	US-09-864-761-21643

Sequence	Score	Length	ID	Description	
Sequence 67, Appl	300	20.7	3346	9	US-09-764-868-67
Sequence 490, App	291	20.1	688	9	US-09-764-868-490
Sequence 336, App	283.5	19.6	2040	12	US-10-044-090-336
Sequence 3, Appl1	278.5	19.2	19797	10	US-09-832-246-3
Sequence 1, Appl1	276.5	19.1	570	12	US-10-104-484-1
Sequence 3, Appl1	275.5	19.1	570	12	US-10-104-484-3
Sequence 25, Appl	272.5	18.8	551	10	US-09-765-298A-25
Sequence 27, Appl	264.5	18.3	930	10	US-09-765-298A-27
Sequence 285, App	259.5	17.9	536	10	US-09-801-368-285
Sequence 556, Ap	255.5	17.6	1271	12	US-10-044-090-110
Sequence 110, App	254	17.5	942	10	US-09-962-832-256
Sequence 256, App	249	17.2	847	10	US-09-822-949A-40
Sequence 40, Appl	245.5	16.9	969	10	US-09-801-368-287
Sequence 287, App	244	16.8	952	10	US-09-917-800A-1389
Sequence 189, Ap	241.8	16.4	2479	9	US-09-764-868-84
Sequence 84, Appl	237	16.4	2479	9	US-09-764-868-69
Sequence 69, Appl	236.5	16.3	1085	9	US-10-067-813-3
Sequence 3, Appl1	236.5	16.3	1085	9	US-10-067-813-3
Sequence 4253, Ap	231.5	16.0	452	10	US-09-960-352-4253
Sequence 1616, Ap	226	15.6	1088	10	US-09-917-800A-1616
Sequence 5830, Ap	225.5	15.6	454	10	US-09-960-352-5830
Sequence 111, App	225	15.5	1191	12	US-10-044-090-111
Sequence 983, App	214.5	14.8	1296	9	US-09-954-531-983
Sequence 1378, Ap	214.5	14.8	1296	9	US-09-954-531-1378
Sequence 6794, Ap	208	14.4	412	10	US-09-954-531-6794
Sequence 10, Appl	206	14.2	1199	10	US-09-794-257-10
Sequence 1, Appl1	203	14.0	1224	10	US-09-972-529-1
Sequence 3, Appl1	203	14.0	3192	10	US-09-788-654A-1
Sequence 91, Appl	200.5	13.8	612	10	US-09-972-529-3
Sequence 44, Appl	194.5	13.4	836	10	US-09-770-445-674
Sequence 501, Appl	194	13.4	1274	10	US-09-925-302-91
Sequence 674, App	193	13.3	752	9	US-09-764-868-501
Sequence 12, Appl	192	13.3	401	10	US-10-108-605-44
Sequence 515, Appl	192	13.3	552	10	US-09-960-352-6793
Sequence 42, App	190.5	13.1	884	10	US-09-770-445-515
Sequence 489, App	187	13.1	774	10	US-09-919-580-42
Sequence 2, Appl1	185.5	12.8	666	9	US-09-938-842A-420
	185.5	12.8	2734	9	US-09-764-868-489
	185.5	12.8	2964	9	US-10-091-613-2

ALIGNMENTS

RESULT 1
US-09-778-963A-1
; Sequence 1, Application US/09778963A
; Patent No. US20020115172A1
; GENERAL INFORMATION:
; APPLICANT: NEELAM, Beena et al
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
; FILE REFERENCE: C1001112
; CURRENT APPLICATION NUMBER: US/09/778, 963A
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-778-963A-1

Alignment Scores:
Pred. No.: 6.21e-102
Score: 883.00
Percent Similarity: 77.78%
Best Local Similarity: 62.01%
Query Match: 60.94%
DB: 10
Gaps: 4

Prior Filing Date:	2001-01-30
Prior Application Number:	PCT/US01/00665
Prior Filing Date:	2001-01-30
Prior Application Number:	PCT/US01/00668
Prior Filing Date:	2001-01-30
Prior Application Number:	PCT/US01/00663
Prior Filing Date:	2001-01-30
Prior Application Number:	PCT/US01/00662
Prior Filing Date:	2001-01-30
Prior Application Number:	PCT/US01/00670
Prior Filing Date:	2001-01-30
Prior Application Number:	US 60/234,687
Prior Filing Date:	2000-09-21
Prior Application Number:	US 09/608,408
Prior Filing Date:	2000-06-30
Prior Application Number:	US 09/774,203
Number Of Seq ID NOS:	49117
Software:	Annotmax Sequence Listing Engine vers. 1.1
Seq ID NO:	21643
Length:	368
Type:	DNA
Organism:	Homo sapiens
Feature:	
OTHER INFORMATION:	MAP TO AL022334.1
OTHER INFORMATION:	EXPRESSED IN BONE MARROW, SIGNAL = 2.8
OTHER INFORMATION:	EXPRESSED IN LUNG, SIGNAL = 3.2
OTHER INFORMATION:	EXPRESSED IN HEPA, SIGNAL = 3
OTHER INFORMATION:	EXPRESSED IN HEART, SIGNAL = 2.6
OTHER INFORMATION:	EXPRESSED IN PLACENTA, SIGNAL = 3
OTHER INFORMATION:	EXPRESSED IN HBL100, SIGNAL = 3
OTHER INFORMATION:	EXPRESSED IN FETAL LIVER, SIGNAL = 2.9
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OTHER INFORMATION:	EXPRESSED IN BR474, SIGNAL = 2.7
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OTHER INFORMATION:	SWISSPROT HIT: P13856, EVALUATE 8.00e-12
OTHER INFORMATION:	EST_HUMAN HIT: BE389944.1, EVALUATE 0.00e+00
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Score:	370.00
Percent Similarity:	89.01%
Best Local Similarity:	75.82%
Query Match:	25.53%
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: : :	Conservative: 12
: : :	Mismatches: 10
: : :	Indels: 0
: : :	Gaps: 0
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RESULT 5	


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RESULT 7
US-10-044-090-336
: Sequence 336, Application US/100444090
: Patent No. US20020137081A1
: GENERAL INFORMATION:
: APPLICANT: Olga Bandman
: TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
: FILE REFERENCE: PA-0028 US
: CURRENT APPLICATION NUMBER: US/10/044,090
: CURRENT FILING DATE: 2002-01-09
: NUMBER OF SEQ ID NOS: 850
: SOFTWARE: perl Program
: SEQ ID NO 336
: LENGTH: 2040
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No. US20020137081A1 3110662CB1
US-10-044-090-336

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US-10-104-484-1
 ; Sequence 1, Application US/10104484
 ; Patent No. US20020150566A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Guan, Kun-Lian
 ; APPLICANT: Stewart, Scott
 ; TITLE OF INVENTION: METHOD OF INHIBITING CANCEROUS CELL PROLIFERATION USING RAS MUTAN
 ; TITLE OF INVENTION: GDP-BOUND CONFORMATION
 ; FILE REFERENCE: UMICH-0010
 ; CURRENT APPLICATION NUMBER: US/10/104,484
 ; PRIORITY FILING DATE: 2002-03-25
 ; PRIOR APPLICATION NUMBER: 60/277,959
 ; PRIORITY FILING DATE: 2001-03-23
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 570
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Nucleotide sequence of the GDP-bound Ras mutant, RasN17N69.
 US-10-104-484-1

Alignment Scores:

Pred. No.:	4,53e-26	Length:	570
Score:	276.50	Matches:	72
Percent Similarity:	52.74%	Conservative:	34
Best Local Similarity:	35.82%	Mismatches:	73
Query Match:	19.08%	Indels:	23
DB:	12	Gaps:	6

US-09-709-103-2 (1-281) x US-10-104-484-1 (1-570)

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 DB 10 TATAAGCTGTGTGGTGGCGCGCGGTGGCAAGATGCGTACATCCACTG 69
 QY 45 LeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPheHisArgLysPhe 64
 DB 70 ATCCAGAACCACTTTGTGGAGCAATGACCCCACTATAGAGATTCCTCCGGAACAG 129
 QY 65 TyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisPro 84
 DB 130 GTGTCATATGATGGAGACAGCTGCTGTGGACATCTGTGATACCGCGGCGAGAGAG 189
 QY 85 PheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSer 104
 DB 190 TACAGCGCATGTGGCAACAGTACATGCGCACCGGGAGGCGTCTGTGTGTGTGCC 249
 QY 105 LeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGlnIleLeuAspThr 124
 DB 250 ATCAACAAACCAAGCTCTTTGAGGACATCCACAGTACAGGAGCAGATC----- 300
 QY 125 LysSerCysLeuLysAsnLysThrLysGlnAsnValAspValProLeuValIleCysGly 144
 DB 301 -----AAACGGGTGAAGAGACTCGGATACCTGCCACAGTGGTGGG 345
 QY 145 AsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGlnIleGlnLeuVal 164
 DB 346 AACAAAGTGTACCTG---GCTGCACGCACTGTGAATCTCGGAGGCTCAGGACTGCC 402
 QY 165 GlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLysAsnSerLeu 184
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 QY 185 AspGlnMetPheArgAlaLeu-----PheAlaMetAlaLysLeu--- 197
 DB 457 GAGGATGCTTCTACAGCTTGTGGTGGATCGGACAGCAACAGCTCGGAAGCTGAAC 516
 QY 198 ---ProSerGlnMetSerProAspLeuHisArgLysValSerValGlnTyrCysAspVal 216
 DB 517 CTTCTGTGTGTGAGTGGCCCGG---CTGCAT-----GAGCTGCAAGTGTGTGCTCTG 566

QY 217 Leu 217
 DB 567 CTG 569

RESULT 10

US-10-104-484-3
 ; Sequence 3, Application US/10104484
 ; Patent No. US20020150566A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Guan, Kun-Lian
 ; APPLICANT: Stewart, Scott
 ; TITLE OF INVENTION: METHOD OF INHIBITING CANCEROUS CELL PROLIFERATION USING RAS MU
 ; TITLE OF INVENTION: GDP-BOUND CONFORMATION
 ; FILE REFERENCE: UMICH-0010
 ; CURRENT APPLICATION NUMBER: US/10/104,484
 ; PRIORITY FILING DATE: 2002-03-25
 ; PRIOR APPLICATION NUMBER: 60/277,959
 ; PRIORITY FILING DATE: 2001-03-23
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 570
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Nucleotide sequence of the wild type Ras mutant, RasN17N69.
 US-10-104-484-3

Alignment Scores:

Pred. No.:	4,53e-26	Length:	570
Score:	276.50	Matches:	72
Percent Similarity:	52.74%	Conservative:	34
Best Local Similarity:	35.82%	Mismatches:	73
Query Match:	19.08%	Indels:	23
DB:	12	Gaps:	6

US-09-709-103-2 (1-281) x US-10-104-484-3 (1-570)

QY 25 TyrArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIleValSerArgPhe 44
 DB 10 TATAAGCTGTGTGGTGGCGCGCGGTGGCAAGATGCGTACATCCACTG 69
 QY 45 LeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPheHisArgLysPhe 64
 DB 70 ATCCAGAACCACTTTGTGGAGCAATGACCCCACTATAGAGATTCCTCCGGAACAG 129
 QY 65 TyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSerGlyAsnHisPro 84
 DB 130 GTGTCATATGATGGAGACAGCTGCTGTGGACATCTGTGATACCGCGGCGAGAGAG 189
 QY 85 PheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIleLeuValPheSer 104
 DB 190 TACAGCGCATGTGGCAACAGTACATGCGCACCGGGAGGCGTCTGTGTGTGTGCC 249
 QY 105 LeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGlnIleLeuAspThr 124
 DB 250 ATCAACAAACCAAGCTCTTTGAGGACATCCACAGTACAGGAGCAGATC----- 300
 QY 125 LysSerCysLeuLysAsnLysThrLysGlnAsnValAspValProLeuValIleCysGly 144
 DB 301 -----AAACGGGTGAAGAGACTCGGATACCTGCCACAGTGGTGGG 345
 QY 145 AsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGlnIleGlnLeuVal 164
 DB 346 AACAAAGTGTACCTG---GCTGCACGCACTGTGAATCTCGGAGGCTCAGGACTGCC 402
 QY 165 GlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLysAsnSerLeu 184
 DB 403 CGAAGC-----TACGGCATCCCTTACATCGAGACTCGGCCAAGACCCGCGAGAGTG 456
 QY 185 AspGlnMetPheArgAlaLeu-----PheAlaMetAlaLysLeu--- 197
 DB 457 GAGGATGCTTCTTACAGCTTGTGGTGGATCGGACAGCAACAGCTCGGAAGCTGAAC 516

CTA GCT GAT GAC GCA GCG CTC CTT GTC GGC CTC GCT GCC GCT GCC CTT
 L A D D A A L L V L G L A A A A A L A G L
 S L M T Q R S A P C P W P G C R R W P S
 CTC GCG GAT GTA CAT GAG GTC GCT TAC GCT GCG CCG GCG GCG GAA GCG TGC
 L A D V H E V A V Y A G P A R E G C
 S R M Y M R S L C T L G R R A K G A
 R G C T . G R C V R W A G A R R V P
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 H D A K G V A R V A A A A A A A G P
 T M P K A S P G S P P P P P L P A R
 R C Q R R R P G R R R R R C R P A
 CAG CAG CTT CTT GTT CCG CAG CCG CTT GTG CAG CAC GTC GCA GTA CTG CAC
 Q O L L V P Q R L L V Q H V A V L L H
 S S F L F R S A F L C S T S Q Y C T
 A A S C S A A P S C A A R R S T A P
 CGA GAC CTT GCG GTC CAG GTC TGG GCT CAT CTC GCT GCG CAG CTT GCG CAT GCG
 R D L A V Q V W A H L A G O L L G H G
 E T L R C R S G L I S L G S L A M A
 R P C G A G L G S S R W A W P W R
 GAA GAG CCG GCG GAA CAT CTG GTC GCT GCT CTT CTT GCG CGA GAT CTC
 E R A A E H L V O A A V L L G R D L
 K S A R N I W S R L L F F L A E I S
 R A R G T S G P G C C S S W P R S R
 GAA GTA GCG GCA GCG CTC GCG GTC GCG CAC CAG CTC CTT CTT CTT CTT CTT
 E V G A A L G V V A H O L L L A L
 K A O R W G S S P T S C S I S R A
 S R R S A G G R R P P A A A S R A G
 GTC CAC CTC GCG GTA GAA GTC GCG GCT GCT GCT GCT GCT GCT GCT GCT GCT
 V H L A V E V A V T L V A A D D O G
 S T S R . K S R S P L L P O M T R G
 P P R G R S R G H P C C R R . P G A
 CAC GTC CAC GTC CTT GGT TTT GTT GAG GCA AGA CTT GGT GTC GAG GAT
 H V H V L L G F V L E A R L G V E D
 T S T F S L V L F L R O D L V S R I
 R P R S P W F C S . G K T W C R G S
 CTG CTG CCT GAG CCG CTC CAC CTC GAA GGA GTC GCG GTC GTC CAG ACT GAA
 L L P E P L L L L L E G V A V V O T E
 C C L S R C T S S K E S R L S R L N
 A A . A A A P P R R S R G C P D . T
 CAC CAG GAT GAA AAC GTC TCC TGT TGT GAG GAT GGA GCG CCG CAT GCG GCG GAA
 H Q D E N V S C E D G E A P H G G E
 T R M K T S P V R M E R R M A G N

P G . K R L L . G W R G A A W R G T
 CCG GTG GTC GCG GCA CGT GTC GAG GAT GTC GAG CTC GTC GTC GTC GTC GTC
 R V V A G R V E D V E L V D L A A D
 G W L P D V S R M S S W . T S P R M
 G G C R T C R G C R A G R P R G W
 GGA GTA GAA CTT GCG GTC GAA GTC GAT GAT GAT GAT GAT GAT GAT GAT GAT
 G V E L A V E V L D G R R V G V L E
 E . N L R W K S S M V G V . A S S K
 S R T C G G S P R W . A C R R P R S
 GCG GCC GGT GAG GAA GCG CGA CAC GAT GAT GAT GAT GAT GAT GAT GAT GAT
 A A G E E A R H D G R L A H L G R A
 R P V R K R D T M A V L P T L D E P
 G R . G S A T R W P S C P P W T S R
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 R M T M R . O F L A G I L S S E S L
 G . P C D S S S W P G Y S A P S R S
 CCG GCA CAT CTT GAT CAT GAT GAT GAT GAT GAT GAT GAT GAT GAT GAT GAT
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 G T S S . S S R P V S
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 US-09-709-103-3
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 G I P S G A G A P S P S R A O P E O
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 N S E R S R S P K P E P R P A R A E
 AGC CCT CCA GCG GCT CAC CCG GCG TGC CAC CCG AGC GAC CCT CAG CCG CCG TCT
 S P P A A H P A C H P S D P O P L S
 A L O P L T P R A T P A T L S R S L
 P S S R S P R V P P O R P S A A L C
 AGC CTT CTC TCG GCG CCG CCG CCG TCG CCG CCG CCG CCG CCG CCG CCG CCG
 A L L S A P R P P S R P L C P M K L
 P F S R P R A R P R G P S A O . N W
 P S L G P A P A L A A P L P N E T G
 GCC GCG ATG ATC AAG AAG AAG TGC CCG AGC GAC TCG GAG CTG AGT ATC CCG GCG
 A A M I K K M C P S D S E L S I P A
 P R () S R R C A R A T R S . V S R P
 R D () Q E D V P E R L G A E Y P G O
 AAG AAC TGC TAT CGC AAG GTC ATC CTC GCG TCG TCC AAG GTC GCG AAG AAG GCG
 K N C Y R M V I L G S S K V G K T A
 R T A I A W S S S A R P R W A R R P

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 US-09-709-103-3
 Seq 3, frame 1, 1-999

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R V A L P H R P L R G R L H A Y H R
GAG GAC TTC CAC CGC AAG TTC TAC TCC ATC CGC GGC GAG GTC TAC CAG CTC GAC 351 378
E D F H R K F Y S I R G E V Y Q L D
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G L P P Q V L L H P R R G L P A R H
ATC CTC GAC ACG TCC GGC AAC CAC CGC TTC CCC GCC ATG CGG CGC CTC TCC ATC 405 432
I L D T S G N H P F P A M R R L S I
S S T P A T T R S P P C G A A S P S
P R H V R Q P P V P R H A A P L H P
CTC ACA GGA GAC GTT TTC ATC CTC GTG TTC AGT CTC GAC ACC AAG TCT TGC CTC TTC 459 486
L T G D V F I L V F S L D N R D S F
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E V Q R L R Q I L D T K S C L K
R R C S G S G S S S T P S L A S R
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P R L L P R G P A R D R A A G G R
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K E D L F V K S N P T A R C A P G R
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S A R G L A S P L P A I R P Q H W G
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G A T E P R R D G H L L R K E R E
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G O D W D Y S P P P V P H G P P
A K T G T I P H P R S P I E A R H P
CCC ATA ACT TTG GGA GGC AAG GCC CAG CCG AAG GTG GAT TTA TCT TCT CAA AGA 1269 1296
P I T L G A R A Q P R V D L S S Q R D
H N F G S E G P A E G G F I F S K T
CCT AAG AGT GAG CGC GGC GTG GGC GGA TGT GAA GTT ATC CAG CCT CTG CTA 1323 1350
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L R V S A G W G R D V K L S S L C
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G F K K P S C P L E G Q D P R G I I

A S R N R H A R L R V R T H G A L S
L Q E T V M P A . G S G P T G H Y L

TTG TCT GTG ATT CCG GGT TGC TGT GAC ACC CGG TAG AGC CTC TGC CCT CCC GAA
L S V I P G C C D S R S L C P P E
C L . F R V A V T A G R A S L P K
V C D S G L L . Q P V E P L P S R N

ACT AAG CGG GGG GGC GTG GGT CAA ATC ATA GCC AAG TGA CTT GTT TAC ATG TGA
T K R G G V G Q I A K . L V Y M .
L S G G A W V K S . P S D L F T C E
A G G R G S N H S Q V T C L H V S

GTG AAA CTG CAC AAA GGA ACA CAA AAC AAA ACT TGC ACT TTA ACG GTA GTT CCG
V K L H K G T Q N K T C T L T V V P
N C T K E T K T L A L . R . F R
E T A Q R N T K Q N L H F N G S S G

GTG TCA ACA TGG ACA CGA ACA AAA CCT TAC CCA GGT GTT TAT ACT GTG TGT GTG
V S T W T R T K P Y P G V Y T V C V
C Q H G H E Q N L T P Q V F I L C V C
V N M D T N K T L P R C L Y C V C V

TGA GGT CTT TAA AGT TAT TGC TTT TGG TTT TAT AAT ATA CAA TAA AAT AAT
G L . S Y C F I W F F N I O . N N
E V F K V I A L F G F L I Y N K I I
R S L K L L L Y L V F . Y T I K . F

TTA AAA TGG AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA
L K W K K K K K K K K K K K K K K K K
K N G K K K K K K K K K K K K K K K K
K M E K K K K K K K K K K K K K K K K

AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA
K K K K K K K K K R P L E H A S R G P H
K K K K K K K K S G R S S M H L E G R I
K K K K K K K A A R A C I . R A A A S

CAT GTA ATT AGT TAT GAA C
H V I S Y E
M . L V M N
C N . L

US-09-709-103-3' - numbering increases in 5' to 3' direction

GTG CAT AAC TAA TTA CAT GAT GCG GCC CTC TAG ATG CAT GCT CGA GCG GCC GGT
V H N . L H D A A L . M H A R A A A
F I T N Y M M R P S R C M L E R P L
S . L I T . C G P L D A C S S G R F

TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT
F F F F F F F F F F F F F F F F F
81 108

F F F F F F F F F F F F F F F F

TTT TTT TTT TCC ATT TTA AAT TAT TTT ATT GTA TAT TAA AAA ACC AAA TAA AGC
F F F S I L N Y F I V Y I K K T K . S
F F F F F F F F F F F F F F F F F
F F F F F F F F F F F F F F F F F

AAT AAC TTT AAA GAC CTC ACA CAC ACA CAG TAT AAA CAC CTC GGT ANG GTT TTG
N N F K D L T H T Q Y K H L G K V L
I T L K T S H T H S I N T W V R F C
L . R P H T H T V . T P G . G F V

TTG GTG TCC ATG TTG ACA CCG GAA CTA CCA TTA AAG TGC AAG TTT TGT TTT GTG
F V S M L T P E L P L K C K F C F V
S C P C . H R N Y R . S A S F V L C
R V H V D T G T T V K V Q V L F C V

TTG CTT TGT GCA GTT TCA CTC ACA TGT AAA CAA CAA GTC ACT TGG CTA TGA TTT GAC
F L C A V S L T C K Q V T W L . F D
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P L C S F T H M . T S H L A M I . P

CCA CCG CCC GCT TAT TGA AGC CTA GCA GAG GGC AGA GGC TCT ACC GGC TGT CAC AGC
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T P P R L L V S G G Q R L Y R L S Q

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T R N H R Q D N A P W V L T L K R A
P G I T D K I M P R G S . P S S G H

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R F L E A . Q R L D . N F T S L P T
D G F L K P S R G W I T S H P S P T

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P R S L L G L . E D K S T L G W A L

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S P S L G P F S F L P E Q M T V P S

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L G S V A P P Q C W G R I A G R G D
S V Q W R L P S A G G S P G G E T
R F S G A S P V L G A D R R E G R R
729 756
GCC AGT CCG GCG CCT CCG GCC TGG GGC GCA CCG GGC CGT TGG ATT TGA CTT
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P V R A R S R P G A H R A V G F D L
Q S A R A P G L G R T G P L D L T
783 810
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N K K V L L L C R Q R G G A P S
T K R S S L G C V A S A A G L L A D
Q K G P P V V S P A R R G S L M
837 864
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D A A L L V L G L A A G L L A F S R M
T Q R S L S L A W L P A L A F S R M
891 918
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C T G R C V R W A G A R R V P R C
V H E V A V Y A G P A R E G C H D A
Y M R S L C T L G R R A K G A T M P
945 972
CAA AGC CGT CCG CCG GGT CGC CCG CGC CGC TGC CCG CCC GCA GCA GGT
O R R A P G R R R R R C R P A A L
K G V A R V A A A A A G P Q L
K A S P G S P P P P L P A R S S F
999 1026
TCT TGT TCC GCA GCG CCT TGT TGT GCA GCA CGT CGC AGT ACT GCA CCG AGA CCT
S C S A A P S C A A R R S T A P R P
L V P Q R L L V Q H V A V L H R D L
L F R S A F L C S T S Q Y C T E T L
1053 1080
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C G A G L G S S R W A A W P W R R A
A V O V W A H L A G Q L G H G E R
R C R S G L I S L G S L A M A K S A
1107 1134
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R G T S G P G C C S S W P R S R S R
A E H L V Q A A V L L G R D L E V G
R N I W S R L L F F L A E I S K A
1161 1188
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R S A L G G R R P A A A R S R A G P P
Q A L G V V A H Q L L D L A L V H L
Q R W G S S P T S C S I S R W S T S
1215 1242
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R G R S R G H P C C R R P G A R P

A V E V A V T L V A A D D O G H V H
R K S R S P L L P Q M T R G T S T
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R S P W F C S G K T W C R G S A A P
V L L G F V L E A R L G V E D L L P
F S L V L F L R Q D L V S R I C C L
1323 1350
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E P L H L L E G V A V V Q T E H Q D
S R C T S S K E S R L S R L N T R M
1377 1404
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E N V S C E D E A P H G G E R V V
K T S P V R M E R R R M A G N G W L
1431 1458
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A G R V E D V E L V D L A A D G V E
P D V S R M S S W T S P R M E N
1485 1512
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L A V E V L D G R R V G V L E A A G
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R K R D T M A V L P T L D E P R M T
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M R Q F L A G I L S S E S L G H I
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R L R S E F
G S A R N S
A P L G I

TRANSLATE (Six-Frame, One-Letter): q

SEQ: q

No changes made since last save, file(s) not written.

GenCore version 5.1.3
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OM protein - nucleic search, using frame_p2n model

Run on: December 30, 2002, 14:39:31 ; Search time 3141 Seconds
(without alignments)
2612.859 Million cell updates/sec

Title: US-09-709-103-1f1

Perfect score: 1450

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Xgapop 10.0, Xgapext 0.5
Fgapop 10.0, Fgapext 0.5
Delop 6.0, Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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41: em_hcgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1449	99.9	846	9	AF498923 Homo sapi
2	1449	99.9	979	9	AF172846 Homo sapi
3	1449	99.9	1187	9	AF153192 Homo sapi
4	1449	99.9	1740	9	AF069506 Homo sapi
5	1449	99.9	1758	9	BC018041 Homo sapi
6	1436	99.9	1746	9	AF177335 Homo sapi
7	1405.5	96.9	1612	10	BC034166 Mus muscu
8	1405.5	96.9	1623	10	AF009246 Mus muscu
9	1399.5	96.5	1616	10	AF239157 Rattus no
10	1387	95.7	1833	9	AF222979 Homo sapi
11	1387	95.7	1833	9	AF222979 Homo sapi
12	1384	95.4	1541	9	AF262018 Homo sapi
13	1370	94.5	1791	10	AF603710 Mouse DNA
14	1370	94.5	2478	2	AC025909 Mus muscu
15	1356	93.5	1835	2	AC090608 Homo sapi
16	1355	93.4	5888	2	AC073621 Homo sapi
17	985	67.9	1625	2	AC122995 Rattus no
18	893	61.6	2832	6	AX393244 Sequence
19	893	61.6	2832	9	AF279143 Homo sapi
20	893	61.6	2973	6	AX393267 Sequence
21	867	59.8	3020	6	BC013419 Homo sapi
22	867	59.8	3020	6	AX393362 Sequence
23	867	59.8	3469	10	AF134409 Rattus no
24	790	54.5	2659	9	HSMB03172 Homo sapi
25	526	36.3	1147	9	HS569D19 Human DNA
26	512	35.3	2110	10	AC076974 Mus muscu
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31	342	23.6	4412	9	AB062937 Macaca fa
32	334	23.0	1875	9	BC008065 Homo sapi
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RESULT 1

ALIGNMENTS

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ACCSSON AF498923.1 GI:20379021
VERSION AF498923.1
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SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Puhl, H.L., Ikeda, S.R. and Aronstam, R.S.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2002) cDNA Resource Center, Guthrie Research Institute, One Guthrie Square, Sayre, PA 18840, USA
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Query Match: 99.93% Indels: 0
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ACCESSION AF172846.1 GI:6014488
VERSION AF172846.1
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Tu, Y. and Wu, C.
TITLE Cloning, expression and characterization of a novel human Ras-related protein that is regulated by glucocorticoid hormone
JOURNAL Biochim. Biophys. Acta 1489 (2-3), 452-456 (1999)
MEDLINE 20135605
PUBMED 10673050
REFERENCE 2 (bases 1 to 979)
AUTHORS Tu, Y. and Wu, C.
TITLE Direct Submission
JOURNAL Submitted (27-JUL-1999) Department of Cell Biology, University of Alabama at Birmingham, 1670 University Blvd., Birmingham, AL 35294, USA
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REFERENCE
1 (bases 1 to 1187)
AUTHORS
Kempainen, R.J.
TITLE
Identification of human pituitary Dextral
JOURNAL
Unpublished
2 (bases 1 to 1187)
AUTHORS
Kempainen, R.J.
TITLE
Direct Submission
JOURNAL
Submitted (20-MAY-1999) Anatomy & Physiology, Auburn University,
College of Veterinary Medicine, Auburn, AL 36849, USA
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Pred. No.:      2.13e-127      Length:      1187
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 VERSION AF069506.1 GI:4959037
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 ORGANISM Homo sapiens
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 1 (bases 1 to 1740)
 Cismowski,M.J., Takesono,A., Ma,C., Lizano,J.S., Xie,X.,
 Fuernkranz,H., Lanier,S.M. and Duzic,E.
 Genetic screens in yeast to identify mammalian nonreceptor
 modulators of G-protein signaling
 Nat. Biotechnol. 17 (9), 878-883 (1999)
 JOURNAL 99403338
 MEDLINE
 PUBMED 10471929
 REFERENCE 2 (bases 1 to 1740)
 Cismowski,M.J., Fuernkranz,H., Ma,C., Spruyt,M., Xie,X.,
 Lanier,S.M. and Duzic,E.
 Direct Submission
 TITLE Receptor Pharmacology/Biochemistry, Cadus
 JOURNAL Submitted (01-JUN-1998)

Pharmaceutical Corporation, 777 Old Saw Mill River Rd., Tarrytown,
 NY 10591, USA
 Location/Qualifiers
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 BOLVDDPQRCAYFEISAKNSSLDMQFRALFAMAKLPSEMSPLDHRKVSVOYCDVLH
 KKALRNKKLLRAGSGGGGPDGAFGIVAFARRPSVHSDLMVIREKASAGSQAKDE
 RCVIS"
 BASE COUNT 422 a 546 c 483 g 289 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 3.37e-127 Length: 1740
 Score: 1449.00 Matches: 281
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.93% Indels: 0
 DB: 9 Gaps: 0
 US-09-709-103-1F1 (1-282) x AF069506 (1-1740)
 Qy 1 MetLysLeuAlaAlaMetIleLysLysMetCysProSerAspSerGluLeuSerIlePro 20
 Db 146 ATGAAACTGGCGCGCATGATCAAGAAGATGTGCCGAGCGACTCGAGCTGAGTATCCG 205
 Qy 21 AlaLysAsnCysTyrArgMetValIleLeuGlySerSerLysValGlyThrAlaIle 40
 Db 206 GCCAAGAAGTCTATCGCATGTCTCGCTCGCTCGCTCAAGGTGGCGAGCGCCATC 265
 Qy 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
 Db 266 GGTCTCGCGCTTCTCACCAGCGCGCTTCGAGGAGCGCTACACGCTTACCATCGAGACTTC 325
 Qy 61 HisArgLysPheTyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSer 80
 Db 326 CACCGCAAGTTCTACTCTCATCGGGCGAGGTCTACAGCTCGACATCTCTCGACACGTCC 385
 Qy 81 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIle 100
 Db 386 GGCAACACCGGTTTCCGCCATCGGGCGCTCTCCATCTCTCAGAGAGAGCTTTTCATC 445
 Qy 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGln 120
 Db 446 CTGTGTGTTTCAGCTTGACAAACCGGACCTCTTCGAGGAGGTGGACCGGCTCAGGACGAG 505
 Qy 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeu 140
 Db 506 ATCTCTGACACCAAGTCTTGCTCTCAAGAACAAACCAAGGAGAAAGCTGGAGCTGCCCTG 565
 Qy 141 ValIleCysGlyAsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIle 160
 Db 566 GTCATCTCGGGCACAAGGTTGACCGGACTTCTACCGGAGGTGGACCGGAGATC 625
 Qy 161 GluGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLys 180
 Db 626 GAGCAGCTGTGTGGCGAGGACCGCGCTGCGCTACTTCGAGATCTCGGCCAAGAAG 685

QY 181 AamSerSerleuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGlu 200
 DB 686 AACAGAGAGCTGGACCAAGATGTTCCGGCGCTCTTCGCCATGCGCAAGCTGCCAGCAG 745
 QY 201 MetSerProAspLeuHisArgLysValSerValGlnTyrCysAspValLeuHisLysLys 220
 DB 746 ATGAGCCCAAGACTGCAACGCAAGGCTCTGGTGACAGTACTGACAGCTGTGTGCAAGAAG 805
 QY 221 AlaLeuArgAsnLysLysLeuLeuArgAlaGlySerGlyGlyGlyGlyGlyGlyGlyGly 240
 DB 806 GGCGTCGGAACAAGAGAGCTGCTGGCGCGCGGCGAGGCGGCGGCGGCGGCGGCGGCGG 865
 QY 241 AspAlaPheGlyTyrValAlaProPheAlaArgArgProSerValHisSerAspLeuMet 260
 DB 866 GACGCTTTGGCATGCTGGACCTTCCTGGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGG 925
 QY 261 TyrLeuArgGluLysAlaSerAlaGlySerGlnAlaLysAspGluArgCysValIle 280
 DB 926 TACATCCGCGAAGAGCGCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 985
 QY 281 Ser 281
 DB 986 AGC 988

RESULT 5
 LOCUS BC018041 1758 bp mRNA linear PRI 06-DEC-2001
 DEFINITION Homo sapiens, RAS, dexamethasone-induced 1, clone MGC:26290
 IMAGE:4797482, mRNA, complete cds.

ACCESSION BC018041.1 GI:17390075
 KEYWORDS MGC.

ORGANISM Homo sapiens.
 Homo sapiens
 Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 1 (bases 1 to 1758)
 Strausberg, R.
 Direct Submission
 Submitted (03-DEC-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabbs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcdpaxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAX Plate: 32 Row: f Column: 11.

FEATURES
 source Location/Qualifiers

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 /clone="MGC:26290 IMAGE:4797482"
 /tissue_type="Brain, hypothalamus"
 /clone_id="NH_MGC_96"
 /lab_host="DH10B"
 /note="Vector: pBluescript"
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 EDLVGDPPORCAVFETSAKNSLDQMPALPAMKLPSKSPDLHRRVSVQCVLH
 KALNRKKLLRAGSGGGGDDPDAGFVAFARPSPVSHSDIMYIREKASGQADKX
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 RCVIS"

BASE COUNT 387 a 576 c 501 g 294 t
 ORIGIN

Alignment Scores:
 Pred. No.: 3,42e-127 Length: 1758
 Score: 1449.00 Matches: 281
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.93% Indels: 0
 DB: 9 Gaps: 0

US-09-709-103-1F1 (1-282) x BC018041 (1-1758)

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 QY 21 AlaLysAsnCysTyrArgMetValIleLeuGlySerSerLysValGlySerThrAlaIle 40
 DB 273 GCCAAGACTGCTATGCCAGTCACTCTGCTGCTCCTCAAGTGGGCAAGAGCGGCATC 332
 QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspHe 60
 DB 333 GTGTGGCGCTTCTCTCACCGCGCGCTTCGAGAGCGCTTACACGCTTCACTCAGAGACTTC 392
 QY 61 HisArgPheThrSerIleArgGlyGluValTyrGluLeuAspIleLeuAspThrSer 80
 DB 393 CACCGAGTTCTACTCCATCCGCGGAGGTCTACAGCTCAACATCTCCAGACAGTCC 452
 QY 81 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIle 100
 DB 453 GGCAACCAACCGCTTCCCGCGCAAGCGCGCTTCTCATCTCAGAGACGTTTCACTC 512
 QY 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGln 120
 DB 513 CTGGTGTTCAGTCTGGAACAACCGCACTCCTTCGAGAGAGGTGACGCGCTCAGAGCAG 572
 QY 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeu 140
 DB 573 ATCTTCGACCAAGGCTTGTCTCAAGAAACAAACAGAGAACTGACGTCCTCG 632
 QY 141 ValIleCysGlyAsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIle 160
 DB 633 GTCACTGCGCGCAACAAGGTGACCGGACTTCTACCGGAGGTGACCAAGCGCGAGATC 692
 QY 161 GluGluLeuValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLys 180
 DB 693 GACGAGCTGGTGGGCGACGACCCCGAGCGCTGCTTCACTTCCAGAGTCTCGGCAAGAAG 752
 QY 181 AamSerSerleuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSerGlu 200
 DB 753 AACAGAGAGCTGGACCAAGATGTTCCGGCGCTCTTCGCCATGCGCAAGCTGCCAGCAG 812
 QY 201 MetSerProAspLeuHisArgLysValSerValGlnTyrCysAspValLeuHisLysLys 220
 DB 813 ATGAGCCCAAGACTGCAACGCAAGGCTCTGGTGACAGTACTGCAAGCTGTGTGCAAGAAG 872
 QY 221 AlaLeuArgAsnLysLysLeuLeuArgAlaGlySerGlyGlyGlyGlyGlyGlyGlyGly 240
 DB 873 GGCGTCGGAACAAGAGAGCTGCTGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 932
 QY 241 AspAlaPheGlyTyrValAlaProPheAlaArgArgProSerValHisSerAspLeuMet 260
 DB 933 GACGCTTTGGCATGCTGGACCTTCCTGGCGCGCGGCGGCGGCGGCGGCGGCGGCTG 992

DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcdpax11.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILM, at: <http://image.llnl.gov>
 Series: IRAX Plate: 58 Row: 9 Column: 5
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6677672.

FEATURES

source

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 /map="FVB/N"
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 /clone_1lb="NCI CGAP_C024"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"
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 EQLVDDDPQRCAYFEISAKNSLDQMFALFPAKLPSEMSPDLHRKVSQVCDVLA
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 CIVIS"

CDS

BASE COUNT 417 a 424 c 420 g 351 t
 ORIGIN

Alignment Scores:

Pred. No.: 3.88e-123 Length: 1612
 Score: 1405.50 Matches: 274
 Percent Similarity: 98.58% Conservative: 3
 Best Local Similarity: 97.51% Mismatches: 3
 Query Match: 96.93% Indels: 1
 DB: 10 Gaps: 1

US-09-709-103-1F1 (1-282) x BC034166 (1-1612)

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 Db 108 ATGAAACTGGCGCGATGATCAAGAAGATGCCCAAGGACTCTGAACCTGATCCCG 167
 QY 21 AlAlSAsnCySTyArGmEVallleuGllySerSerlySValGlylThrAlle 40
 Db 166 GCCAAGAACTGCTACGATGATGATCTCTCGGCTCATCCAAAGTGCGCAAGCGGCACTT 227
 QY 41 ValSerArgPheLeuThglYArGpHeGluAspAlaYrThProThrllsGluAspPhe 60
 Db 228 GGTGCGGCTTCTCACGGCGCTTTCAGATGCTTACACCCCTACATGAGGAGACTTC 287
 QY 61 HisAlGlySphEtySerlleArgGlylVallylGlnLeuAspilleuAspThSer 80
 Db 288 CACCAAAATTTTACTCGATCCGCGCGAAGCTCACAGTTGACATACCTGACACATCC 347
 QY 81 GlYAsnHisPProPhProAlaMeArGrArgLeuSerlleuThGlyAspValPheIle 100
 Db 348 GGCATCATCCCTTCCCGCATGCGGCGCTCTCTATCTTACAGAGACGCTTTTCATT 407
 QY 101 LeuValPheSerleuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGln 120
 Db 408 CTGGGTTCAGCTTAGACAACCGCGACTCATTCGAAGAGGTGCAAAAGCTCAACACGACG 467
 QY 121 lleleuAspThlySerSeryleuAsnlySthlylGluAsnValAspValProleu 140

Db 468 ATCTTAGACACCAAGTCTGTCTCAAGAACAAACCAAGAGATGTGACGTGCCGTG 527
 QY 141 VallleCysGlyAsnlySglYAspArgAspPheTyArgGluValAspGlnArgGluile 160
 Db 528 GTCACTTGGCGGTAAACAAGGGGACCGGACTTCTTACCGGAAGTAGACGCGGGAGATT 587
 QY 161 GluGlnLeuValGlyAspAspProGlnArgCysAlaTyPheGluIleSeralAlSlys 180
 Db 588 GAGCAGCTGGTGGGTGACGACCTCAGCGCTTGTGCTTACATTCAGATCTCAGCAAGAAG 647
 QY 181 AsnSerSerleuAspGlnMetPheArgAlaLeuPheAlaMetAlaIlySleuProSerGlu 200
 Db 648 AACGACGCTTGACCAAGAGTTCGCGCTTGTCCATGCGCAAGCTGCTTACCGAG 707
 QY 201 MetSerProAspLeuHisArglySValSerValGlnTyPheCysAspValleuHislySlys 220
 Db 708 ATAGAGCCCACTTGACCGCAAGGATGTCTGTCACTGACGACGATCTGCAACGAAG 767
 QY 221 AlAleuArgAsnlySlySleuLeuArgAlaGlySerGlyGlyGlyGlyAspProGly 240
 Db 768 GCTCTGAGAAACAAGAGCTTTCGCGCGGCGGAGC--GAGAGCGGGGGCGACACGCG 824
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RESULT 8

AF009246

LOCUS

DEFINITION

AF009246

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

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BASE COUNT 412 a 437 c 417 g 357 t
 ORIGIN

Alignment Scores:

Pred. No.: 3,91e-123 Length: 1623
 Score: 1405.50 Matches: 274
 Percent Similarity: 98.58% Conservative: 3
 Best Local Similarity: 97.51% Mismatches: 3
 Query Match: 96.93% Indels: 1
 DB: 10 Gaps: 1

US-09-709-103-1F1 (1-282) x AF009246 (1-1623)

Qy 1 MetLysLeuAlaAlaMetIleLysLysMetCysProSerAspSerGluLeuSerIlePro 20
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 Qy 21 AlaLysAsnCysTyrArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIle 40
 Db 202 GCCAAGAAGCTCTACAGGATGTGATCCTCGGCTCATCCAAAGTGGCAAGCGGCCATT 261
 Qy 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
 Db 262 GTGTGCGGCTTCTCAGCGGCGGTTTTCAGGATGCTTACACCTTACATCGAGGACTTC 321
 Qy 61 HisArgLysPheTyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSer 80
 Db 322 CACCGAAGTTTACTCGATCGCGCGGGAAGTCTACAGTTGGACATCTGGACACATCC 381
 Qy 81 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThrGlyAspValPheIle 100
 Db 382 GGCAATCATCGTTTCCCGCATCGCGGCGCTCTCTATCCTCACAGAGACGTTTTCATT 441
 Qy 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGlnGln 120
 Db 442 CTGGTGTTCAGCTTAGACAACCGGACTCATTCGAAGAGTGTGAAGGCTCAACAGCAG 501
 Qy 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsnValAspValProLeu 140
 Db 502 ATCTAGACACCAAGTCTGTCTCAAGAACAAACCAAGAGATGTGGAGTGGCGCTG 561
 Qy 141 VallIeCysGlyAsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGluIle 160
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 Qy 161 GluGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLysLys 180
 Db 622 GAGCAGCTGGTGGTGAGACCTCAGCGTTGTGCTTCTCGAGATCTCAGCCAGAGAG 681
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 Db 919 TACATTCGTGAAAAAACCAAGTGTCCGACCGCAGGCTAAGGACAAAGGACGCGCTGTGTCATC 978

Qy 281 Ser 281
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RESULT 9

AF239157 1616 bp mRNA linear ROD 06-JUL-2001
 LOCUS Rattus norvegicus DEXRAS1 (Dexras1) mRNA, complete cds.

DEFINITION AF239157

ACCESSION AF239157

VERSION AF239157.1 GI:7230767

KEYWORDS

SOURCE

ORGANISM

Rattus norvegicus.

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 1616)

Fang, M., Jaffrey, S.R., Sawa, A., Ye, K. and Snyder, S.H.

Dexras1: a G protein specifically coupled to neuronal nitric oxide

synthase via CAPON

Neuron 28 (1), 183-193 (2000)

20537828

11086993

2 (bases 1 to 1616)

Fang, M., Jaffrey, S.R., Sawa, A., Ye, K. and Snyder, S.H.

Direct Submission

Submitted (24-FEB-2000) Neuroscience, Johns Hopkins University, 725

N. Wolfe St, Baltimore, MD 21205, USA

Location/Qualifiers

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/organism="Rattus norvegicus"

/db_xref="taxon:10116"

1..1616

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musculus DEXRAS1 encoded by GenBank Accession Number

AF009246"

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LTGRFEDAYPTTIEDFHRKFYSIRGEVYQDLDTSGNHPFPAMRRLSILTDGVFIIV

FSLNDRDSFEVORLQOILDTKSNKTKENVDPLVICGNKGDYDFREVEQREI

EQLVGGDDPORCAFYETISAKNSLDDQFRALFAMAKLPSEMSPLDHRKVSQYCDVLH

KKAIRNKKLLRAGSGGGGDHDAFGLAPFARRPSVHSDLMYIREKTSVSSQAKDKER

CVIS"

BASE COUNT 403 a 436 c 413 g 363 t 1 others

ORIGIN

Alignment Scores:

Pred. No.: 1.43e-122 Length: 1616

Score: 1399.50 Matches: 273

Percent Similarity: 98.22% Conservative: 3

Best Local Similarity: 97.15% Mismatches: 4

Query Match: 96.52% Indels: 1

DB: 10 Gaps: 1

US-09-709-103-1F1 (1-282) x AF239157 (1-1616)

Qy 1 MetLysLeuAlaAlaMetIleLysLysMetCysProSerAspSerGluLeuSerIlePro 20

Db 118 ATGAACCTGGCGCGATGATCAAGAAGATGTGCCAAGCGACTCTGAACCTGATCCCG 177

Qy 21 AlaLysAsnCysTyrArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIle 40

Db 178 GCCAAGAAGCTCTACAGGATGTGATCCTCGCTCATCCAAAGTGGCAAGCGGCCATC 237

Qy 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60


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Db 238 GTGTCGCGCTTCTCAACGGGCGCTTCGAGAGACGCTTACACCCCTTACCATGAGACTTC 297
Qy 61 H1sArgLysPheTyrSerTleArgGlyValTyrGlnLeuAspIleLeuAspThrSer 80
Db 298 CACCGAAAGTTTACTCGATCCGCGGAGATCTACAGTTCAGTACATGAGACATCT 357
Qy 81 G1AsnHisProPheProAlaMetArgLysSerIleLeuThrGlyAspValPheIle 100
Db 358 GGCAGATCAACCGTTCCCGCCATGGCGGCGCTCTCATCTCACAGGAGACGTTTCACT 417
Qy 101 LeuValPheSerLeuAspAsnArgAspSerPheGluGluValGlnArgLeuArgGln 120
Db 418 CTGCTGTTAGCTTACAGACACCGCGACTCTTCGAGAGAGCTCAAGGCTCAACAGCAG 477
Qy 121 IleLeuAspThrLysSerCysLeuLysAsnLysThrLysGluAsnValAspValPro 140
Db 478 ATCTTAGACACCAAGTCTGCTCAAGAACCAACCAAGAGAGATGAGACGTCGCGCTG 537
Qy 141 ValIleCysGlyAsnLysGlyAspArgAspPheTyrArgGluValAspGlnArgGlu 160
Db 538 GTCATTTGGGTTACAAAGGGAGCGCGGACTTCTACCGGAGATGAGAGCGGAGATT 597
Qy 161 GluGlnLeuValGlyAspAspProGlnArgCysAlaTyrPheGluIleSerAlaLys 180
Db 598 GAGCACTGCTGGCGCATGACCTTCAGCGTTCCTTACGATCTCGGCGCAAGAG 657
Qy 181 AsnSerSerLeuAspGlnMetPheArgAlaLeuPheAlaMetAlaLysLeuProSer 200
Db 658 AATAGAGCGCTGACCAAGATGTTCCGTCGCTTTGCAATGAGCCCAAGGCTGAGCGAG 717
Qy 201 MetSerProAspLeuHisArgLysValSerValGlnTyrCysAspValLeuHisLys 220
Db 718 ATGAGCGCTGACTTGACCGCAAGGTGTCTGTGCACTGAGTGTGACAAAAG 777
Qy 221 AlaLeuArgAsnLysLysLeuLeuArgAlaGlySerGlyGlyGlyGlyAspProGly 240
Db 778 GCTCTAGAGAACAAAGAGCTTCTGCTGCGGCGAGC---GAGAGTGGGCGCAACGCA 834
Qy 241 AspAlaPheGlyIleValAlaProPheAlaArgArgProSerValHisSerAspLeu 260
Db 835 GATGCTTTGGCAATCTTGGCGCTTGTCTGCGAGACTGAGCTGATGCGACTCATG 894
Qy 261 TyrIleArgGlyLysAlaSerAlaGlySerGlnAlaLysAspLysGluArgCysVal 280
Db 895 TACATTCGTGAGAAACCAAGTCTCAGACAGCAGGCTTAAGACAGAGCGCTGTCTC 954
Qy 281 Ser 281
Db 955 AGT 957

RESULT 10
AF222979 4990 bp DNA linear PRI 02-JAN-2001
LOCUS Homo sapiens activator of G-protein signaling gene, complete cds.
DEFINITION AF222979
ACCESSION AF222979
VERSION AF222979.1 GI:12004991
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 4990)
AUTHORS Cismowski,M.J., Xie,X. and Duzic,E.
TITLE Genomic sequence of the human ras-related G-protein activator AGS1
JOURNAL Unpublished
2 (bases 1 to 4990)
AUTHORS Cismowski,M.J., Xie,X. and Duzic,E.
TITLE Direct Substitution
JOURNAL Submitted (10-JAN-2000) OSI Pharmaceuticals, 777 Old Saw Mill River
Road, Terrytown, NY 10591, USA
FEATURES
Location/Qualifiers
1..4990
/organism="Homo sapiens"

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in-situ hybridization analysis"
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join(2903..3188,3400..3959)
/note="ras-related protein; AGS1"
/codon_start=1
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/protein_id="A044256.1"
/db_xref="GI:12004992"
/translation="MKLAAMIKMCPDSELSIPANCYRYVILGSSKVGKTAIVSRF
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EQLVGDPPORCAVEISAKNSLDQMFPAKALFSESPDLHRKVSVDVCLH
KMLRNKKLLRAGSGGGGDPDAFQIVAPFARBSVHSDLMYIREKASGQAKDE
RCVIS"
BASE COUNT 1049 a 1507 c 1509 g 925 t
ORIGIN
Alignment Scores:
Pred. No.: 8,38e-121 Length: 4990
Score: 1387.00 Matches: 281
Percent Similarity: 79.83% Conservative: 0
Best Local Similarity: 79.83% Mismatches: 71
Query Match: 95.66% Indels: 71
Gaps: 1
US-09-709-103-1F1 (1-282) x AF222979 (1-4990)
Qy 1 MetLysLeuAlaAlaMetIleLysLysMetCysProSerAspSerGluLeuSerIlePro 20
Db 2903 ATGAACTGGCGCGAGATGATCAAGAAATGTCGCCGAGCACTGGAGCTGAGTATCCG 2262
Qy 21 AlaLysAsnCysTyrArgMetValIleLeuGlySerSerLysValGlyLysThrAlaIle 40
Db 2963 GCCAAGAACTGCTATCCGATGTCATCTCGGCTCGTCCAGAGTGGCAAGAGCGGCATC 3022
Qy 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
Db 3023 GTGTCGCGCTTCTCACCGCGCGCTTCGAGAGCGCTTACACAGCTTACATCAGGACTTC 3082
Qy 61 HisArgLysPheTyrSerIleArgGlyGluValTyrGlnLeuAspIleLeuAspThrSer 80
Db 3083 CACGCAAGTTCTACTCCATCCGCGGAGGTCATCAAGCTCGACATCTCGACAGCTTC 3142
Qy 81 G1AsnHisProPheProAlaMetArgLysSerIleLeuThr----- 95
Db 3143 GGCACACACCGCTTCCCGCATCGCGGCGCTTCTCCATCTCACAGGTGAGCGGGGGCC 3202
Qy 95 ----- 95
Db 3203 GGGCAGTGGCGGAGGAAGGCGGGAACCTTCGCGCAGGCGCCCCGAGCGCGGT 3262
Qy 95 ----- 95
Db 3263 CCGGCTGCGCGCGCGCGAGTAGTGCGCTTCGCTTAGAGAGCTAGCGCGCGCGCG 3322
Qy 95 ----- 95
Db 3323 GCTCAAGTAGACGCCGACCTGTCCCTGGCGGCGCACCCCTCACTTCTCTTCTGCT 3382
Qy 96 -----G1AspValPheIleLeuValPheSerLeuAspAsnArgAspSe 110
Db 3383 CTGTGTGCCCTCTAGAGAGCGTTTTCATCTGTGTTCAGTGTGACAAACCGCGACTC 3442
Qy 110 rPheGluGluValGlnArgLeuArgGlnGlnIleLeuAspThrLysSerCysLeuLysAs 130
Db 3443 CTTCAGAGAGGTGACGCGCTCAGGCGAGCATCTCGACACCAAGTCTTGCTTCAAGAA 3502

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QY 130 nlystThrlyGluAenValAspValProLeuValileCysGlyAsnLysGlyAspArgAs 150
Db 3503 CAAACCAAGGAGACGTGGACGTCCCTCGTTCATCTGCGGCAACCAAGGAGTGCACCGCA 3562
QY 150 pPheTyArgGluValAspGlnAtrGluileGluLnuValGlyAspAspProGlnAr 170
Db 3563 CTTCTACCGGAGGTGGACCGGAGATCGAGCAGCTGGTGGCGGACGACCCCGGCG 3622
QY 170 gCysAlaTyRheGluileSerAlaLysLysAsnSersSerLeuAspGlnMetPheArgAl 190
Db 3623 CTGCGCTTACTTCGAGATCTCGGCCAAGCAAGACAGCAGCCTGGACACAGATGTTCCGCGC 3682
QY 190 LeuPheAlaMetAlaLysLeuProSerGluMetSerProAspLeuHisArgLysValSe 210
Db 3693 GCTCTTCGCCATGGCCAGCTGCCAGCGAGATGAGCCACAGCTGACCGCAAGGTCTC 3742
QY 210 rValGlnTyRyCysAspValLeuHisLysLysAlaLeuArgAsnLysLysLeuLeuArgAl 230
Db 3743 GGTGAGTACTCGGACGTCTGCACAGAGAGCGCTGCCGGAACAGAAAGCTGTGCCGGC 3802
QY 230 aGlySerGlyGlyGlyGlyAspProGlyAspAlaPheGlyileValAlaPropheAl 250
Db 3803 CGCAGCGCGCGCGCGCGCGCGACCCGCGCGACGCTTTGGCATCGTGGCACCCTTCGC 3862
QY 250 aArgArgProSerValHisSerAspLeuMetTyRileArgGluLysAlaSerAlaGlySe 270
Db 3863 CGCGCGCGCGCGCGCGCGACCTCATGTATCATCGCGAGAAGCGCGCGCGCGAG 3922
QY 270 rGlnAlaLysAspLysGluArgCysValileSer 281
Db 3923 CCAGCCCAAGACAGAGAGCGCTGGCTCATCAGC 3956

RESULT 11
LOCUS AC020558 183334 bp DNA linear PRI 09-JAN-2002
DEFINITION Homo sapiens BAC clone RP11-524F11 from 17, complete sequence.
ACCESSION AC020558
VERSION AC020558.4 GI:13242397
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 183334)
Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
99063792
MEDLINE
PUBMED 9847074
2 (bases 1 to 183334)
Mulvaney, E., Maupin, R., LaPlant, Y. and Bielicki, L.
The sequence of Homo sapiens BAC clone RP11-524F11
Unpublished (2001)
3 (bases 1 to 183334)
Waterston, R.H.
Direct Submission
Submitted (03-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 183334)
Waterston, R.H.
Direct Submission
Submitted (07-MAR-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 183334)
Waterston, R.
Direct Submission
Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Mar 7, 2001 this sequence version replaced gi:7631041.
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Genome Center
Center: Washington University Genome Sequencing Center

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Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc>
 Contact: sapiens@watson.wustl.edu
 ----- Summary Statistics -----
 Center project name: H_NH0524F11

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RP11-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tatenio, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is AC073621. Actual start of this position is at base position 1 of RP11-524F11; actual end is at base position 183334 of RP11-524F11.

The sequence from position 1987 to 2253 was derived from PCR product of RP11-524F11 BAC DNA.

FEATURES	Location/Qualifiers	source
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	/clone_lib="RPC1-11"	
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	/note="similar to EST AI968384 (NID:g5765202) wu02e05.x1"	
misc_feature	339..738	
	/note="similar to EST AI289781 (NID:g3931622) qw12a07.x1"	
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	/note="similar to EST AW072137 (NID:g6027135) wz98e07.x1"	
misc_feature	340..767	
	/note="similar to EST AI014398 (NID:g3228779) ou93b12.s1"	
misc_feature	340..686	
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	/note="similar to EST AI359064 (NID:g4110685) qy25e07.x1"	
misc_feature	405..884	
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misc_feature	782..1335	
	/note="similar to EST BF042464 (NID:g10759519)"	
misc_feature	822..1319	
	/note="similar to EST BE864687 (NID:g10385980)"	
misc_feature	834..2931	
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repeat_region 6583..6891 /rpt_family="Alu"
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repeat_region 6960..7153 /rpt_family="L1"
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repeat_region 7525..7838 /rpt_family="Alu"
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repeat_region 7851..8487 /rpt_family="L1"
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repeat_region 9000..9104 /rpt_family="L2"
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Alignment Scores:

Pred. No.:	6.38e-119	Length:	183334
Score:	1387.00	Matches:	281
Percent Similarity:	79.83%	Conservative:	0
Best Local Similarity:	79.83%	Mismatches:	0
Query Match:	95.66%	Indels:	71
DB:	9	Gaps:	1

US-09-709-103-1f1 (1-282) x AC020558 (1-183334)

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Qy 1 MetLysLeuAlaIleMetIleLysLeuMetCysProSerAspSerGluLeuSerIlePro 20
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Db 2080 ATGAAACTGGCGCGGATGATCAAGAAATGTGCCAGCACTCGAGAGCTGATATCCG 2021
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Qy 21 AlaLysAncCysTyrArgMetValIleLeuGlySerSerIleValGlyLysThrAlaIle 40
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Db 2020 GCCAAGAACTGCTATCCAGTATGATCTCGCTCGTCCCAAGTGGGCAAGCGGCATC 1961
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Qy 41 ValSerArgPheLeuThrArgPheGluAspAlaThrProThrIleGluAspPhe 60
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Db 1960 GTGTGGGCTTCTCCACCGCGCGCTTGAGAGAGCCCTACACGCTACCATCGAGACTTC 1901
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Qy 61 HisArgLysPheTyrSerIleArgGlyValTyrGlnLeuAspIleLeuAspThrSer 80
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Db 1900 CACCGCAAGTCTACTCTCATCTCCGCGGAGAGTCTACCAAGCTCCAGACACTCC 1841
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Qy 81 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThr----- 95
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Qy 95 ----- 95
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Db 1720 CCGGCTGCGCGCGCCGCAATAGTGCCTTGGCGCTTAGAGAGCTACGGCGCCCGCGG 1661
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Qy 95 ----- 95
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QY 170 gCysAlaTyPheGluIleSerAlaLysLysAsnSerSerIeuAspGlnMetPheArgAl 190
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 QY 190 aLeuPheAlaMetAlaLysLeuProSerGluMetSerProAspLeuHisArgLysValSe 210
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 QY 230 aGlySerGlyGlyGlyGlyGlyAspProGlyAspAlaPheGlyIleValAlaProPheAl 250
 Db 1180 CGCGAGCGCGCGCGCGCGCGAGCCCGCGGACGCCCTTGGCATCGTGGCACCCCTTCGC 1121
 QY 250 aArgProSerValHisSerAspLeuMetTyrlleArgGluLysAlaSerAlaGlySe 270
 Db 1120 GCGCGCGCGCGCGCGCGAGCCTCATGTACATCCGGAAGAGCGCGCGCGAG 1061
 QY 270 rGlnAlaLysAspLysGluArgCysValIleSer 281
 Db 1060 CCAGGCCAAGGACAAGGAGCGCTGCTATCAGC 1027
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 DEFINITION gene, complete cds.
 ACCESSION AF262018
 VERSION AF262018.1 GI:8118456
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 SOURCE Homo sapiens.
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 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 5141)
 Kempainen,R.J. and Behrend,E.N.
 Human Dextral gene
 Unpublished
 2 (bases 1 to 5141)
 Kempainen,R.J. and Behrend,E.N.
 Direct Submission
 Submitted (30-APR-2000) Anatomy & Physiology, Auburn University,
 College of Veterinary Medicine, Auburn, AL 36832, USA
 Location/Qualifiers
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BASE COUNT 1090 a 1579 c 1522 g 950 t
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Alignment Scores:
 Pred. No.: 1.67e-120 Length: 5141
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 Percent Similarity: 79.83% Conservative: 1
 Best Local Similarity: 79.55% Mismatches: 0
 Query Match: 95.45% Indels: 71
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 US-09-709-103-1f1 (1-282) x AF262018 (1-5141)
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 QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyThrProThrIleGluAspPhe 60
 Db 2668 GTGTCCGCTTCTTCCACCGCGCTTCGAGGACGCTACACGCTTACCATCGAGACTTC 2727
 QY 61 HisArgLysPheTySerIleArgGlyGluValTyGlnLeuAspIleLeuAspThrSer 80
 Db 2728 CACCGCAAGTTCTACTCCATCCGCGCGAGGTCTACAGCTCGACATCTCTGACACGTC 2787
 QY 81 GlyAsnHisProPheProAlaMetArgArgLeuSerIleLeuThr----- 95
 Db 2788 GGCAACACCCCGTTCCCGCCATGCGCGCTCTTCCATCTCACAGGTGAGCGCGGGGCC 2847
 QY 95 ----- 95
 Db 2848 GGGCAGTCCGGGAGGGAAGCGGGGAACCTCTCGGCAGCGGCCCGCGAGCGCGGT 2907
 QY 95 ----- 95
 Db 2908 CCGGTGCGCGCGCGGAGTAGTGTGCGCTTAGAGAGGCTAGCGCGCCCGCGCG 2967
 QY 95 ----- 95
 Db 2968 GCCTCAAAGTCAGCCGACTTGTCCCTGGGCGGCCACCTCACCTTCTCTTTTCTGCT 3027
 QY 96 -----GlyAspValPheIleLeuValPheSerLeuAspAsnArgAspSe 110
 Db 3028 CTCTGTGCCCCCTTAGGAGACGTTTTCATCTGTGTTCAGTCTGGAACAACCGCGACTC 3087
 QY 110 rPheGluGluValGlnArgLeuArgGlnIleLeuAspThrLysSerCysLeuLysAs 130
 Db 3088 CTTGAGGAGGTGCGAGCGGCTCAAGCAGCAGATCTCTGACACCAAGTCTTGCTCAAGAA 3147
 QY 130 nLysThrLysGluAsnValAspValProLeuValIleCysGlyAsnLysGlyAspArgAs 150
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 QY 150 pPheTyArgGluValAspGlnArgGluIleGluGlnLeuValGlyAspAspProGlnAr 170
 Db 3208 CTTTACCCGAGGTGGACACGACGCGAGATGAGCAGCTGTGGCGACGACGCCACGCG 3267
 QY 170 gCysAlaTyPheGluIleSerAlaLysLysAsnSerSerLeuAspGlnMetPheArgAl 190
 Db 3268 CTGGCCTACTTCGAGATCTCGGCCAAGAAACAGACGCTGGACACAGATGTTCCGGCG 3327
 QY 190 aLeuPheAlaMetAlaLysLeuProSerGluMetSerProAspLeuHisArgLysValSe 210
 Db 3328 GCTCTTGGCCATGGCCAGCTGCCAGCGAGATGAGCCAGACCTGACCCGCAAGGTCTC 3387
 QY 210 rValGlnTyrcysAspValLeuHisLysLysAlaLeuArgAsnLysLysLeuLeuArgAl 230
 Db 3388 GGTGAGTACTCGAGCTGCTGCAAGAAGCGCTCGGAACAGAGCTGTGCGGGC 3447
 QY 230 aGlySerGlyGlyGlyGlyGlyAspProGlyAspAlaPheGlyIleValAlaProPheAl 250
 Db 3448 CGGCAGCGCGCGCGCGCGGCGACCCCGCGCGAGCGCTTGTGCGATCGTGGCACCTTTCG 3507

QY 250 aArgaPProSerValHisSerAspLeuMetTyrIleArgIuValAsaSerAlaGlySe 270
Db 3508 GGGCCGGCCAGGCTACAGACGACCTCATGTACATCCGAGAGGCGAGCGGCGAG 3567

QY 270 rGlnAlaValAspIleuValArgCysValIleSer 281
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RESULT 13
AL603710/c
LOCUS AL603710 179124 bp DNA linear ROD 05-APR-2002
DEFINITION Mouse DNA sequence from clone RP23-247B13 on chromosome 11,
complete sequence.
ACCESSION AL603710
VERSION AL603710.8 GI:2068514
KEYWORDS HTG
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS 1
TITLE Almeida J.
JOURNAL Direct Submission
Submitted (04-APR-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 7, 2002 this sequence version replaced gi:18070899.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

COMMENT
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em: EMBL; SW:
SWISSPROT; Tr: TrEMBL; Wp: WormPeP; Information on the WormPeP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-247B13 is
from the RP23-23 Mouse PAC Library
constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/dacpac/home.htm
VECTOR: pBACe3.6.

FEATURES
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/clone="RP23-247B13"
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Location/Qualifiers

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ORIGIN

Alignment Scores:
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Score: 1370.00 Matches: 274
Percent Similarity: 83.43% Conservative: 3
Best Local Similarity: 82.53% Mismatches: 3
Query Match: 94.48% Indels: 52
DB: 10 Gaps: 2

US-09-709-103-1F1 (1-282) x AL603710 (1-179124)

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QY 21 AlaLysAsnCysTyrArgMetValIleLeuGlySerSerLysValGlySerThralaIle 40
Db 122365 GCCAAGAACTGTACAGAGATGTATCTCTCGCTCATTCMAAGTGGCAAGAGCGCATTT 122306

QY 41 ValSerArgPheLeuThrGlyArgPheGluAspAlaTyrThrProThrIleGluAspPhe 60
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QY 61 HisArgLysPheTyrSerIleArgGlyGluValIleTyrGluLeuAspIleLeuAspThrSer 80
Db 122245 CACCGAAGATTCTTACTGATCCCGGGAGAGTTTACCACTTGAGACATCTCGACATCC 122186

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QY 130 AsnLysThrLysGluAsnValAspValProLeuValIleGlyGlyAsnLysGlyAspArg 149
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QY 150 AspPheTyrArgGluValAspGlnArgGlnIleGluGlnLeuValGlyAspAspProGln 169
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DEFINITION Mus musculus chromosome 11 clone RP23-82E8, WORKING DRAFT SEQUENCE,
6 unordered pieces.
ACCESSION AC025909
VERSION AC025909.28 GI:14547761
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.


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RESULT 15
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LOCUS Homo sapiens chromosome 17 clone RP11-524F11 map 17, *** SEQUENCING
DEFINITION IN PROGRESS ***, 2 unordered pieces.
AC090608.7 GI:19683171
VERSION HTG; HTGS PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 183598)
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE Homo sapiens chromosome 17, clone RP11-524F11
JOURNAL Unpublished
2 (bases 1 to 183598)
O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
Phunhahang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R.,
Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M.,
Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S., Severy, P.,
Sougez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Travers, M., Travis, N., Trigglio, J., Vassiliev, H., Viel, R., Vo, A.,
Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J.,
Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (03-MAR-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 183598)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,
Boukhalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J. S., Dodge, S.,
Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
Gande, S., Gordon, S., Goyette, M., Graham, L., Grand, P., Hargreaves,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., Labocque, R., Lamazares, R.,
Lander, T., Lehoczkv, J., Levine, R., Lindblad-Toh, K., Liu, G.,
Maclean, C., MacDonald, P., Major, J., Margulis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Meneus, L.,
Mhova, T., Mlenka, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
Norbu, C., Norman, C. H., O'Connor, T., O'Neill, D., Oliver, J., Peterson, K.,
Phunhahang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R.,
Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M.,
Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S., Severy, P.,
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Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Travers, M., Travis, N., Trigglio, J., Vassiliev, H., Viel, R., Vo, A.,
Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J.,
Zembek, L., Zimmer, A. and Zody, M.

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Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 22, 2002 this sequence version replaced gi:16445176.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L11985
Center clone name: 524_F_11
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 178216 178315: gap of 100 bp
* 178316 183598: contig of 5283 bp in length.
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Human Male BAC"
BASE COUNT 40950 a 47626 c 49185 g 45565 t 272 others
ORIGIN
Alignment Scores:
Pred. No.: 5,34e-116 Length: 183598
Score: 1356.00 Matches: 279
Percent Similarity: 78.81% Conservative: 0
Best Local Similarity: 78.81% Mismatches: 2
Query Match: 93.52% Indels: 73
Gaps: 1
Db: 2
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